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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:57:31 ; Search time 41.59 Seconds
(without alignments)
4.329 Million cell updates/sec

Title: 09-185908-1E
Perfect score: 8
Sequence: 1 WXXXSYXG 8

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000 .

Post-processing: Listing first 50 summaries

Database :

Issued_Patents_AA:*
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5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	37.5	104	1 US-08-488-113B-153	Sequence 153, App
2	3	37.5	104	1 US-08-477-484B-153	Sequence 153, App
3	3	37.5	104	1 US-08-107-669D-17	Sequence 17, Appl
4	3	37.5	104	1 US-08-472-788A-17	Sequence 17, Appl
5	3	37.5	104	2 US-08-477-531B-17	Sequence 17, Appl
6	3	37.5	104	2 US-08-646-360-153	Sequence 153, App
7	3	37.5	104	2 US-08-082-842A-17	Sequence 17, Appl
8	3	37.5	104	4 US-08-839-765-153	Sequence 153, App
9	3	37.5	104	2 US-09-136-389-153	Sequence 153, App
10	3	37.5	226	2 US-08-428-188-1	Sequence 1, Appl
11	3	37.5	526	4 US-08-895-590-5	Sequence 5, Appl
12	3	25.0	3	1 US-08-165-545-8	Sequence 8, Appl
13	3	25.0	3	1 US-08-305-768-27	Sequence 27, Appl
14	3	25.0	3	1 US-08-256-771-17	Sequence 17, Appl
15	3	25.0	3	1 US-08-381-984-17	Sequence 17, Appl
16	3	25.0	3	2 US-08-871-163-27	Sequence 27, Appl
17	3	25.0	3	2 US-08-767-903-27	Sequence 27, Appl
18	2	25.0	3	5 PCT-US95-1172A-27	Sequence 27, Appl
19	2	25.0	4	1 US-07-895-300A-8	Sequence 8, Appl
20	2	25.0	4	1 US-08-165-545-7	Sequence 7, Appl
21	2	25.0	4	1 US-08-190-802A-265	Sequence 265, App
22	2	25.0	4	1 US-08-332-071B-16	Sequence 16, App
23	2	25.0	4	1 US-08-176-938-20	Sequence 20, Appl
24	2	25.0	4	1 US-08-215-137-11	Sequence 11, Appl
25	2	25.0	4	1 US-08-487-006-150	Sequence 150, App
26	2	25.0	4	1 US-08-487-006-151	Sequence 151, App
27	2	25.0	4	1 US-08-487-006-152	Sequence 152, App

28	2	25.0	4	1	US-08-487-006-153	Sequence 153, App
29	2	25.0	4	1	US-08-256-771-16	Sequence 16, Appl
30	2	25.0	4	1	US-08-170-360-17	Sequence 17, Appl
31	2	25.0	4	1	US-08-222-851-22	Sequence 22, Appl
32	2	25.0	4	1	US-08-458-367-8	Sequence 8, Appl
33	2	25.0	4	1	US-08-381-984-16	Sequence 16, Appl
34	2	25.0	4	2	US-08-441-871-1	Sequence 1, Appl
35	2	25.0	4	2	US-08-441-871-55	Sequence 55, Appl
36	2	25.0	4	2	US-08-441-871-65	Sequence 65, Appl
37	2	25.0	4	2	US-08-592-646A-62	Sequence 62, Appl
38	2	25.0	4	2	US-08-637-759B-108	Sequence 108, App
39	2	25.0	4	2	US-08-685-589A-6	Sequence 6, Appl
40	2	25.0	4	2	US-08-488-659A-150	Sequence 150, App
41	2	25.0	4	2	US-08-488-659A-151	Sequence 151, App
42	2	25.0	4	2	US-08-488-659A-152	Sequence 152, App
43	2	25.0	4	2	US-08-488-659A-153	Sequence 153, App
44	2	25.0	4	2	US-08-645-193B-27	Sequence 27, Appl
45	2	25.0	4	2	US-08-722-806A-7	Sequence 7, Appl
46	2	25.0	4	3	US-08-871-355A-108	Sequence 108, App
47	2	25.0	4	3	US-09-222-373-49	Sequence 49, Appl
48	2	25.0	4	3	US-09-222-373-50	Sequence 50, Appl
49	2	25.0	4	3	US-09-112-656-14	Sequence 14, Appl
50	2	25.0	4	3	US-08-981-122-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-488-113B-153
; Sequence 153, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-153

Query Match 37.5%; Score 3; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 syxg 8
1111
Db 85 SYXG 88

RESULT 2
US-08-477-484B-153
Sequence 153, Application US/08477484B
Patent No. 5756599
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
TITLE OF INVENTION: Proteins
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155

TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-153

Query Match 37.5%; Score 3; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 syxg 8
1111
Db 85 SYXG 88

RESULT 3
US-08-107-669D-17
Sequence 17, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalè
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-17

Query Match 37.5%; Score 3; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 syxg 8
1111
Db 85 SYXG 88

RESULT 4
US-08-472-788A-17
Sequence 17, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalia, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-17

Query Match 37.5%; Score 3; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 syxg 8
||||
Db 85 syxg 88

RESULT 5
US-08-477-531B-17
Sequence 17, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington

STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-17

Query Match 37.5%; Score 3; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 syxg 8
||||
Db 85 syxg 88

RESULT 6
US-08-646-360-153
Sequence 153, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-153

Query Match 37.5%; Score 3; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 syxg 8
1111
Db 85 syxg 88

RESULT 7
US-08-082-842A-17
Sequence 17, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110220S09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889

NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-17

Query Match 37.5%; Score 3; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 syxg 8
1111
Db 85 syxg 88

RESULT 8
US-08-839-765-153
Sequence 153, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110220S09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-153

Query Match 37.5% Score 3; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 syxg 8
||||
Db 85 SYXG 88

RESULT 9

US-09-136-389-153
Sequence 153, Application US/09136389
Patent No. 6146850

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-153

Query Match 37.5% Score 3; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 syxg 8
||||
Db 85 SYXG 88

RESULT 10

US-08-428-188-1
Sequence 1, Application US/08428188
Patent No. 5861262

GENERAL INFORMATION:
APPLICANT: Chaudhrie, Jean
APPLICANT: Lemainque, Arnaud
APPLICANT: Malette, Patricia
TITLE OF INVENTION: Method for the Specific Immunoassay of
TITLE OF INVENTION: Human Plasma Glutathione Peroxidase, Kit for its
TITLE OF INVENTION: Implementation, Oligopeptides and Antibodies Specific for
TITLE OF INVENTION: the Method
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,188
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 10504
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Holman, John C.
REGISTRATION NUMBER: 22,769
REFERENCE/DOCKET NUMBER: 7696/P58648NA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 226 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 73
OTHER INFORMATION: /note="Amino acid at position 73
OTHER INFORMATION: is selenocysteine"

US-08-428-188-1

Query Match 37.5%; Score 3; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 syxg 8
 ||||
 Db 71 SYXG 74

RESULT 11
 US-08-895-590-5
 ; Sequence 5, Application US/08895590
 ; Patent No. 6207410
 ; GENERAL INFORMATION:
 ; APPLICANT: Hall, Linda M.
 ; APPLICANT: Ren, Dejian
 ; APPLICANT: Zheng, Wei
 ; APPLICANT: Dubald, Manuel Marcel Paul
 ; TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314-3187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,590
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,888
 ; FILING DATE: 19-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm M.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 022650-263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 526 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-895-590-5

Query Match 37.5%; Score 3; DB 4; Length 526;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 syxg 8
 ||||
 Db 72 SYXG 75

RESULT 12
 US-08-165-545-8
 ; Sequence 8, Application US/08165545
 ; Patent No. 5424396
 ; GENERAL INFORMATION:
 ; APPLICANT: Memoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptide and
 ; TITLE OF INVENTION: Antimicrobial Agent
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: DisplayWrite
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/165,545
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/871,981
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-8850
 ; TELEFAX:
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; HYPOTHETICAL:
 ; ANTI-SENSE:
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM:
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:
 ; TISSUE TYPE:
 ; CELL TYPE:
 ; CLONING:
 ; IMMEDIATE SOURCE:
 ; LIBRARY:
 ; CLONE:
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT:
 ; MAP POSITION:
 ; UNITS:
 ; FEATURE:
 ; NAME/KEY:
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION:
 ; PUBLICATION INFORMATION:
 ; AUTHORS:
 ; TITLE:
 ; JOURNAL:
 ; VOLUME:
 ; ISSUE:
 ; PAGES:
 ; DATE:
 ; DOCUMENT NUMBER:
 ; FILING DATE:
 ; PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wr 2
11
Db 2 wr 3

RESULT 13
US-08-305-768-27
Sequence 27, Application US/08305768
Patent No. 5602097

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antifungal peptides

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/305,768

FILING DATE: 12-SEPT-1994

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wr 2
11
Db 1 wr 2

RESULT 14

US-08-256-771-17

Sequence 17, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,771

FILING DATE: July 22, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 wr 2
11
Db 2 wr 3

RESULT 15

US-08-381-984-17

Sequence 17, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/381,984

FILING DATE: April 11, 1995

CLASSIFICATION: 252

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-17

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 16
US-08-871-163-27
Sequence 27, Application US/08871163
Patent No. 5885782
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,163
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-871-163-27

Query Match 25.0%; Score 2; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 1 wr 2

RESULT 17
US-08-767-903-27
Sequence 27, Application US/08767903
Patent No. 6020312
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,903
FILING DATE:
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-767-903-27

Query Match 25.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 1 wr 2

RESULT 18
PCT-US95-11724-27
Sequence 27, Application PC/TUS9511724
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11724
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 25.0%; Score 2; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 1 wr 2

RESULT 19
US-07-895-300A-8
Sequence 8, Application US/07895300A
Patent No. 5279823
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/895,300A
FILING DATE: 19920608
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-895-300A-8

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sy 6
11
Db 2 sy 3

RESULT 20
US-08-165-545-7
Sequence 7, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 3 wr 4

RESULT 21
US-08-190-802A-265
Sequence 265, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTA peptide
US-08-190-802A-265

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 1 wr 2

RESULT 22
US-08-332-071B-16
Sequence 16, Application US/08332071B
Patent No. 5556836
GENERAL INFORMATION:
APPLICANT: ROEDER, ERICH G.
APPLICANT: KESSLER, HORST
APPLICANT: KUTSCHER, BERNHARD
APPLICANT: BERND, MICHAEL
APPLICANT: KLENNER, THOMAS
TITLE OF INVENTION: USE OF D-GLUCOPHRANDRONIC ACIDS AND
THEIR DERIVATIVES FOR INCORPORATION IN PHARMACOLOGICALLY
TITLE OF INVENTION: ACTIVE PEPTIDES AND THEIR SALTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,071B
FILING DATE: 01-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 326/216933
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944

TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-071B-16

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sy 6
11
Db 1 sy 2

RESULT 23
US-08-176-938-20
Sequence 20, Application US/08176938
Patent No. 5602099
GENERAL INFORMATION:
APPLICANT: Schiller, Peter W.
TITLE OF INVENTION: New Peptides
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,938
FILING DATE: 04-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-354-8113
TELEFAX: 212-819-8783
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= Tlc
OTHER INFORMATION: /note= "1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /label= Phg
OTHER INFORMATION: /note= "phenylglycine"
US-08-176-938-20

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 yxg 8
111
Db 1 YXG 3

RESULT 24
US-08-215-137-11
; Sequence 11, Application US/08215137
; Patent No. 5614370
; GENERAL INFORMATION:
; APPLICANT: Konteatis, Zenon
; APPLICANT: Siciliano, Salvatore J
; APPLICANT: Springer, Martin S
; TITLE OF INVENTION: ASSAY TO IDENTIFY HUMAN C5A ANTAGONISTS
; TITLE OF INVENTION: AND ACONISTS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,137
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bengen, Gerard H
; REGISTRATION NUMBER: 35,745
; REFERENCE/DOCKET NUMBER: 19108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3901
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label="Tic
; OTHER INFORMATION: /note="tetrahydroisoquinoline carboxyllic acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label="dcha
; OTHER INFORMATION: /note="D-cyclohexylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label="darg
; OTHER INFORMATION: /note="D-arginine"
US-08-215-137-11

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wr 2

Db 3 WR 4

RESULT 25
US-08-487-006-150
; Sequence 150, Application US/08487006
; Patent No. 5641861
; GENERAL INFORMATION:
; APPLICANT: Dooley, Colette T.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
; TITLE OF INVENTION: Agonists and Antagonists
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,006
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-TP 1706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 2
; OTHER INFORMATION: /note="Xaa is (D)Nve"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 4
; OTHER INFORMATION: /note="Xaa is Nap."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 4
; OTHER INFORMATION: /note="Amino acid is amidated at
; OTHER INFORMATION: the C-terminal."
US-08-487-006-150

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 yxg 8
111
Db 1 YXG 3

Search completed: January 14, 2002, 07:57:31
Job time: 376 sec

1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 07:58:37 ; Search time 45.4 Seconds
(without alignments)
13.423 Million cell updates/sec

Title: 09-185908-1F
Perfect score: 8
Sequence: 1 wrxxxxyxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : PIR_68: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	37.5	113	2 A41073	thyroglobulin - ra
2	2	25.0	5	2 E60274	major protein anti
3	2	25.0	5	2 S68326	blood cell protein
4	2	25.0	7	2 PC2132	FMRFamide-related
5	2	25.0	7	2 S33245	neuromodulatory pe
6	2	25.0	8	2 S68802	nitrate reductase
7	2	25.0	8	2 PT0311	Ig heavy chain CRD
8	2	25.0	9	2 S66607	guinoline 2-oxidor
9	2	25.0	9	2 B57444	neuropeptide Grp-A
10	2	25.0	9	2 C57444	neuropeptide Grp-A
11	2	25.0	10	2 C45474	chompospondin 2 -
12	2	25.0	10	2 S62880	polygalacturonase
13	2	25.0	10	2 PT0309	Ig heavy chain CRD
14	2	25.0	10	2 I48778	small nuclear ribo
15	2	25.0	11	2 PT0081	protein QA300023 -
16	2	25.0	11	2 S78026	ribosomal protein
17	2	25.0	11	2 A34662	Achalasia cardio-ex
18	2	25.0	11	2 B41946	T-cell receptor ga
19	2	25.0	12	1 A53709	alpha-conotoxin im
20	2	25.0	12	2 S01122	photosystem II 3.7
21	2	25.0	12	2 PA0019	photosystem II 3.7
22	2	25.0	12	2 PA0037	acidic ribosomal p
23	2	25.0	12	2 PA0016	plastocyanin 2 - A
24	2	25.0	12	2 PH0930	ribosomal protein
25	2	25.0	12	2 PC2122	T-cell receptor be
26	2	25.0	13	2 S01119	aminotransferase c
27	2	25.0	13	2 PN0176	photosystem II pro
28	2	25.0	13	2 PQ0700	acidic ribosomal p
29	2	25.0	13	2 A60379	unidentified 6.3/4
					factor X activator

30	2	25.0	13	2 A33660	osteoclast functio
31	2	25.0	13	2 PT0290	Ig heavy chain CRD
32	2	25.0	13	2 S47368	T-cell antigen rec
33	2	25.0	13	2 S47372	T-cell antigen rec
34	2	25.0	13	2 S47384	T-cell antigen rec
35	2	25.0	13	2 S54344	glyceradehyde-3-p
36	2	25.0	13	2 PH0786	T-cell receptor al
37	2	25.0	13	2 PC4391	cysteine proteinas
38	2	25.0	13	2 S66558	serine proteinase
39	2	25.0	14	1 LFECH	trp operon leader
40	2	25.0	14	1 LFEHWC	trp operon leader
41	2	25.0	14	1 LFEHWT	trp operon leader
42	2	25.0	14	1 B85761	trp operon leader
43	2	25.0	14	2 E81280	probable proteolys
44	2	25.0	14	2 PA0013	photosystem II oxy
45	2	25.0	14	2 PT0026	calotropin DI - mu
46	2	25.0	14	2 G44957	photosystem II oxy
47	2	25.0	14	2 PA0096	pyruvate decarboxy
48	2	25.0	14	2 B39111	Ig heavy chain V r
49	2	25.0	14	2 PT0232	Ig heavy chain CRD
50	2	25.0	14	2 PH0915	T-cell receptor be

ALIGNMENTS

RESULT 1
A41073
thyroglobulin - rabbit (fragments)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 31-Oct-1997
C:Accession: A41073
R:Dunn, A.D.; Crutchfield, H.E.; Dunn, J.T.
J. Biol. Chem. 266, 20198-20204, 1991
A:title: Thyroglobulin processing by thyroidal proteases. Major sites of cleavage by
A:Reference number: A41073; MUID:92041846
A:Accession: A41073
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-113 <DUN>
C:superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat ho

Query Match 37.5%; Score 3; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
| | | |
Db 64 AYXG 67

RESULT 2
E60274
Major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274
R:Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:title: Isolation and partial characterization of major protein antigens in the cult
A:Reference number: A60274; MUID:91099989
A:Accession: E60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6

Db 1 AY 2

RESULT 3

S68326

blood cell protein B - Ascidia ceratodes (fragment)

N:Alternate names: Abcp-B

C:Species: Ascidia ceratodes

C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999

C:Accession: S68326

R:Taylor, S.W.; Koss, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A:Reference number: S68325; MUID:96132650

A:Accession: S68326

A:Molecule type: protein

A:Residues: 1-5 <TAY>

F:4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 3 AY 4

RESULT 4

PC2132

FMRFamide-related heptapeptide - Panagrellus redivivus

C:Species: Panagrellus redivivus

C:Date: 03-May-1994 #sequence_revision 15-Oct-1994 #text_change 11-Jul-1997

C:Accession: PC2132

R:Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, T.G.; Thim,

Biochem. Biophys. Res. Commun. 200, 973-980, 1994

A:Title: KSAVMRFamide: a novel FMRFamide-related heptapeptide from the free-living nemat

A:Reference number: PC2132; MUID:94235053

A:Accession: PC2132

A:Molecule type: protein

A:Residues: 1-7 <MAU>

C:Keywords: amidated carboxyl end

F:7/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 3 AY 4

RESULT 5

S33245

neuromodulatory peptide Wwamide-2 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33245

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33245

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 1 WR 2

RESULT 6

S68802

nitrate reductase (NADH) inhibitor - spinach (fragment)

C:Species: Spinacia oleracea (spinach)

C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998

C:Accession: S68802

R:Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.

FEBS Lett. 387, 127-131, 1996

A:Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spin

A:Reference number: S68802; MUID:96244508

A:Accession: S68802

A:Molecule type: protein

A:Residues: 1-8 <BAC>

A:Experimental source: leaves; strain cv. Bloomsdale

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 6 AY 7

RESULT 7

PT0311

Ig heavy chain CRD3 region (clone 6-100) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0311

R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0311

A:Molecule type: DNA

A:Residues: 1-8 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 3 AY 4

RESULT 8

S66607

guinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)

C:Species: Comamonas testosteroni

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S66607

R:Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingsens, F.

Eur. J. Biochem. 232, 536-544, 1995

A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase fr

A:Reference number: S66606; MUID:96035889

A:Accession: S66607

A:Molecule type: protein

A:Residues: 1-9 <SCH>

A:Experimental source: strain 63

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
DB 7 AY 8

RESULT 9

BS7444

neuropeptide Grb-AST B2 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)

C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996

C:Accession: BS7444

R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket

A:Reference number: AS7444; MUID:95403341

A:Accession: BS7444

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
DB 2 WR 3

RESULT 10

CS7444

neuropeptide Grb-AST B3 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)

C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996

C:Accession: CS7444

R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket

A:Reference number: AS7444; MUID:95403341

A:Accession: CS7444

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
DB 2 WR 3

RESULT 11

CA5474

thrombospondin 2 - bovine (fragment)

N:Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Aug-1998

C:Accession: CA5474

R:Peillerin, S.; Lafouillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Pei

J. Biol. Chem. 268, 4304-4310, 1993

A:Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by ad

A:Reference number: A45474; MUID:93179438

A:Accession: CA5474
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <PEL>
A:Experimental source: adrenocortical cells
A:Note: sequence extracted from NCBI backbone (NCBI:125844)
C:Superfamily: Thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
DB 1 AY 2

RESULT 12

S62880

polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)

C:Species: Aspergillus sp.

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S62880

R:Stratillova, E.; Dzuurova, M.; Markovic, O.; Joernvall, H.

FEBS Lett. 382, 164-166, 1996

A:Title: An essential tyrosine residue of Aspergillus polygalacturonase.

A:Reference number: S62880; MUID:96196586

A:Accession: S62880

A:Molecule type: protein

A:Residues: 1-10 <STR>

A:Keywords: glycosidase; hydrolase

F:4/Active site: Tyr #status predicted

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
DB 3 AY 4

RESULT 13

PT0309

Ig heavy chain CRD3 region (clone 6-94) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0309

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0309

A:Molecule type: DNA

A:Residues: 1-10 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
DB 9 AY 10

RESULT 14

I48778

small nuclear ribonucleoprotein E - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I48778
R;Fautsch, M.P.; Thompson, M.A.; Holicky, E.L.; Schultz, P.J.; Hallett, J.B.; Wieben, E.
Genomics 14, 883-890, 1992
A;Title: Conservation of coding and transcriptional control sequences within the snRNP R
A;Reference number: A44368; MUID:93122798
A;Accession: I48778
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: EMBL:X65703; NID:g312006; PIDN:CAA4625.1; PID:g312007.

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 2 AY 3

RESULT 15
PT0081
protein QA30023 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C;Accession: PT0081
R;Tsugita, A.; Kano, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PN0173
A;Accession: PT0081
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: Leaf
A;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
||
Db 5 AY 6

RESULT 16
S78026
ribosomal protein yml29, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)
C;Species: Saccharomyces cerevisiae
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997
C;Accession: S78026
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wiltma
Eur. J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr
A;Reference number: S78018; MUID:97296414
A;Accession: S78026
A;Molecule type: protein
A;Residues: 1-11 <KIP>
A;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrial; protein biosynthesis; ribosome

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6

Db 4 AY 5
||

RESULT 17
A34662
Achatina cardio-excitatory peptide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
C;Accession: A34662
R;Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, T.; Muneeke, Y.; Kobayashi, M.
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A;Title: A novel cardio-excitatory peptide isolated from the atria of the African gia
A;Reference number: A34662; MUID:90211261
A;Accession: A34662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FUJ>
A;Keywords: amidated carboxyl end
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 5 WR 6

RESULT 18
B41946
T-cell receptor gamma chain (1t.57) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: B41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A;Reference number: A41946; MUID:92049316
A;Accession: B41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
A;Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 5 WR 6

RESULT 19
A53709
alpha-conotoxin ImI - cone shell (Conus imperialis)
N;Alternate names: alpha-CTX-ImI
C;Species: Conus imperialis (imperial cone)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53709
R;McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; O
J. Biol. Chem. 269, 16733-16739, 1994
A;Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conot
A;Reference number: A53709; MUID:94266889
A;Accession: A53709
A;Molecule type: protein
A;Residues: 1-12 <MCIT>
A;Note: structure confirmed by chemical synthesis
C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Superfamily: alpha-conotoxin
A:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot
E:2-8,3-12/Dissulfide bonds: #status experimental
F:12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 10 wr 11

RESULT 20
S01122
photosystem II 3.7k protein - spinach (fragment)

C:Species: Spinacia oleracea (spinach)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: S01122
R:Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.
FEBS Lett. 235, 289-292, 1988

A:Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
A:Reference number: S01120

A:Accession: S01122
A:Molecule type: protein
A:Residues: 1-12 <SCH>
C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 25.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
11
DB 5 ay 6

RESULT 21
PA0019
acidic ribosomal P2-like protein - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Apr-1995
C:Accession: PA0019
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A:Reference number: PA0001

A:Accession: PA0019
A:Molecule type: protein
A:Residues: 1-12 <KAM>
A:Experimental source: callus

Query Match 25.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
11
DB 6 ay 7

RESULT 22
PA0037
plastocyanin 2 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0037
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0037
A:Molecule type: protein
A:Residues: 1-12 <KAM>
A:Experimental source: stem

Query Match 25.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
11
DB 9 ay 10

RESULT 23
PN0160
ribosomal protein S16 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C:Accession: PN0160
R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JPIID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A:Reference number: PN0160
A:Accession: PN0160
A:Molecule type: protein
A:Residues: 1-12 <FUK>
C:Keywords: protein biosynthesis; ribosome

Query Match 25.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
11
DB 1 ay 2

RESULT 24
PH0930
T-cell receptor beta chain V-D-J region (clone 1) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0930
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857
A:Accession: PH0930

A:Molecule type: mRNA
A:Residues: 1-12 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the codon GGA for residue 8 as Arg

C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
11
DB 4 ay 5

RESULT 25
PC2122
aminotransferase chimera DY237 - synthetic (fragment)
C:Species: synthetic

C:Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
 C:Accession: PC2122
 R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
 J. Biochem. 115, 568-577, 1994
 A:Title: Construction of aminotransferase chimeras and analysis of their substrate speci
 A:Reference number: JX0315; MUID:94334304
 A:Accession: PC2122
 A:Molecule type: DNA
 A:Residues: 1-12 <MTV>
 C:comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC
 C:comment: The parental enzymes catalyze the reversible amino group transfer reaction be
 C:Keywords: aminotransferase

Query Match 25.0%; Score 2; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
 II
 Db 7 Ay 8

Search completed: January 14, 2002, 07:58:37
 Job time: 387 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:08:23 ; Search time 30.66 Seconds

(without alignments)
9.567 Million cell updates/sec

Title: 09-185908-1f

Perfect score: 8

Sequence: 1 wixxayxg 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.5	80	1	VA0H_BOVIN	P81103 bos taurus
2	25.0	7	1	OVN_LEPDE	P42985 leptomastix
3	25.0	7	1	ALL2_CARMA	P81805 carcinus ma
4	25.0	7	1	PAR3_HABCO	P81298 haemophilus
5	25.0	7	1	PAR3_PANRE	P41874 panagrellus
6	25.0	7	1	MNP1_LEPDE	P42984 leptomastix
7	25.0	8	1	MMAL_ACHFU	P35919 achalina fu
8	25.0	8	1	UP06_MOUSE	P38644 mus musculu
9	25.0	10	1	O20B_COMTE	P80465 comamonas t
10	25.0	11	1	CEP1_ACHFU	P22790 achalina fu
11	25.0	12	1	CXAL_CONIM	P50983 conus imper
12	25.0	12	1	PSF3_PHYPA	P80662 physcomitre
13	25.0	13	1	PSBP_PIPNS	P81668 pinus pinas
14	25.0	13	1	UVRD_SALTY	P00531 salmonella
15	25.0	14	1	CAL1_CALGI	P20728 caltropis
16	25.0	14	1	ECDC_LYMDI	P80940 lymantiria d
17	25.0	14	1	LPW_CITFR	P03056 citrobacter
18	25.0	14	1	LPW_ECOLI	P03053 escherichia
19	25.0	14	1	LPW_SALTY	P03054 salmonella
20	25.0	15	1	SODM_ENTAE	P22799 enterobacte
21	25.0	15	1	UC08_MAIZE	P80614 zea mays (m
22	25.0	15	1	UC14_MAIZE	P80620 zea mays (m
23	25.0	15	1	VAA3_RHOPA	P02006 rhodospheudo
24	25.0	16	1	ALRX_PSEPU	P17916 pseudomonas
25	25.0	16	1	ARCD_PSEPU	P41147 pseudomonas
26	25.0	16	1	CAT9_FASHE	P80333 fasciola he
27	25.0	16	1	UPAB_HUMAN	P19335 homo sapien
28	25.0	17	1	ATPI_PAVLU	P28529 pavlova lut
29	25.0	17	1	GAST_MACMU	P33714 macaca mula
30	25.0	17	1	LPW_CONGL	P06556 corynebacte
31	25.0	17	1	YPRK_SALTY	P93495 salmonella
32	25.0	18	1	AGI_EUPMA	P33889 euphorbia m
33	25.0	18	1	ALL2_CYDPO	P82153 cydia pomon

ALIGNMENTS

RESULT	ID	STANDARD	PRT	80 AA.
1	VA0H_BOVIN			
AC	P81103; 018981;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT)			
DE	(VACUOLAR PROTON PUMP H SUBUNIT) (V-ATPASE M9.2 SUBUNIT) (V-ATPASE			
DE	9.2 KDA MEMBRANE ACCESSORY PROTEIN).			
GN	ATP6H.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID:9913;			
RN	[1]			
RP	SEQUENCE OF 1-19, AND SEQUENCE OF 19-80 FROM N.A.			
RC	TISSUE=Adrenal medulla;			
RX	MEDLINE:9825166; PubMed:9556572;			
RA	Ludwig J., Kerschner S., Brandt U., Pfeiffer K., Getzlav F., Apps D.K.,			
RT	Schagger H.;			
RT	"Identification and characterization of a novel 9.2-kDa membrane			
RT	sector-associated protein of vacuolar proton-ATPase from chromaffin			
RT	granules.";			
RL	J. Biol. Chem. 273:10939-10947(1998).			
CC	-1- FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY			
CC	OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.			
CC	-1- SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, HEART, SPLEEN, KIDNEY AND			
CC	ADRENAL GLAND. NOT FOUND IN BRAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: Y15285; CAA75570.1; "			
KW	Hydrolase; Hydrogen ion transport; Transmembrane.			
FT	TRANSMEM 7			
FT	TRANSMEM 35			
FT	TRANSMEM 55			
FT	SEQUENCE 80 AA: 9129 MW: 87B2CEB7D47E5427 CRC64:			
SO	SEQUENCE			
Query Match	37.5%; Score 3; DB 1; Length 80;			
Best Local Similarity	100.0%; Pred. No. 1.9e+02;			
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

34	2	25.0	18	1	GALS_SALTY	P41030 salmonella
35	2	25.0	18	1	UC03_MAIZE	P80609 zea mays (m
36	2	25.0	19	1	CAT3_FASHE	P80532 fasciola he
37	2	25.0	20	1	LPB2_HUMAN	P56642 homo sapien
38	2	25.0	20	1	MCRG_METTE	P22950 methanosarc
39	2	25.0	20	1	RIC1_HALMA	P12740 halocarcula
40	2	25.0	20	1	SYR_RAT	P40329 rattus norv
41	2	25.0	21	1	MDH_BURCE	P80537 burkholderi
42	2	25.0	22	1	MDH_PSEIN	P80538 pseudomonas
43	2	25.0	22	1	CYSP_TRIVA	P33404 trichomonas
44	2	25.0	22	1	TXI_HETFU	P82850 heterometru
45	2	25.0	22	1	VHV4_LACHE	P22296 lactobacill
46	2	25.0	23	1	CYSP_TRIRO	P33403 tritrichomo
47	2	25.0	23	1	FLAL_SULSH	P94066 sulfolobus
48	2	25.0	23	1	TX2_HETFU	P82851 heterometru
49	2	25.0	24	1	ACHB_ELEEL	P09689 electrophor
50	2	25.0	24	1	CAMT_PIPNS	P81081 pinus pinas

QY 5 ayyx 8
 ||||
 Db 1 AYYG 4

RESULT 2

OVN_LEPDE
 ID OVM_LEPDE STANDARD; PRT; 6 AA.
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Phytophaga; Chrysomelidae; Chrysomelidae;
 OC Chrysomelinae; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RX MEDLINE=91271080; PubMed=2052497;
 RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
 RA Proost P., Torrekens S., de Loof A.;
 RT *Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RT decemlineata".
 RL Peptides 12:31-36(1991).
 CC -I- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 CC Neuropeptide; Amidation.
 KW MOD.RES 6
 FT SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
 SQ

Query Match 25.0%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
 ||
 Db 2 AY 3

RESULT 3

ALL2_CARMA
 ID ALL2_CARMA STANDARD; PRT; 7 AA.
 AC P81805;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 2.
 OS Carcinus menas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT *Isolation and identification of multiple neuropeptides of the
 RT allatostatatin superfamily in the shore crab Carcinus menas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW MOD.RES 7
 FT SEQUENCE 7 AA; 770 MW; 672879CDB5DB70 CRC64;
 SQ

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
 ||
 Db 2 AY 3

RESULT 4

FAR3_HAECO
 ID FAR3_HAECO STANDARD; PRT; 7 AA.
 AC P81298;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE).
 OS Haemochus contortus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloida;
 OC Trichostrongyloidea; Haemonchidae; Haemonchidae; Haemonchus.
 OX NCBI_TaxID=6289;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Neuron;
 RX Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Geary T.G.,
 RA Thompson D.P., Shaw C.;
 RL Submitted (MAY-1998) to the SWISS-PROT data bank.
 CC -I- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
 CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD.RES 7
 FT SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;
 SQ

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
 ||
 Db 3 AY 4

RESULT 5

FAR3_PANRE
 ID FAR3_PANRE STANDARD; PRT; 7 AA.
 AC P41874;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94235053; PubMed=8179635;
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
 RA Geary T.G., Thim L.;
 RT *KSAYMRFamide: a novel FMRFamide-related heptapeptide from the free-
 RT living nematode, Panagrellus redivivus, which is myoactive in the
 RT parasitic nematode, Ascaris suum.";
 RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
 CC -I- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
 CC MUSCLE TENSION INCREASE.
 CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: PC2132; PC2132.
 KW Neuropeptide; Amidation.

```
FT MOD.RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 902 MW: 69D406B5DC5B350 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
   1 1
   3 AY 4

DB 3 AY 4

RESULT 6
NMPI_LEPDE
ID NMPI_LEPDE STANDARD: PRT: 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
DE Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phycophaga; Chrysomelidae; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
XX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE. AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Splitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., Van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 15:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC Neuropeptide; Amidation.
KW MOD.RES 7 7 AMIDATION.
FT SEQUENCE 7 AA: 705 MW: 6DD73768745B5DB0 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
   1 1
   1 AY 2

DB 1 AY 2

RESULT 7
WMAL_ACHFV
ID WMAL_ACHFV STANDARD: PRT: 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAMIDE-1.
OC Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wmamide-1, -2 and -3, novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
```

```
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR: S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD.RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 993 MW: 7362D5B69B041310 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   1 1
   1 WR 2

DB 1 WR 2

RESULT 8
UF06_MOUSE
ID UF06_MOUSE STANDARD: PRT: 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P50) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 KDA.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 817 MW: A35DD878676B05B1 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
   1 1
   7 AY 8

DB 7 AY 8

RESULT 9
Q2OB_COMTE
ID Q2OB_COMTE STANDARD: PRT: 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE QUINOLINE 2-OXIDOREDUCTASE, BETA CHAIN (EC 1.3.99.11) (FRAGMENT).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuka B., Feltner S., Lings F.;
RT "Quinolene 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
```

CC 1,2-DIHYDROQUINOLINE.
CC -1- CATALYTIC ACTIVITY: QUINOLINE + ACCEPTOR + H(2)O = ISOUINOLIN-
CC 1(2H)-ONE + REDUCED ACCEPTOR.
CC -1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
CC (3-METHYL-)QUINOLINE.
CC -1- SUBUNIT: HETEROHXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KM Oxioreductase; Flavoprotein; FAD; Molybdenum.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1241 MW; C2EC25DD9CDC769 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ay 6
DB 7 AY 8

RESULT 10
CEPI_ACHFV STANDARD; PRT; 11 AA.
ID CEPI_ACHFV
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBL_TaxId=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=232251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
CC MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD.RES 11 11
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
DB 5 WR 6

RESULT 11
CXAL_CONIM STANDARD; PRT; 12 AA.
ID CXAL_CONIM
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA-CONOTOXIN IMI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBL_TaxId=35631;
RN [1]
RP SEQUENCE. AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=9426689; PubMed=8206995;
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
RA Gray W.R., Olivera B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin Imi.";
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
RA McIntosh J.M.;
RT "Alpha-conotoxin Imi exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; PubMed=10194298;
RA Rogers J.P., Lugibuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
RA Wenner D.E.;
RT "NMR solution structure of alpha-conotoxin Imi and comparison to
RT other conotoxins specific for neuronal nicotinic acetylcholine
RL receptors.";
RN Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; PubMed=10050774;
RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
RA Metfessel C., Tsetlin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin Imi reveals a common
RT scaffold in snail and snake toxins recognizing neuronal nicotinic
RT acetylcholine receptors.";
RL FEBS Lett. 444:275-280(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; PubMed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic
RT resonance.";
RL J. Med. Chem. 42:2364-2372(1999).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
CC RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
CC WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGET NEURONAL
CC NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
CC WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
CC WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
CC ALPHA-2/BETA-2, ALPHA-3/BETA-2, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
CC PDB; 1IM1; 15-JUN-99.
DR PDB; 1IM1; 23-APR-99.
DR PDB; 1CNL; 27-MAY-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT DISULFID 2 12
FT DISULFID 3 12
FT MOD.RES 12 12
SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA5A54A176A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
DB 10 WR 11

RESULT 12
PSP3_PHYPA STANDARD: PRT: 12 AA.
ID PSP3_PHYPA
AC P80662:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (24 KDA SUBUNIT OF OXYGEN
EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
OS Physcomitrella patens (Moss).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Bryophyta:
Bryopsida: Funariidae: Funariales: Funariaceae: Physcomitrella.
OX NCBI_TaxId=3218;
RN NCBI_TaxId=3218;
RN NCBI_TaxId=3218;
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kaestn B., Buck F., Nuske J., Reski R.;
RT "Cytochrome c affects nuclear- and plastome-encoded energy-converting
plastid enzymes.";
RT Planta 201;261-272(1997).
RL -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
WITH THE PHOTOSYSTEM II COMPLEX.
CC -1- INDUCTION: BY LIGHT.
CC -1- SIMILARITY: BELONGS TO THE PSBP FAMILY.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
KW Multigene family.
FT NON_TER 12
FT SEQUENCE 12 AA: 1182 MW: 8028054D7C44DC5 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 AY 2

RESULT 13
PSBP_PINPS STANDARD: PRT: 13 AA.
ID PSBP_PINPS
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN
EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
OS PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Coniferopsida: Coniferales: Pinaceae: Pinus.
OX NCBI_TaxId=71647;
RN NCBI_TaxId=71647;
RN NCBI_TaxId=71647;
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99774088; PubMed=10344291;
RA Costa P., Plomancu C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RT Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
(SPOT N179) IS: 5.9, ITS MW IS: 22 KDA.
CC -1- SIMILARITY: BELONGS TO THE PSBP FAMILY.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13
FT SEQUENCE 13

SQ SEQUENCE 13 AA: 1294 MW: C6772B0D54D7C44D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 AY 2

RESULT 14
UVRD_SALTY STANDARD: PRT: 13 AA.
ID UVRD_SALTY
AC Q05311;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE DNA HELICASE II (EC 3.6.1.-) (FRAGMENT).
GN UVRD.
OS Salmonella typhimurium.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Salmonella.
OX NCBI_TaxId=602;
RN NCBI_TaxId=602;
RN NCBI_TaxId=602;
RP SEQUENCE FROM N.A.
RX MEDLINE=93300795; PubMed=8314774;
RA Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.;
RT "Sequence and topology of the Cora magnesium transport systems of
Salmonella typhimurium and Escherichia coli. Identification of a new
RT class of transport protein.";
RT J. Biol. Chem. 268:14071-14080(1993).
RL -1- FUNCTION: HAS BOTH ATPASE AND HELICASE ACTIVITIES. UNWINDS DNA
DUPLICATES WITH 3' TO 5' POLARITY WITH RESPECT TO THE BOUND STRAND
AND INITIATES UNWINDING MOST EFFECTIVELY WHEN A SINGLE-STRANDED
REGION IS PRESENT. INVOLVED IN THE POSTCISION EVENTS OF
NUCLEOTIDE EXCISION REPAIR AND METHYL-DIRECTED MISMATCH REPAIR.
CC -1- SIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.
CC -----
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CC -----
DR EMBL: L11043; AAA02965.1; -
DR StyGene: SG10414; UVRD.
KW DNA repair; DNA replication; SOS response; Helicase; ATP-binding;
KW DNA-binding.
FT NON_TER 1
FT SEQUENCE 13 AA: 1492 MW: D7967B28B09ACB5D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 6 AY 7

RESULT 15
CALI_CALGI STANDARD: PRT: 14 AA.
ID CALI_CALGI
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALOTROPIN DI (EC 3.4.22.-) (FRAGMENT).
DE

OS Calotropis gigantea (Madar) (Bowstring hemp).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
 OC Asclepiadeae; Calotropis.
 OC NCBI_TaxID=4066;
 RN [1]
 RP SEQUENCE.
 RA Bhattacharya D., Sengupta A., Sinha N.K.;
 RT "Chemical modification and amino terminal sequence of calotropin DI
 from Calotropis gigantea.";
 RL Phytochemistry 26:633-636(1987).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOL PROTEASES.
 CC PIR; PT0026; PT0026.
 DR MEROPS; C01.011; -;
 DR InterPro; IPR00169; ThiolProt_act_site.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolyase; Thiol protease.
 FT MOD_RES 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 DB 8 wr 9

RESULT 16
 ECDC_LYMDI STANDARD; PRT; 14 AA.
 AC P80940;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE TESTIS ECDYSTIOTROPIN PEPTIDE C (TE).
 OS Lymantria dispar (Gypsy moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Lymantriidae; Lymantria.
 OC NCBI_TaxID=13123;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97387807; PubMed=9243792;
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
 RA Bell R.A.;
 RT "Naturally occurring analogs of Lymantria testis ecdystiotropin, a
 gonadotropin isolated from brains of Lymantria dispar pupae.";
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
 CC -I- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
 CC OF LARVAE AND PUPAE.
 SQ SEQUENCE 14 AA; 1553 MW; 17FA79531A685CB8 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 DB 6 ay 7

RESULT 17
 LPW_CITFR

ID LPW_CITFR STANDARD; PRT; 14 AA.
 AC P03056;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OC NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83007061; PubMed=6749821;
 RA Blumenberg M., Yanofsky C.;
 RT "Evolutionary divergence of the Citrobacter freundii tryptophan
 operon regulatory region: comparison with other enteric bacteria.";
 RL J. Bacteriol. 152:57-62(1982).
 CC -I- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.
 CC -----
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 CC -----
 DR EMBL; J01557; -; NOT_ANNOTATED_CDS.
 DR PIR; A03592; LFEBC.
 KW Tryptophan biosynthesis; leader peptide.
 SQ SEQUENCE 14 AA; 1720 MW; 5B792A473E8048E7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 DB 11 wr 12

RESULT 18
 LPW_ECOLI STANDARD; PRT; 14 AA.
 AC P03053;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL OR TRPEE OR B1265 OR Z2545 OR ECS1837.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82150258; PubMed=7038627;
 RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
 RA Horowitz H., van Cleemput M., Wu A.M.;
 RT "The complete nucleotide sequence of the tryptophan operon of
 Escherichia coli.";
 RL Nucleic Acids Res. 9:6647-6668(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=76240562; PubMed=781271;
 RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
 RA Yanofsky C.;
 RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
 Escherichia coli.";

```
RL J. Mol. Biol. 103:351-381(1976).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RL secondary structure involving the tryptophan codon region.";
RN Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RN Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck J., Davis N.W., Llm A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RN Nature 409:529-533(2001).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RN DNA Res. 8:11-22(2001).
RN
RP -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
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DR EMBL: J01714; AAA57296.1; -
DR EMBL: A04494; CAA00361.1; -
DR EMBL: AE000224; AAC74347.1; -
DR EMBL: AE005380; AAG56550.1; -
DR EMBL: AP002556; BAB35260.1; -
DR PIR: A03589; LFECEM.
DR Ecogen: EG11274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;
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LPW_SALTY
ID LPW_SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRP OPERON LEADER PEPTIDE.
GN TRP OR TRPEE.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmnella.
OX NCBI_TaxID=602;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=78196931; PubMed=351195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
RT regions of the tryptophan operons of Escherichia coli and Salmonella
RT typhimurium.";
RN J. Mol. Biol. 121:193-217(1978).
RN
RP -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
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-----
DR EMBL: M24960; -; NOT_ANNOTATED_CDS.
DR PIR: A03590; LFECEM.
DR StyGene: SG10400; trpL.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;
```

Query Match 25.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 wr 2
   11
Db 11 wr 12
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RESULT 19

RESULT 20

ID	SODM_ENTAE	STANDARD	PRT	15 AA
AC	P22799;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1) (FRAGMENT).			
GN	SODA.			
OS	Enterobacter aerogenes (Aerobacter aerogenes).			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Enterobacter.			
OX	NCBI_TaxID=548;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=91248479; PubMed=1368658;			
RA	Kim S.W., Lee S.O., Lee T.H.;			
RT	"Purification and characterization of superoxide dismutase from			
RT	Aerobacter aerogenes";			
RL	AgriC. Biol. Chem. 55:101-108(1991).			
CC	-1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE			
CC	CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.			
CC	-1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE			
CC	FAMILY.			

DR PIR: P00137; P00137.
 DR HSSP: P00448; 1MM.
 DR InterPro: IPR001189; SOD_MI.
 DR Pfam: PF00081; SODte; 1.
 DR PROSITE: PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Manganese.
 FT NON_TER 15
 SO SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 ||
 DB 1 AY 2

RESULT 21
 UC08_MAIZE
 ID UC08_MAIZE STANDARD; PRT: 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huët J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:97-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KDA.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 CC Maize-2DPAGE: P80614; COLEOPTILE.
 DR MaizeDB: 123934; -.
 FT NON_TER 1 15
 FT NON_TER 15
 SO SEQUENCE 15 AA; 1785 MW; 1978B1D6A84DDF8D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 ||
 DB 3 WR 4

RESULT 22
 UC14_MAIZE
 ID UC14_MAIZE STANDARD; PRT: 15 AA.
 AC P80620;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 258)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huët J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:97-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.9, ITS MW IS: 34.6 KDA.
 DR Maize-2DPAGE: P80620; COLEOPTILE.
 DR MaizeDB: 123944; -.
 FT NON_TER 1 1
 FT NON_TER 15
 SO SEQUENCE 15 AA; 1564 MW; CF0BBA087DE658 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 ||
 DB 1 AY 2

RESULT 23
 YAA3_RHOA
 ID YAA3_RHOA STANDARD; PRT: 15 AA.
 AC Q02006;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN AADR 3' REGION (FRAGMENT).
 OS Rhodospseudomonas palustris.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Rhodospseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=CGA009;
 RC MEDLINE=92394882; PubMed=1522059;
 RA Dispensa M., Thomas C.T., Kim M.K., Perrotta J.A., Gibson J.,
 RA Harwood C.S.;
 RT "Anaerobic growth of Rhodospseudomonas palustris on 4-hydroxybenzoate
 RT is dependent on Aadr, a member of the cyclic AMP receptor protein
 RT family of transcriptional regulators";
 RL J. Bacteriol. 174:5803-5813(1992).
 CC -----
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 CC -----
 CC EMBL: M92426; AAA26091.1; -.
 DR PIR: C43334; C43334.
 DR Hypothetical protein.
 FT NON_TER 15
 FT NON_TER 15
 SO SEQUENCE 15 AA; 1926 MW; 149B01A548D7C202 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 ||
 DB 7 AY 8

RESULT 24
ID ALRX_PSEPU STANDARD: PRT: 16 AA.
AC P17916;
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BROAD-SPECIFICITY AMINO ACID RACEMASE (EC 5.1.1.-) (FRAGMENT).
OS Pseudomonas putida.
CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=303;
RN [1]
RP SEQUENCE.
RC STRAIN=AKU 0813;
RX MEDLINE=85072810; PubMed=6439237;
RA Roise D., Soda K., Yagi T., Walsh C.T.;
RT "Inactivation of the Pseudomonas striata broad specificity amino acid
racemase by D and L isomers of beta-substituted alanines: kinetics,
stereochemistry, active site peptide, and mechanistic studies.";
RL Biochemistry 23:5195-5201(1984).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
DR -1- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
DR PIR: A29520; A29520.
DR InterPro: IPR000821; Ala_racemase.
DR PROSITE: PS00395; ALANINE_RACEMASE; 1.
KW isomerase; Pyridoxal phosphate.
FT BINDING 6 6 PYRIDOXAL PHOSPHATE.
FT NON_TER 16 16
SQ SEQUENCE 16 AA: 1572 MW: 866C2DA154362E07 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 9 ay 10

RESULT 25
ID ARCD_PSEPU STANDARD: PRT: 16 AA.
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ARGININE/ORNITHINE ANTIPORTER (FRAGMENT).
CN ARCD.
OS Pseudomonas putida.
CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_Taxid=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/Genbank/DDAJ databases.
CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
ARGININE DEIMINASE PATHWAY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
(POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
PERMEASES.

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CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL: U07185; AAA16963.1; -
KW Transport; Amino-acid transport; Transmembrane; Inner membrane.
FT NON_TER 1 1
SQ SEQUENCE 16 AA: 1644 MW: 90B48A7C8FAA9705 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 6 ay 7

Search completed: January 14, 2002, 08:08:23
Job time: 708 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:07:34 ; Search time 81.98 Seconds
(without alignments)
14.274 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 8
Sequence: 1 wxxxxxxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146273229 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	34	13	057591	057591 fugu rubrip
2	37.5	163	2	Q9EW42	Q9EW42 streptococ
3	37.5	171	5	Q24837	Q24837 entamoeba h
4	37.5	663	8	Q9MS52	Q9MS52 goyazia rup
5	37.5	699	8	Q9T182	Q9T182 dipelta ven
6	25.0	8	2	Q9S443	Q9S443 pseudomonas
7	25.0	8	10	P82324	P82324 pisum sativ
8	25.0	8	11	Q62721	Q62721 rattus norv
9	25.0	9	5	Q9TVP1	Q9TVP1 trypanosoma
10	25.0	9	8	Q9MMG9	Q9MMG9 buteo buteo
11	25.0	9	8	Q9MMF4	Q9MMF4 buteo rufin
12	25.0	10	12	Q86324	Q86324 rous sarcom
13	25.0	10	12	Q86325	Q86325 rous sarcom
14	25.0	10	12	Q86326	Q86326 rous sarcom
15	25.0	11	2	P96319	P96319 desulfobact
16	25.0	11	2	Q68237	Q68237 borrelia bu
17	25.0	11	5	Q99292	Q99292 dirosophila
18	25.0	11	6	Q9TRR7	Q9TRR7 cryctolagus
19	25.0	12	4	Q9UMZ8	Q9UMZ8 homo sapien

20	25.0	12	7	077919	077919 pseudotroph
21	25.0	13	2	Q55234	Q55234 synchocyst
22	25.0	13	3	Q10721	Q10721 pseudallesc
23	25.0	13	4	Q9UJ52	Q9UJ52 homo sapien
24	25.0	13	4	Q9UEE3	Q9UEE3 homo sapien
25	25.0	13	5	Q9TMR4	Q9TMR4 tillyus serr
26	25.0	13	6	Q9TU76	Q9TU76 ovis aries
27	25.0	13	10	P82432	P82432 nicotiana t
28	25.0	13	11	P82808	P82808 rattus norv
29	25.0	13	12	P90442	P90442 spodoptera
30	25.0	14	2	Q54081	Q54081 saccharopol
31	25.0	14	2	P96347	P96347 helicobacte
32	25.0	14	2	Q9PMT9	Q9PMT9 campylobact
33	25.0	14	8	Q9MRU0	Q9MRU0 arabidopsis
34	25.0	14	9	Q38469	Q38469 bacterioph
35	25.0	14	10	P82433	P82433 nicotiana t
36	25.0	14	11	Q9QVFX	Q9QVFX rattus sp.
37	25.0	15	1	Q9UMH6	Q9UMH6 thermococcu
38	25.0	15	2	Q9RSF2	Q9RSF2 seriatia ma
39	25.0	15	2	Q9RSL9	Q9RSL9 bacillus st
40	25.0	15	4	Q9UBK0	Q9UBK0 homo sapien
41	25.0	15	5	Q9TWL6	Q9TWL6 echinococcu
42	25.0	15	6	Q9TRG9	Q9TRG9 bos taurus
43	25.0	15	10	Q9S8Z0	Q9S8Z0 hordium vul
44	25.0	15	11	Q9QUW3	Q9QUW3 rattus sp.
45	25.0	15	12	Q69353	Q69353 herpes simp
46	25.0	15	12	Q9PXC1	Q9PXC1 human immu
47	25.0	16	2	Q9R633	Q9R633 helicobacte
48	25.0	16	2	Q53399	Q53399 bacillus th
49	25.0	16	4	Q9UP51	Q9UP51 homo sapien
50	25.0	16	4	Q9UC99	Q9UC99 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	34 AA.
ID	057591			
AC	057591			
DT	01-JUN-1998 (TREMBLrel. 06, last sequence update)			
DT	01-JUN-1998 (TREMBLrel. 06, last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
DE	ARGININOSUCCINATE SYNTHETASE (FRAGMENT).			
GN	ASS.			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Tetraodontidae; Acanthopterygii; Percomorpha; Tetraodontiformes;			
OC	NCBI_TaxID=31033;			
OX	NCBI_TaxID=31033;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98077503; PubMed=9414319;			
RA	Ames N., Gilley J., Fried M.;			
RT	"The comparative genomic structure and sequence of the surfelt gene			
RT	homologs in the puffer fish Fugu rubripes and their association with			
RT	CpG-rich islands.";			
RL	Genome Res. 7:1138-1152(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Fried M.;			
RL	submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Gilley J.;			
RL	submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; Y15170; CA75440.1; -.			
DR	InterPro; IPR001518; Arginosuc_synth.			
DR	Pfam; PF00764; Arginosuc_synth; 1.			
DR	ProDom; PD003544; Arginosuc_synth; 1.			
FT	NON_TER			
SQ	SEQUENCE 34 AA; 3713 MW; 0DC816A13998B4B8 CRC64;			

Query Match 37.5%; Score 3; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayyx 8
 ||||
 Db 9 AXXG 12

RESULT 2
 ID Q9EM42 PRELIMINARY; PRT; 163 AA.
 AC Q9EM42;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 GN PENICILLIN BINDING PROTEIN 1A (FRAGMENT).
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=950473;
 RA Overweg K., Boggett D., Sluifker M., de Groot R., Hermans P.W.M.;
 RT "Molecular characterization of Streptococcus pneumoniae penicillin-
 resistance in the Netherlands."
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ403979; CAC20961.1; -.
 FT NON_TER 1 1
 FT NON_TER 163 163
 SQ SEQUENCE 163 AA; 18350 MW; 02B96CAE2DB26ACF CRC64;

Query Match 37.5%; Score 3; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayyx 8
 ||||
 Db 149 AXXG 152

RESULT 3
 ID Q24837 PRELIMINARY; PRT; 171 AA.
 AC Q24837;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE OFR 1.5 (FRAGMENT).
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HM-1;JMS5;
 RX MEDLINE=94099892; PubMed=8274224;
 RA Bruchhaus I., Leippe M., Lioutas C., Tannich E.;
 RT "Unusual gene organization in the protozoan parasite Entamoeba
 histolytica.";
 RL DNA Cell Biol. 12:925-933(1993).
 DR EMBL; X70851; CAA50201.1; -.
 FT NON_TER 1 1
 FT NON_TER 171 171
 SQ SEQUENCE 171 AA; 20070 MW; AB7A93347AB43F74 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 171;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayyx 8
 ||||
 Db 25 AXXG 28

RESULT 4
 ID Q9MS52 PRELIMINARY; PRT; 663 AA.
 AC Q9MS52;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE NADH DEHYDROGENASE (FRAGMENT).
 GN NDHF.
 OS Goyazia rupicola.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Gesneriaceae; Goyazia.
 OX NCBI_TaxID=125973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith J.F.;
 RT "The phylogenetic relationships of Lemnocarpos and Goyazia
 (Gesneriaceae) based on ndhf sequences."
 RL Ann. Mo. Bot. Gard. 0:0-0(2000).
 CC -I- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
 CC -I- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CC CHAINS.
 DR EMBL; AF257485; AAF75262.1; -.
 DR InterPro: IPR001750; Oxidored_q1.
 DR InterPro: IPR002128; Oxidored_q1_C.
 DR InterPro: IPR001516; Oxidored_q1_N.
 DR Pfam: PF00361; oxidored_q1; 1.
 DR Pfam: PF01010; oxidored_q1_C; 1.
 DR Pfam: PF00662; oxidored_q1_N; 1.
 KW Chloroplast; NAD; Oxidoreductase; Plastocyanine.
 FT NON_TER 1 1
 FT NON_TER 663 663
 SQ SEQUENCE 663 AA; 74858 MW; BB002498EACE32AE CRC64;

Query Match 37.5%; Score 3; DB 8; Length 663;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayyx 8
 ||||
 Db 601 AXXG 604

RESULT 5
 ID Q9T182 PRELIMINARY; PRT; 699 AA.
 AC Q9T182;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT F (FRAGMENT).
 GN NDHF.
 OS Dipelta ventricosa.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Dipsacales; Limnaceae; Dipelta.
 OX NCBI_TaxID=105266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pyck N., Roels P., Smets E.;
 RT "Tribal relationships in Caprifoliaceae: evidence from a cladistic
 analysis using ndhf sequences."
 RL Syst. Geogr. Plants 69:145-159(1999).

RN [2]
RN SEQUENCE FROM N.A.
RA Pyck N., Smets E.:
RT "A search for the phylogenetic position of the seven-son flower
RT (hepaticodium, dipsacales): combining molecular and morphological
RT evidence."
RL Plant Syst. Evol. 0:0-0(2000).
CC -1- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CC CHAINS
DR EMBL: AF161295; AAF18383.2.
DR Interpro: IPR001750; Oxidored_q1.
DR Interpro: IPR002128; Oxidored_q1_C.
DR Interpro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1_1.
DR Pfam: PF01010; oxidored_q1_C; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
DR Chloroplast; NAD; Oxidoreductase; Plastoguinone.
FT NON_TER 1
FT NON_TER 699
SQ SEQUENCE 699 AA; 78769 MW; 76D0753B53E50592 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 699;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 rxray 6
DB 114 RXRAY 118

RESULT 6
O9S443 PRELIMINARY; PRT; 8 AA.
AC O9S443;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE beta-LACTAMASE (FRAGMENT).
OS PSE2.
CN Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R345;
RA Roy D., Coulombe M., Perron K., Roy P.H.;
RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
RT gene aac(6')-IIC from the integron of a Chinese Pseudomonas aeruginosa
RT clinical isolate."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162771; AAD46628.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 930 MW; EBD85DDDD9D1A336 CRC64;

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 6 AY 7

RESULT 7
P82324 PRELIMINARY; PRT; 8 AA.
AC P82324;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF THYLAKOID (SPOT105) (FRAGMENT).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Pelletier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wilk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.7, ITS MW IS: 16.8 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 839 MW; DDC68B5DDDC2D2D5 CRC64;

Query Match 25.0%; Score 2; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 5 AY 6

RESULT 8
O62721 PRELIMINARY; PRT; 8 AA.
AC O62721;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes."
RL Gene 158:291-294(1995).
DR EMBL: U17178; AAA86692.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 25.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 2 WR 3

RESULT 9

Q9TVF1
ID Q9TVF1 PRELIMINARY; PRT: 9 AA.
AC Q9TVF1;
DT 01-OCT-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MUCIN-LIKE PROTEIN (FRAGMENT).
GN EMUC-19C8.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN NCBI_TaxID=5693;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CL-BRENNER;
RA MEDLINE=98225151; PubMed=9556557;
DI Nola J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
RT "The Trypanosoma cruzi mucin family is transcribed from hundreds of
RT genes having hypervariable regions."
RL J. Biol. Chem. 273:10843-10850(1998).
DR EMBL: AF036447; AAC14246.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 896 MW; DBA831BBD72D CRC64;

Query Match 25.0%; Score 2; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 4 AY 5

RESULT 10
Q9MMG9
ID Q9MMG9 PRELIMINARY; PRT: 9 AA.
AC Q9MMG9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 6 (FRAGMENT).
GN ND6.
OS Buteo buteo vulpinus (western steppe-buzzard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Falconiformes; Accipitridae;
OC Accipitridae; Buteo.
OX NCBI_TaxID=115228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VUL-1;
RA Haring E., Riesing M.J., Pinsker W., Gamauf A.;
RT "Evolution of a pseudo-control region in the mitochondrial genome of
RT Palearctic Buzzards (genus Buteo)."
RL J. Zool. Syst. Evol. Res. 37:185-194(1999).
DR EMBL: AF202197; AAF61879.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1026 MW; C24E272732C9DB5D CRC64;

Query Match 25.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 2 AY 3

RESULT 11
Q9MMF4
ID Q9MMF4 PRELIMINARY; PRT: 9 AA.

AC Q9MMF4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 6 (FRAGMENT).
GN ND6.
OS Buteo rufinus rufinus (Long-legged buzzard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Falconiformes; Accipitridae;
OC Accipitridae; Buteo.
OX NCBI_TaxID=116585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RUF-1;
RA Haring E., Riesing M.J., Pinsker W., Gamauf A.;
RT "Evolution of a pseudo-control region in the mitochondrial genome of
RT Palearctic Buzzards (genus Buteo)."
RL J. Zool. Syst. Evol. Res. 37:185-194(1999).
DR EMBL: AF202212; AAF61894.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1026 MW; C24E272732C9DB5D CRC64;

Query Match 25.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 2 AY 3

RESULT 12
Q86324
ID Q86324 PRELIMINARY; PRT: 10 AA.
AC Q86324;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE GP37 (FRAGMENT).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCHMIDT-RUPPIN SUBGROUP A (NY);
RA Hara H., Kaji A.;
RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U41726; AAB60580.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 25.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 1 AY 2

RESULT 13
Q86325
ID Q86325 PRELIMINARY; PRT: 10 AA.
AC Q86325;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE GP37 (FRAGMENT).

GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroel viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCMIDT-RUPPIN SUBGROUP A (NY);
RL Hara H., Kajl A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
EMBL: U41727; AAB60581.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 25.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 AY 2

RESULT 14
O68326 PRELIMINARY; PRT; 10 AA.
AC O68326;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE GP37 (FRAGMENT).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroel viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCMIDT-RUPPIN SUBGROUP A (NY);
RL Hara H., Kajl A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SCMIDT-RUPPIN SUBGROUP A (NY);
RX MEDLINE=82271824; PubMed=6287213;
RA Takeya T., Hanafusa H., Junghans R.P., Ju G., Skalka A.M.;
RT "Comparison between the viral transforming gene (src) of recovered
avian sarcoma virus and its cellular homolog.";
RL Mol. Cell. Biol. 1:1024-1037(1981).
DR EMBL: U41729; AAA84421.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 25.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 AY 2

RESULT 15
P66319 PRELIMINARY; PRT; 11 AA.
AC P66319;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CODED PORTION OF PROTEOLYSIS TAG (FRAGMENT).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
OX NCBI_TaxID=876;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27774;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL: U68081; AAB48023.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1250 MW; 85776D58CB5ABB5A CRC64;

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 8 AY 9

RESULT 16
O68237 PRELIMINARY; PRT; 11 AA.
AC O68237;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE PLASMID CP32-4, POSSIBLE PARTITION PROTEINS, COMPLETE CDS (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-4.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RA Stevenson B., Casjens S., Rosa P.;
RL Microbiology 0:0-0(1998).
DR EMBL: AF022481; AAC35449.1; -.
KW Plasmid.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1237 MW; 50E3B714D45B5D07 CRC64;

Query Match 25.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 5 AY 6

RESULT 17
Q99292 PRELIMINARY; PRT; 11 AA.
AC Q99292;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BICOID PROTEIN (FRAGMENT).
GN BCD.
OS Drosophila heteroneura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=32382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91184004; PubMed=2081457;
RA Macdonald P.M.;
RT "Dicoid mRNA localization signal: phylogenetic conservation of
function and RNA secondary structure.";

RL Development 110:161-171(1990).
 CC -1- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES
 CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.
 CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH
 CC ITS HOMODOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE
 CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.
 DR EMBL: M32125; AAA28386.1; -.
 DR FLYBASE: FBgn0012352; Dmel\bcd.
 KW Homeobox: DNA-binding; Developmental protein; Nuclear protein;
 KM Segmentation polarity protein; Transcription regulation; RNA-binding.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1221 MW; 8CE802305DD9D6C1 CRC64;

Query Match 25.0%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 Db 7 AY 8

RESULT 18
 OYTRR7
 ID OYTRR7 PRELIMINARY; PRT; 11 AA.
 AC OYTRR7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
 DE 1-13 FRAGMENT.
 OS Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92250478; PubMed=1533622;
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
 RT "A calyculin-associated protein is a newly identified member of the
 RT CA2+/phospholipid-binding proteins, annexin family.";
 RT J. Biol. Chem. 267:8919-8924(1992).
 SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match 25.0%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 Db 7 AY 8

RESULT 19
 OYQM28
 ID OYQM28 PRELIMINARY; PRT; 12 AA.
 AC OYQM28;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE COAGULATION FACTOR VIII (FRAGMENT).
 DE F8C.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vidal F., Farsac E., Gallardo D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: J0168366; AAD50437.1; -.

FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1453 MW; 2CCABC3DB252D6C7 CRC64;

Query Match 25.0%; Score 2; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 Db 3 WR 4

RESULT 20
 OY7919
 ID OY7919 PRELIMINARY; PRT; 12 AA.
 AC OY7919;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II B LOCUS 4 (FRAGMENT).
 OS Pseudotropheus sp. 'Pseudotropheus tropheus complex'.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Pseudotropheus.
 OC NCBI_TaxID=51796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Madaga-Trillo E., McAndrew B., Vlncek V., Zaleska-Rutczynska Z.,
 RA Snelman N., Figueroa F., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
 RT class II B loci.";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050032; AAC41371.1; -.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1529 MW; 6C2ABFACD5A5B734 CRC64;

Query Match 25.0%; Score 2; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 Db 4 WR 5

RESULT 21
 OY5234
 ID OY5234 PRELIMINARY; PRT; 13 AA.
 AC OY5234;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE 2-HYDROXYACID DEHYDROGENASE HOMOLOGUE (FRAGMENT).
 OS Synechocystis sp. (Strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA Terauchi K., Ikeuchi M., Ohmori M.;
 RT "A putative fd-GOGAT gene involved in protection against
 RT photoinhibition in Synechocystis PCC 6803.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D78371; BAA11378.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1564 MW; CC84E4282B1CA5B9 CRC64;

Query Match 25.0%; Score 2; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 10 AY 11

RESULT 22
ID 010721 PRELIMINARY; PRT; 13 AA.
AC 010721.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE ALKALINE EXTRACELLULAR PROTEASE (EC 3.4.21.-) (AEP) (FRAGMENT).
OS Pseudallescheria boydii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Microascales; Microasaceae; Pseudallescheria.
OX NCBI_TaxID=5597;
RN [1]
RP SEQUENCE.
RX MEDLINE=96207571; PubMed=8670095;
RA Larcher G., Climon B., Symons F., Tronchin G., Chabasse D.,
RA Bouchara J.-P.;
RT "A 33 kDa serine proteinase from *Scedosporium apiospermum*."
RL Blochem. J. 315:119-126(1996).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: SECRETED
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
SUBTILASE FAMILY.
KW Hydrolase; Serine protease; zymogen.
FT NON_TER 13
FT SEQUENCE 13 AA: 1292 MW: 9DD5F3294A68D861 CRC64;

Query Match 25.0%; Score 2; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 AY 2

RESULT 23
ID 09UJ52 PRELIMINARY; PRT; 13 AA.
AC 09UJ52.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE LATROPILIN-2 (FRAGMENT).
GN LPHN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99153747; PubMed=10030676;
RA White G.R.M., Varley J.M., Helgway J.;
RT "Isolation and characterisation of a human homologue of the
latrophilin gene from a region of 1p31.1 implicated in breast
cancer".
RL Oncogene 17:3513-3519(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA White G.R.M., Varley J.M., Helgway J.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ244500; CAB60202.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA: 1637 MW: 4161F9BECF72A1A3 CRC64;

Query Match 25.0%; Score 2; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 10 AY 11

RESULT 24
ID 09UEE3 PRELIMINARY; PRT; 13 AA.
AC 09UEE3.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE ERGB TRANSCRIPTION FACTOR (FRAGMENT).
GN FLI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oyata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RT "Molecular analysis on the breakpoint region of a t(11;22)
translocation in Ewing's sarcoma."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB012624; BAA32805.1; -.
FT NON_TER 1
FT NON_TER 13
FT SEQUENCE 13 AA: 1529 MW: 629F6FEC6A649A5BB CRC64;

Query Match 25.0%; Score 2; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 11 AY 12

RESULT 25
ID 09TWR4 PRELIMINARY; PRT; 13 AA.
AC 09TWR4.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE PEPTIDE T-BRADYKININ POTENTIATOR.
OS Tityus serrulatus (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butidae; Butidae; Tityus.
OX NCBI_TaxID=6887;
RN [1]
RP SEQUENCE.
RX MEDLINE=94024945; PubMed=8212046;
RA Ferreira L.A., Alves E.W., Henriques O.B.;
RT "Peptide T, a novel bradykinin potentiator isolated from *Tityus*
serrulatus scorpion venom".
RL Toxicon 31:941-947(1993).
SQ SEQUENCE 13 AA: 1604 MW: 35770B0644FC02D7 CRC64;

Query Match 25.0%; Score 2; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches	2;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	5	ay	6						
		11							
Db	12	AY	13						

Search completed: January 14, 2002, 08:07:35
Job time: 765 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:56:31 ; Search time 81.39 Seconds
(without alignments)
7.281 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 8
Sequence: 1 wrxxayxg 8

Scoring table:
OLIGO
Gapop 60.0 , Capext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

A_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	37.5	9	21	AAV51341 sphingolipid desat
2	3	37.5	13	22	AAB37631 Cholestyrolin pe
3	3	37.5	86	18	AAW20310 H. pylori cytoplas
4	3	37.5	91	21	AAAG22631 Zea mays protein f
5	3	37.5	110	18	AAW27779 Amino acid sequenc
6	3	37.5	121	21	AAAG22630 Zea mays protein f
7	3	37.5	185	18	AAW20262 H. pylori secreted
8	3	37.5	185	18	AAW24622 H. pylori secreted
9	3	37.5	275	12	AAAI0204 Mutant subtilisin
10	3	37.5	277	22	AAAG75013 Human colon cancer
11	3	37.5	284	21	AAB56744 Human prostate can

12	3	37.5	401	12	AAAP12129 ORF 1 of Igg Light
13	3	37.5	489	20	AAW84298 Consensus sequence
14	3	37.5	498	20	AAW84183 Consensus sequence
15	3	37.5	500	22	AAW40758 Human polypeptide
16	3	37.5	513	20	AAAY38787 Neisseria meningit
17	3	37.5	515	9	AAAP60575 Mutated alpha-amy1
18	3	37.5	688	17	AAW17559 Bacillus CGTase va
19	3	37.5	688	17	AAW17577 Bacillus CGTase va
20	3	37.5	688	17	AAW17573 Bacillus CGTase va
21	3	37.5	689	17	AAW17570 Bacillus CGTase va
22	3	37.5	689	17	AAW17574 Bacillus CGTase va
23	3	37.5	689	17	AAW17578 Lactoferrin derive
24	2	25.0	3	15	AAAR8523 Boveine lactoferrin
25	2	25.0	3	16	AAAR84691 Peptide for anti-u
26	2	25.0	3	17	AAAR8547 Lactoferrin derive
27	2	25.0	3	19	AAAR90601 Anti-Inflammatory
28	2	25.0	3	19	AAAR56219 Apoptosis inducer
29	2	25.0	3	19	AAW41282 FMRF neuropeptide
30	2	25.0	3	22	AAAR92005 Generic enkephalin
31	2	25.0	4	2	AAAP10370 Enkephalin-like an
32	2	25.0	4	2	AAAP10372 Enkephalin-like an
33	2	25.0	4	2	AAAP10373 Enkephalin-like an
34	2	25.0	4	2	AAAP10375 Enkephalin-like an
35	2	25.0	4	2	AAAP10386 Generic analgesic
36	2	25.0	4	2	AAAP10599 N-adamantane tetra
37	2	25.0	4	2	AAAP10433 Analgesic tetrapep
38	2	25.0	4	2	AAAP10401 Agonist peptide.
39	2	25.0	4	2	AAAP10620 Analgesic tetrapep
40	2	25.0	4	2	AAAP10625 Analgesic tetrapep
41	2	25.0	4	3	AAAP20208 Analgesic and neur
42	2	25.0	4	3	AAAP20210 Analgesic and neur
43	2	25.0	4	5	AAAP40339 Sequence of enkep
44	2	25.0	4	7	AAAP61656 Sequence of peptid
45	2	25.0	4	8	AAAP71313 Peptide component
46	2	25.0	4	10	AAAP91630 Motif useful in to
47	2	25.0	4	11	AAAR47670 Cyclic enkephalin
48	2	25.0	4	11	AAAR07020 Enkephalin analogu
49	2	25.0	4	11	AAAR07103 Melanocyte-stimula
50	2	25.0	4	12	AAAR13032 Isenin deriv. Syn

ALIGNMENTS

RESULT 1	
AAV51341	
17 AAV51341 standard; Protein: 9 AA.	
XX	
AC AAV51341:	
XX	
DT 27-APR-2000 (first entry)	
XX	
DE Sphingolipid desaturase protein fragment #7.	
XX	
XX Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;	
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;	
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;	
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;	
KW pharmaceutical; food; chemical raw material.	
XX	
OS Unidentified.	
XX	
FT Key Location/Qualifiers	
FT Misc-difference 3 /label= Any-amino_acid	
FT	
XX DE19828850-A1.	
PN	
XX 30-DEC-1999.	
PD	
XX 27-JUN-1998; 98DE-1028850.	
PF	
XX 27-JUN-1998; 98DE-1028850.	
PR	

XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX Heinz E, Zaehring U, Schmidt H, Sperling P;
 PI WPI; 2000-127549/12.
 XX
 DR
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 XX
 PS Claim 4; Page 23; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that
 CC selectively introduces a double bond into the sphingobase of the ceramide
 CC residue of sphingolipids and capnoids. A DNA sequence encoding the
 CC sphingolipid desaturase, or a vector containing the DNA sequence, can be
 CC used to produce transgenic plants, especially crop plants, with an
 CC increased or decreased delta-8-unsaturated long-chain base content or an
 CC altered delta-8-unsaturated long-chain base cis/trans ratio, especially
 CC to compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or
 CC capnoids can be used in cosmetics, pharmaceuticals and foods and as
 CC chemical raw materials. AY51335-Y51344 represent sphingolipid desaturase
 CC protein fragments described in the method of the invention.
 CC
 XX Sequence 9 AA:
 SQ

Query Match 37.5%; Score 3; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 aysxg 8
 ||||
 Db 1 aysxg 4

RESULT 2
 AAB37631
 ID AAB37631 standard; peptide; 13 AA.
 XX
 AC AAB37631;
 XX
 DT 23-MAR-2001 (first entry)
 DE
 XX Cholecystokinin peptide fragment analogue #10.
 DE
 XX Antidiabetic; cytostatic; auditory; cholecystokinin-8; CCK-8; neuropathy;
 KW peripheral nervous system; diabetes mellitus; cancer treatment;
 KW cytotstatic; hearing impairment; visual handicap;
 KW alcohol-induced neuropathy; dystrophy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8 /label= Nle
 FT Modified-site 11 /label= Nle
 FT Modified-site 13 /label= Nle
 FT Modified-site 13 /note= "C-terminal amide"
 FT
 XX WO200066150-A1.
 XX
 XX 09-NOV-2000.
 XX
 XX 03-MAY-2000; 2000WO-SE00870.
 PF
 XX

PR 03-MAY-1999; 99SE-0001578.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Lundeborg T, Manni L;
 XX
 DR WPI; 2001-024739/03.
 XX
 PT Manufacturing a medicament for treating neuropathies in the peripheral
 PT nervous system comprises use of a substance showing cholecystokinin-8
 PT activity -
 XX
 PS Disclosure; Page 4; 38pp; English.
 XX
 CC The present invention relates to peptides showing cholecystokinin (CCK)-8
 CC activity, which can be used to treat neuropathies in the peripheral
 CC nervous system (PNS). The present sequence is one such peptide. The
 CC peptides of the present invention may be used to treat neuropathies in
 CC the PNS associated with diabetes mellitus, cancer treatment such as
 CC cytotstatic, hearing impairment and/or visual handicap, alcohol-induced
 CC neuropathy, damage induced by surgery and dystrophy.
 XX
 SQ Sequence 13 AA:
 OY 5 aysxg 8
 ||||
 Db 6 aysxg 9

Query Match 37.5%; Score 3; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 AAW20310
 ID AAW20310 standard; Protein; 86 AA.
 XX
 AC AAW20310;
 XX
 DT 10-JUL-1997 (first entry)
 DE
 XX H. pylori cytoplasmic protein 24414687.aa.
 DE
 XX Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 XX
 OS Helicobacter pylori.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 27 /label= unknown
 FT Misc-difference 28 /note= "encoded by TSR"
 FT Misc-difference 28 /label= unknown
 FT Misc-difference 37 /note= "encoded by ARA"
 FT Misc-difference 37 /note= "encoded by ACY"
 FT Misc-difference 56 /label= unknown
 FT Misc-difference 68 /note= "encoded by GYT"
 FT Misc-difference 68 /label= unknown
 FT /note= "encoded by TRA"
 FT
 XX WO9640893-A1.
 XX
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US09122.
 PF
 XX 01-APR-1996; 96US-0630405.
 PR

PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR) ASTRA AB.
XX
PI Berglindh OT, Smith D, Mellgaerd BL;
XX WPI: 1997-052306/05.
DR N-PSDB; ANT67516.
XX
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
PS Claim 61; Page 507; 1481pp; English.
XX
CC The present sequence shows a Helicobacter pylori cytoplasmic protein
CC that may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping configs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
XX
SQ Sequence 86 AA:

Query Match 37.5%; Score 3; DB 18; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 rxxy 6
| | | | |
Db 26 rxxy 30

RESULT 4
AAC22631
ID AAC22631 standard; Protein; 91 AA.
XX
AC AAC22631:
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 25635.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132487.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 12-AUG-1999; 99US-0148341.
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PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
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PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.5%; Score 3; DB 21; Length 91;
Best Local Similarity 100.0%; Pred No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ayxg 8
|||
Db 27 ayxg 30

RESULT 5
AAW27779
ID AAW27779 standard; Protein; 110 AA.
XX
AC AAW27779;
XX
DT 21-JUL-1998 (first entry)
XX
DE Amino acid sequence of pseudouridylylate synthase I.
XX
KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW Staphylococcal gene; regulatory element; bacterial gene expression;
KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
toxic shock syndrome.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT MISC-difference 10 /note= "not specified"
FT MISC-difference 18 /note= "not specified"
FT
XX
PN W09730070-A1.
XX
XX 21-AUG-1997.
XX
PD 19-FEB-1997; 97WO-US02318.
XX
PR 20-FEB-1996; 96US-0011888.
XX
PA (SWIK) SMITHKLINE BEECHAM CORP.
XX
PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;
XX
DR WPI; 1997-424969/39.
DR N-PSDB; AAT83748.

XX Novel polypeptide(s) from *Staphylococcus aureus* strain WCUH29 - used
PT to isolate antimicrobial compounds, and in vaccines against *S.*
PT *aureus* infection
XX
PS Claim 6; Page 270; 989pp; English.
XX
CC The present sequence represents a *Staphylococcus aureus* protein, that,
CC based on homology with an *Escherichia coli* protein, is believed
CC to be pseudouridylylase synthase I (pseudouridine synthase I, uracil
CC hydrolyase. The DNA sequence was isolated from a library of clones of
CC *S. aureus* WCUH 29 in *Escherichia coli*. The DNA sequences to control in
CC the construction of ribozymes and antisense sequences to control the
CC expression of *Staphylococcal* genes. The DNA sequence is also useful as
CC a source of regulatory elements for the control of bacterial gene
CC expression. The present protein may be used to produce vaccines to
CC enable a host to produce specific antibodies with antibacterial action.
CC These vaccines and antibodies would protect a host against invasion by
CC *S. aureus*, and conditions relating to *Staphylococcal* infection,
CC e.g. *Staphylococcal* food poisoning, scaled skin syndrome, and toxic
CC shock syndrome.
XX
SQ Sequence 110 AA;
XX
Query Match 37.5%; Score 3; DB 18; Length 110;
Best Local Similarity 100.0%; Pred. No. Se+02; Mismatches 0; Gaps 0;
Matches 4; Conservative 0; Indels 0;
OY 5 ayxg 8
|||
DB 8 ayxg 11
RESULT 6
ID AMG22630
AMG22630 standard; Protein; 121 AA.
XX
AC AMG22630;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zee mays protein fragment SEQ ID NO: 25634.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.
XX
OS Zee mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137328.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.

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PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 03-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.
PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156458.
PR 29-SEP-1999; 9905-0156596.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157865.
PR 07-OCT-1999; 9905-0158029.
PR 08-OCT-1999; 9905-0158232.
PR 12-OCT-1999; 9905-0158369.
PR 13-OCT-1999; 9905-0159293.
PR 13-OCT-1999; 9905-0159294.
PR 13-OCT-1999; 9905-0159295.
PR 14-OCT-1999; 9905-0159329.
PR 14-OCT-1999; 9905-0159330.
PR 14-OCT-1999; 9905-0159331.
PR 14-OCT-1999; 9905-0159637.
PR 14-OCT-1999; 9905-0159638.
PR 18-OCT-1999; 9905-0159584.
PR 21-OCT-1999; 9905-0160741.
PR 21-OCT-1999; 9905-0160767.

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PR 21-OCT-1999; 9905-0160768.
PR 21-OCT-1999; 9905-0160770.
PR 21-OCT-1999; 9905-0160814.
PR 21-OCT-1999; 9905-0160815.
PR 22-OCT-1999; 9905-0160980.
PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
PR 22-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Query Match 37.5%; Score 3; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.3e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
Db 57 ayxg 60

RESULT 7
AAW20262
ID AAW20262 standard; Protein; 185 AA.
XX
AC AAW20262;
XX
DT 30-JUL-1997 (first entry)
XX
DE H. pylori secreted or periplasmic protein 23594833.aa.
XX
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
XX
OS Helicobacter pylori.
XX
FH Key Location/Qualifiers
FT MISC-difference 2 /label= unknown
FT MISC-difference 101 /note= "encoded by YAR"
FT MISC-difference 142 /label= unknown
FT MISC-difference 149 /note= "encoded by RAA"
FT MISC-difference 149 /note= "unknown"
FT MISC-difference 149 /label= unknown
FT MISC-difference 157 /note= "encoded by CSG"
FT MISC-difference 157 /label= unknown
FT MISC-difference 158 /note= "encoded by GAK"
FT MISC-difference 158 /label= unknown
FT MISC-difference 158 /note= "encoded by WAA"

WO9640893-A1.
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09122.
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR ) ASTRA AB.

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XX Berglindh OT, Smith D, Mellgaard BL.
PI WPI: 1997-052306/05.
DR N-PSDB: AAT67760.
XX
XX Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PI infection, and to detect Helicobacter
XX
XX Claim 72: Page 466; 1481pp; English.
XX
CC This sequence is a H. pylori secreted or periplasmic protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
XX
XX Sequence 185 AA;
SQ
XX
XX
XX Query Match 37.5%; Score 3; DB 18; Length 185;
Best Local Similarity 100.0%; Pred. No. 7,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 5 aysxg 8
|||
Db 140 aysxg 143
XX
XX
XX RESULT 8
AAW24622
ID AAW24622 standard; Protein: 185 AA.
XX
XX AAW24622;
XX
XX 11-AUG-1997 (first entry)
XX
XX H. pylori secreted or periplasmic protein 23594833.aa.
XX
XX "Transmembrane; cytoplasmic; cell envelope; flagella; transport;
KW secreted; periplasmic; chronic gastritis; duodenal ulcer disease;
KW activator; inhibitor; bacterial life cycle; vaccine; immunise;
KW detection; antisense; inhibition.
XX
XX Helicobacter pylori.
XX
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "encoded by VAT"
FT Misc-difference 101 /note= "encoded by RAA"
FT Misc-difference 142 /note= "encoded by RAA"
FT Misc-difference 149 /note= "encoded by RAA"
FT Misc-difference 157 /note= "encoded by CSG"
FT Misc-difference 157 /note= "encoded by GAK"
FT Misc-difference 158 /note= "encoded by WAA"
XX
XX W09719098-A1.
XX
XX 29-MAY-1997.
PD

XX
XX 15-NOV-1996; 96W0-US18542.
XX
XX 17-NOV-1995; 95US-0561469.
XX
XX (ASTR) ASTRA AB.
XX
XX Smith DH;
XX
XX WPI: 1997-298052/27.
DR N-PSDB: AAT77440.
XX
XX
XX Helicobacter pylori nucleic acid sequences and related proteins -
PT used for diagnostics and therapeutics
XX
XX Claim 10; Page 153; 1481pp; English.
XX
CC This sequence is a H. pylori secreted or periplasmic protein.
CC Helicobacter pylori has been strongly linked to chronic gastritis and
CC duodenal ulcer disease. The nucleic acid sequences of the invention
CC are used to evaluate compounds, especially activators or inhibitors of
CC bacterial life cycle, for the ability to bind an H. pylori nucleic acid
CC sequence. The nucleic acid sequences, and corresponding proteins, are
CC also useful for generating vaccines for immunising subjects against H.
CC pylori or for use in detecting the presence of Helicobacter species in
CC a sample. Antisense nucleic acid sequences of these sequences are
CC used to inhibit expression of a gene from Helicobacter species. H.
CC pylori whole genomic DNA was isolated and nebulised to a median size of
CC 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique
CC BstXI-linker adapters in 100-1000 fold molar excess. These linkers are
CC complementary to the BstXI-cut PMPX vectors, while the overhang is not
CC self-complementary. Therefore the linkers will not concatamerise nor
CC will the cut vector re-ligate itself easily. The linker-adaptor inserts
CC were ligated to each of the 20 PMPX vectors to construct a series of
CC shotgun subclone libraries. The purified DNA samples were then
CC sequenced.
CC Note: The ORF/protein reference number for this sequence was obtained
CC from the related specification, W09640893.
XX
XX Sequence 185 AA;
SQ
XX
XX
XX Query Match 37.5%; Score 3; DB 18; Length 185;
Best Local Similarity 100.0%; Pred. No. 7,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 5 aysxg 8
|||
Db 140 aysxg 143
XX
XX
XX RESULT 9
AAR10204
ID AAR10204 standard; Protein: 275 AA.
XX
XX AAR10204;
XX
XX 27-MAR-1991 (first entry)
XX
XX Mutant subtilisin polypeptide (I).
XX
XX Mutant; subtilisin; detergent; serine protease.
XX
XX Key Location/Qualifiers
FH Misc-difference 218..218 /label= S, D
FT
XX
XX US4980288-A.
XX
XX 25-DEC-1990.
PD
XX
XX 14-DEC-1987; 87US-0143949.
PF
XX

PR 14-DEC-1987; 87US-0143949.
XX 12-FEB-1986; 86US-0828545.
XX (GENE-) GENEX CORP.
XX
XX Bryan PM, Rollence MJ, Pantoliano MW;
XX WPI; 1991-021675/03.
XX
XX Mutant subtilisin poly-peptide(s) with increased thermal
PT stability - obtd. by muta-genesis of subtilisin gene used in liq.
PT detergent compns.
XX
XX Claim 1; Page 16; 18pp; English.
XX
XX NB: to construct sequences AAR10204-13, the B. subtilis wild-type
CC sequence was retrieved from the GENSEQ database (AAP0095; J01137972-A)
CC and amino acid residues altered according to the mutations described
CC in the specification (Ser/Asp-Asn218).
CC The mutant subtilisin does not lose activity as rapidly when stored
CC in soln. with detergents or when subjected to high heat during use
CC in cleaning. It is used for the removal of proteinaceous stains on
CC fabric. Other stabilising mutants may be introduced into the
CC protein. The stabilising mutations may also be applied to other
CC homologous serine proteases.
XX
SQ Sequence 275 AA;

Query Match 37.5%; Score 3; DB 12; Length 275;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayxg 8
1111
Db 216 ayxg 219

RESULT 10
AAG75013
ID AAG75013 standard; Protein; 277 AA.
XX
XX AAG75013;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:5777.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 14.
XX
XX Homo sapiens.
XX
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US26524.
XX
XX 29-SEP-1999; 99US-0157137.
XX
XX 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX
XX N-PSDB; AAH34418.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 7294-7295; 9803pp; English.

XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 277 AA;

Query Match 37.5%; Score 3; DB 22; Length 277;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ayxg 8
1111
Db 89 ayxg 92

RESULT 11
AAB56744
ID AAB56744 standard; Protein; 284 AA.
XX
XX AAB56744;
XX
XX 13-MAR-2001 (first entry)
XX
XX Human prostate cancer antigen protein sequence SEQ ID NO:1322.
XX
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;
KW vulnereary; gastrointestinal; nephrotoxic; immunofective; gynaecological;
KW antibacterial; gene therapy; neutral; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200055174-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05988.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (ROSE/) ROSEN C A.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587513/55.
XX
XX N-PSDB; AAF15947.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
XX Claim 11; Page 1743-1744; 2338pp; English.

```
XX AAF1566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytoskeletal,
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 284 AA:
SQ
Oy 5 ayxg 8
   ||||
Db 263 ayxg 266

RESULT 12
AA12129
ID AAR12129 standard; Protein: 401 AA.
AC AAR12129;
XX
XX 01-AUG-1991 (first entry)
XX
XX ORF 1 of Igc light chain variable region clone.
XX
XX Immunoglobulin G; light chain; variable region; duplication;
XX passive immunity; group B streptococci.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Peptide 224..336
XX /label= "L/V region
XX /note= "last 3 amino acids of leader and variable
XX region"
XX
XX WO9106305-A.
XX
XX 16-MAY-1991.
XX
XX 06-NOV-1990: 90WO-US06426.
XX
XX 07-NOV-1989: 89US-0432700.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Shuford WW, Harris LJ, Raff HV;
XX
XX WPI; 1991-163947/22.
XX
XX N-PSDB; AAO11879.
XX
XX Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
XX formed by duplicating esp. variable region of light chain of Igc
XX class
XX
XX Example 4; Fig 17; 104pp; English.
XX
XX This sequence is derived from the nucleotide sequence encoding the
XX light chain variable region. The "x" residues represent nonsense
XX codons. The coding sequence has been translated in all 3 reading
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CC frames (see also AAR12130 and AAR12131). The L/V region is duplicated
CC in so-called "aberrant" light chains (see AAO11878), conferring
CC increased avidity on antibodies comprising such aberrant chains.
CC See also AAO11880.
XX
XX SQ Sequence 401 AA:
SQ
Oy 5 ayxg 8
   ||||
Db 27 ayxg 30

RESULT 13
AAW84298
ID AAW84298 standard; Protein: 489 AA.
AC AAW84298;
XX
XX 25-MAR-1999 (first entry)
XX
XX Consensus sequence of GDNFR and GRR2 and GRR3 proteins.
XX
XX GDNFR, glial cell line-derived neurotrophic factor receptor;
XX GDNFR, glial cell line-derived neurotrophic factor; GDNF;
XX neurturin; signal transduction; dopaminergic nerve cell;
XX Parkinson's disease; Alzheimer's disease; amyotrophic lateral
XX neurological disorder; diabetes; glaucoma; sensory neuron;
XX retinal ganglion cell degeneration; sensory neuropathy;
XX retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT MISC-difference 1..489
XX FT /note= "x=not specified"
XX
XX WO9854213-A2.
XX
XX 03-DEC-1998.
XX
XX 27-APR-1998: 98WO-US08486.
XX
XX 30-MAY-1997: 97US-0866354.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D;
XX
XX WPI; 1999-080806/07.
XX
XX New isolated glial cell line-derived neurotrophic factor receptors -
XX used to develop products for treating e.g. improperly functioning
XX dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
XX or amyotrophic lateral sclerosis
XX
XX Claim 51; Fig 26; 318pp; English.
XX
XX The present sequence represents a consensus sequence of glial
XX cell-line derived neurotrophic factor receptor (GDNFR) protein and
XX GDNFR-related (GRR) proteins GRR2 and GRR3. The proteins have similar
XX functions. GDNFR proteins are functionally characterised by the ability
XX to bind glial cell line-derived neurotrophic factor (GDNF) and/or
XX neurturin specifically, and to act as part of a molecular complex which
XX mediates or enhances the signal transduction affects of GDNF and/or
XX neurturin. The proteins can be used for treating improperly functioning
XX dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
XX amyotrophic lateral sclerosis. They can also be used for treating
XX neurological disorders associated with diabetes, glaucoma or other
```

CC diseases and conditions involving retinal ganglion cell degeneration,
CC sensory neuropathy caused by injury to, insults to, or degeneration of,
CC sensory neurons, pathological conditions, or disease or injury-related
CC retinopathies. The products can also be used for detection, diagnosis,
CC drug screening and gene therapy.
XX
SQ Sequence 489 AA;

Query Match 37.5%; Score 3; DB 20; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
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Db 305 ayxg 308

RESULT 14
AAM84183
ID AAM84183 standard; Protein; 498 AA.

XX AAM84183;

DT 25-MAR-1999 (first entry)

XX Consensus sequence of rat and human GDNFR and GRR proteins.

XX G1a1 cell-line derived neurotrophic factor receptor;
KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
KW neurturin; signal transduction; dopaminergic nerve cell;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurological disorder; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy;
KW retinopathy; gene therapy; GDNFR-related protein; GRR.

XX Synthetic.
OS Rattus sp.
OS Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 1..498
FT /note= "x=not specified"

XX WO9854213-A2.

PD 03-DEC-1998.

PF 27-APR-1998; 98WO-US08486.

PR 30-MAY-1997; 97US-0866354.

PA (AMGE-) AMGEN INC.

XX (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Wen D;

XX WPI; 1999-080806/07.

XX New isolated glial cell line-derived neurotrophic factor receptors -
PT used to develop products for treating e.g. improperly functioning
PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
PT or amyotrophic lateral sclerosis
XX
PS Claim 51; Fig 19; 318pp; English.

XX The present sequence represents a consensus sequence of rat and
CC human glial cell-line derived neurotrophic factor receptor (GDNFR)
CC protein and GDNFR-related (GRR) proteins. The proteins have similar
CC functions. GDNFR proteins are functionally characterised by the ability
CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
CC neurturin specifically, and to act as part of a molecular complex which
CC mediates or enhances the signal transduction affects of GDNF and/or
CC neurturin. The proteins can be used for treating improperly functioning

CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
CC amyotrophic lateral sclerosis. They can also be used for treating
CC neurotrophic disorders associated with diabetes, glaucoma or other
CC diseases and conditions involving retinal ganglion cell degeneration,
CC sensory neuropathy caused by injury to, insults to, or degeneration of,
CC sensory neurons, pathological conditions, or disease or injury-related
CC retinopathies. The products can also be used for detection, diagnosis,
CC drug screening and gene therapy.
XX

SQ Sequence 498 AA;

Query Match 37.5%; Score 3; DB 20; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
|||
Db 312 ayxg 315

RESULT 15

AAM40758
ID AAM40758 standard; Protein; 500 AA.

XX AAM40758;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 5689.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0596042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou F, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI59914.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 2; SEQ ID NO 5689; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide


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FT /label=A, V, D
FT /note="Wild-Type is D"
FT Misc-difference 57..57
FT /label=S, C, Y
FT /note="Wild-Type is Y"
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FT /label=F, Y
FT /note="Wild-Type is Y"
FT Misc-difference 61..61
FT /label=V, D
FT /note="Wild-Type is D"
FT Misc-difference 63..63
FT /label=C, F, Y
FT /note="Wild-Type is Y"
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FT /label=D, E
FT /note="Wild-Type is E"
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FT /label=H, R
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FT Misc-difference 127..127
FT /label=T, N
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FT Misc-difference 129..129
FT /label=G, E
FT /note="Wild-Type is E"
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XX EP285123-A.
XX
XX
XX 05-MAY-1988.
XX
XX 30-MAR-1988; 88EP-0105163.
XX
XX 03-APR-1987; 87US-0034819.
XX
XX (SUSO ) SUOMEN SOKERI OY.
XX
XX Lehtovaara P, Knowles J, Kotivula A, Bamford J, Reinikainen T;
XX
XX WPI: 1988-279927/40.
XX
XX
XX Introducing random point mutations into nucleic acids -
XX by prepn of single stranded template, annealing a primer, elongation,
XX misincorporation, completion of molecules and screening.
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Query Match 37.5%; Score 3; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 5 ayyg 8
 | | |
Db 46 ayyg 49

RESULT 18
AAW17569
ID AAW17569 standard; protein: 688 AA.
XX
AC AAW17569;
XX
DT 30-JUN-1997 (first entry)
XX
DE Bacillus CGTase variant beta-cyclodextrin #1.
XX
KW Cyclomalodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
KW Thermoaerobacter; starch; cyclomalodextrin; cyclodextrin; pesticide;
KW transglycosylation; cyclic glucose oligomer; glucose oligosaccharide;
KW cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
KW plastic laminate; biodegradable plastic; mutein.
XX
OS Synthetic.
XX
FH Key
FT Modified-site 21 Location/Qualifiers
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FT Modified-site 89
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FT Modified-site 90
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FT /note= "X= Gln, Lys, Arg, Trp, Phe, Asn, Ser, or absent"
FT Modified-site 99
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FT /note= "X= Gly, Ala"
FT Modified-site 102
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FT /note= "X= Gly, Ala"
FT Modified-site 136
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FT Modified-site 141
FT /label= H140X
FT /note= "X= Ala, Arg, Asn"
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FT Thr, or absent"
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FT /note= "X= Gly, Ser, Asn, Asp"
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PD	W09633267-A1.	
XX		
PD	24-OCT-1996.	
PF	22-APR-1996;	96WO-DK00179.
XX		
PR	16-NOV-1995;	95DK-0001281.
PR	21-APR-1995;	95DK-0000477.
PR	17-OCT-1995;	95DK-0001173.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
PI	Andersen C, Dijkhuizen L, Dijkstra BW, Von Der Osten C;	
XX		
DR	WPl: 1996-485774/48.	
XX		
PT	New variants of cyclo:malto:dextrin glucanotransferase (CGTase) -	
PT	have altered substrate binding, useful for prodn. of cyclodextrin(s)	
PT	or linear oligosaccharide(s), opt. formed in situ in e.g. baked	
PS	goods	
XX		
PS	Claim 31; Page -: 161pp; English.	
XX		
CC	AAW1568-W1579, and AAW1592-W17605 represent mutant versions of the	
CC	cyclomalto-dextrin glucanotransferase (CGTase) of Bacillus circulans	
CC	strain 251 (see AAM06773 for wild type sequence). CGTase catalyses the	
CC	conversion of starch and similar substrates into cyclomalto-dextrins	
CC	(also known as cyclodextrins) via an intramolecular transglycosylation	
CC	reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a	
CC	hydrophobic internal cavity that form inclusion complexes with many	
CC	small hydrophobic molecules. These CGTase mutants have a modified	
CC	substrate binding and/or product selectivity, compared to this sequence.	
CC	The mutants are created using primer mutagenesis to modify the gene	
CC	encoding this sequence. These sequences have greater product selectivity	
CC	and/or reduced product inhibition (better yields) than wild-type CGTase.	
CC	These mutant sequences are used to manufacture the 6 main CD types	
CC	(comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,	
CC	optionally in situ, e.g. during production of baked goods, to stabilise	
CC	chemicals during their manufacture and in detergents. CD are known for	
CC	their usefulness in foods, e.g. as a bread-improving agent, to	
CC	encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals,	
CC	pesticides or fungicides, to bind/remove lipophilic compounds such as	
CC	cholesterol (e.g. in egg yolk or butter), in plastic laminates, films	
CC	etc. and to make biodegradable plastics.	
XX		
SQ	Sequence 688 AA:	
	Query Match	37.5%; Score 3; DB 17; Length 688;
	Best Local Similarity	100.0%; Pred. No. 1.7e+03;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	5 ayxg 8 	
Dd	97 ayxg 100	
RESULT 19		
ID	AAW1577	
XX	AAW1577 standard; protein; 688 AA.	
AC	AAW1577;	
XX		
DT	30-JUN-1997 (first entry)	
XX		
DE	Bacillus CGTase variant beta-cyclodextrin #3.	
XX		
KM	Cyclomalto-dextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;	
KM	transmanarobacter; starch; cyclomalto-dextrin; cyclodextrin; pesticide;	
TW	transglycosylact; cyclic glucose oligomer; glucose oligosaccharide;	

KM		cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
KW		plastic laminate;biodegradable plastic; mutein.
XX		
OS	Synthetic.	
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FT	Modified-site	47 /label= R47X
FT	Modified-site	/note= "X= Ala, Gln, His, Arg, Leu"
FT	Modified-site	87 /label= I87H
FT	Modified-site	88 /label= N88X
FT	Modified-site	/note= "X= Asn, Lys, His"
FT	Modified-site	89 /label= Y89X
FT	Modified-site	/note= "X= Gly, Ala, Lys, Arg, Pro, Tyr, Glu or absent"
FT	Modified-site	90 /label= S90X
FT	Modified-site	/note= "X= Gly, Ala"
FT	Modified-site	91 /label= G91X
FT	Misc-difference	/note= "X= Ala, Val, Ser, Gly"
FT	Misc-difference	92 /note= "possible insertion of Ala, Val, Gly, or Tyr"
FT	Modified-site	94 /label= N93X
FT	Modified-site	/note= "X= Asn, His, Thr, or absent"
FT	Modified-site	95 /label= N94X
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FT	Modified-site	102 /label= W101X
FT	Modified-site	/note= "X= Gly, Ala"
FT	Modified-site	136 /label= D135L
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FT	Modified-site	/note= "X= Ala, Leu, Ile, Phe, Trp, Gly, Tyr, Arg, Asp, or absent"
FT	Modified-site	150 /label= Q148X
FT	Modified-site	/note= "X= Gly, Asn, Ala, Gln"
FT	Modified-site	151 /label= P149W
FT	Modified-site	152 /label= S150A
FT	Modified-site	169 /label= Y167X
FT	Modified-site	/note= "X= Ala, Phe"
FT	Modified-site	170 /label= T168S
FT	Modified-site	181 /label= G179X
FT	Modified-site	/note= "X= Ser, Asn, Asp"
FT	Modified-site	182

FT	/label_ G180X
FT	/note "X= Ser, Asn, Asp"
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FT	/label_ F183X
FT	/note "X= Trp, Tyr, Ala"
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FT	187
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FT	/note "X= Gly, Ala"
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FT	/label_ D196X
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FT	/label_ L197X
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XX	
PN	W09633267-A1.
XX	
PD	24-OCT-1996.
XX	
PE	22-APR-1996; 96MO-DK00179.
XX	
PR	16-NOV-1995; 95DK-0001281.
PR	21-APR-1995; 95DK-0000477.
PR	17-OCT-1995; 95DK-0001173.
XX	
PA	(NOVO) NOVO-NORDISK AS.
XX	
PI	Andersen C, Dijkhuizen L, Dijkstra BW, Von Der Osten C;
XX	
DR	WPI; 1996-48574/48.
XX	
PT	New variants of cyclomalto:dextrin glucanotransferase (CGTase) -
PT	have altered substrate binding, useful for prodn. of cyclodextrin(s)
PT	or linear oligosaccharide(s), opt. formed in situ in e.g. baked
PT	goods
XX	
PS	Claim 40; page -: 161pp; English.
XX	
CC	AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the
CC	cyclomalto:dextrin glucanotransferase (CGTase) of Bacillus circulans

CC	strain 251 (see AAM06773 for wild type sequence). CGTase catalyses the
CC	conversion of starch and similar substrates into cyclomaltohextrins
CC	(also known as cyclodextrins) via an intramolecular transglycosylation
CC	reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a
CC	hydrophobic internal cavity that form inclusion complexes with many
CC	small hydrophobic molecules. These CGTase mutants have a modified
CC	substrate binding and/or product selectivity, compared to this sequence.
CC	The mutants are created using primer mutagenesis to modify the gene
CC	encoding this sequence. These sequences have greater product selectivity
CC	and/or reduced product inhibition (better yields) than wild-type CGTase.
CC	These mutant sequences are used to manufacture the 6 main CD types
CC	(comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,
CC	optionally in situ, e.g. during production of baked goods, to stabilise
CC	chemicals during their manufacture and in detergents. CD are known for
CC	their usefulness in foods, e.g. as a bread-improving agent, to
CC	encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals,
CC	pesticides or fungicides, to bind/remove lipophilic compounds such as
CC	cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
CC	etc. and to make biodegradable plastics.
SQ	Sequence 688 AA:
OY	5 ayxg 8
DG	97 ayxg 100
RESULT	20
AAM17573	
ID	AAM17573 standard; protein: 688 AA.
XX	AAM17573:
DT	30-JUN-1997 (first entry)
DE	Bacillus CGTase variant beta-cyclodextrin #2.
XX	
KW	Cyclomaltoextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
KW	thermoanaerobacter; starch; cyclomaltoextrin; cyclodextrin; pesticide;
KW	transglycosylation; cyclic glucose oligomer; glucose oligosaccharide;
KW	cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
KW	plastic laminate; biodegradable plastic; muten.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Misc-difference
FT	Modified-site

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 FT Modified-site
 FT 94
 FT /label= N93X
 FT /note= "X= Gly, His, Thr, or absent"
 FT Modified-site
 FT 95
 FT /label= N94X
 FT /note= "X= Gln, Lys, Arg, Trp, Phe, Ser, or absent"
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 FT /note= "X= Gly, Ala"
 FT Modified-site
 FT 102
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 XX 24-OCT-1996.
 PD
 XX
 XX 22-APR-1996; 96WO-DK00179.
 PF
 XX
 XX 16-NOV-1995; 95DK-0001281.
 PR 21-APR-1995; 95DK-0000477.
 PR 17-OCT-1995; 95DK-0001173.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX
 PI Andersen C, Dijkhuizen L, Dijkstra BW, Von Der Osten C;
 DR WPI; 1996-485774/48.
 XX
 XX New variants of cyclo:malto:dextrin glucanotransferase (CGTase) -
 PT have altered substrate binding, useful for prodn. of cyclodextrin(s)
 PT or linear oligosaccharide(s), opt. formed in situ in e.g. baked
 PT goods
 XX
 PS Claim 34; Page -; 161pp; English.
 PS
 XX
 CC AAM17568-W17579, and AAM17592-W17605 represent mutant versions of the
 CC cyclomalto-dextrin glucanotransferase (CGTase) of *Bacillus circulans*
 CC strain 251 (see AAM06773 for wild type sequence). CGTase catalyses the
 CC conversion of starch and similar substrates into cyclomalto-dextrins
 CC (also known as cyclodextrins) via an intramolecular transglycosylation
 CC reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a
 CC hydrophobic internal cavity that form inclusion complexes with many
 CC small hydrophobic molecules. These CGTase mutants have a modified
 CC substrate binding and/or product selectivity, compared to this sequence.
 CC The mutants are created using primer mutagenesis to modify the gene
 CC encoding this sequence. These sequences have greater product selectivity
 CC and/or reduced product inhibition (better yields) than wild-type CGTase.
 CC These mutant sequences are used to manufacture the 6 main CD types
 CC (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,
 CC optionally in situ, e.g. during production of baked goods, to stabilise
 CC chemicals during their manufacture and in detergents. CD are known for
 CC their usefulness in foods, e.g. as a bread-improving agent, to
 CC encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals,
 CC pesticides or fungicides, to bind/remove lipophilic compounds such as
 CC cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
 CC etc. and to make biodegradable plastics.
 XX
 SQ Sequence 688 AA;

Query Match 37.5%; Score 3; DB 17; Length 688;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 aysxg 8

||||

Db 97 aysxg 100

RESULT 21

AAW17570 AAW17570 standard; protein; 689 AA.

AC AAW17570;

DT 30-JUN-1997 (first entry)

DE Bacillus CGTase variant gamma-cyclodextrin #1.

XX Cyclomaltopectin glucanotransferase; CGTase; enzyme; Bacillus circulans;

KW thermomicrobacter; starch; cyclomaltopectin; cyclodextrin; pesticide;

KM transglycosylation; cyclic glucose oligomer; glucose oligosaccharide;

KW cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;

XX plastic laminate; biodegradable plastic; mutein.

OS Synthetic.

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PN MO9633267-A1.
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PD 24-OCT-1996.
XX
XX 22-APR-1996; 96WO-DK00179.
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XX 16-NOV-1995; 95DK-0001281.
PR 21-APR-1995; 95DK-0000477.
PR 17-OCT-1995; 95DK-0001173.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Andersen C, Dijkhuizen L, Dijkstra BW, Von Der Osten C;
XX WPI: 1996-485774/48.
XX
XX New variants of cyclo:malto:dextrin glucanotransferase (CGTase) -
PT have altered substrate binding, useful for prodn. of cyclodextrin(s)
PT or linear oligosaccharide(s), opt. formed in situ in e.g. baked
PT goods
XX
XX Claim 31: Page -; 161pp; English.
XX
XX AAM17566-W17579, and AAM17592-W17605 represent mutant versions of the
CC cyclomaltodextrin glucanotransferase (CGTase) of *Bacillus circulans*
CC strain 251 (see AAM06773 for wild type sequence). CGTase catalyzes the
CC conversion of starch and similar substrates into cyclomaltodextrins
CC (also known as cyclodextrins) via an intramolecular transglycosylation
CC reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a
CC hydrophobic internal cavity that form inclusion complexes with many
CC small hydrophobic molecules. These CGTase mutants have a modified
CC substrate binding and/or product selectivity, compared to this sequence.
CC The mutants are created using primer mutagenesis to modify the gene
CC encoding this sequence. These sequences have greater product selectivity
CC and/or reduced product inhibition (better yields) than wild-type CGTase.
CC These mutant sequences are used to manufacture the 6 main CD types
CC (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,
CC optionally in situ, e.g. during production of baked goods, to stabilize
CC chemicals during their manufacture and in detergents. CD are known for
CC their usefulness in foods, e.g. as a bread-improving agent, to
CC encapsulate/stabilize/solubilize vitamins, dyes, pharmaceuticals,
CC pesticides or fungicides, to bind/remove lipophilic compounds such as
CC cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
CC etc. and to make biodegradable plastics.
XX
XX Sequence 689 AA:
SQ

Query Match 37.5%; Score 3; DB 17; Length 689;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
1111
Db 97 ayxg 100

RESULT 22
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ID AAM17574 standard; protein; 689 AA.
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XX AAM17574;
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XX
DT 30-JUN-1997 (first entry)
XX

DE *Bacillus* CGTase variant gamma-cyclodextrin #2.
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XX Cyclomaltodextrin glucanotransferase; CGTase; enzyme: *Bacillus circulans*;
KW thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide;
KW transglycosylation; cyclic glucose oligomer; glucose oligosaccharide;
KW cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
KW plastic laminate; biodegradable plastic; mutain.
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XX 24-OCT-1996.
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XX 22-APR-1996; 96WO-DK00179.
XX
XX 16-NOV-1995; 95DK-0001281.
XX 21-APR-1995; 95DK-0000477.
XX 17-OCT-1995; 95DK-0001173.
XX
XX (NOVO ) NOVO-NORDISK AS.

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XX
PI Andersen C, Dijkhuizen L, Dijkstra BW, Von Der Osten C;
DR WPI: 1996-485774/48.
XX
PT New variants of cyclomalto:dextrin glucanotransferase (CGTase) -
PT have altered substrate binding, useful for prodn. of cyclodextrin(s)
PT or linear oligosaccharide(s), opt. formed in situ in e.g. baked
PT goods
XX
XX Claim 34: Page -: 161pp; English.
XX
CC AAM17568-W17579, and AAM17592-W17605 represent mutant versions of the
CC cyclomalto:dextrin glucanotransferase (CGTase) of Bacillus circulans
CC strain 251 (see AAM06773 for wild type sequence). CGTase catalyses the
CC conversion of starch and similar substrates into cyclomalto:dextrins
CC (also known as cyclodextrins) via an intramolecular transglycosylation
CC reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a
CC hydrophobic internal cavity that form inclusion complexes with many
CC small hydrophobic molecules. These CGTase mutants have a modified
CC substrate binding and/or product selectivity, compared to this sequence.
CC The mutants are created using primer mutagenesis to modify the gene
CC encoding this sequence. These sequences have greater product selectivity
CC and/or reduced product inhibition (better yields) than wild-type CGTase.
CC These mutant sequences are used to manufacture the 6 main CD types
CC (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,
CC optionally in situ, e.g. during production of baked goods, to stabilise
CC chemicals during their manufacture and in detergents. CD are known for
CC their usefulness in foods, e.g. as a broad-improving agent, to
CC encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals,
CC pesticides or fungicides, to bind/remove lipophilic compounds such as
CC cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
CC etc. and to make biodegradable plastics.
XX
SQ Sequence 689 AA;
XX
Query Match 37.5%; Score 3; DB 17; Length 689;
Best Local Similarity 100.0%; Pred. No. 1,7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ayyx 8
| | | |
DB 97 ayyx 100
XX
RESULT 23
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ID AAM17578 standard; protein: 689 AA.
XX
AC AAM17578;
XX
DT 30-JUN-1997 (first entry)
XX
DE Bacillus CGTase variant gamma-cyclodextrin #3.
XX
KW Cyclomalto:dextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
KW thermoanaerobacter; starch; cyclomalto:dextrin; cyclodextrin; pesticide;
KW transglycosylation; cyclic glucose oligomer; glucose oligosaccharide;
KW cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
KW plastic laminate; biodegradable plastic; mucin.
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XX Synthetic.
XX
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PD	24-OCT-1996.
XX	
PR	22-APR-1996; 96WO-DK00179.
XX	
PR	16-NOV-1995; 95DK-0001281.
PR	21-APR-1995; 95DK-0000477.
PR	17-OCT-1995; 95DK-0001173.
XX	
PA	(NOVO) NOVO-NORDISK AS.
XX	
XX	Andersen C, Dijkhuizen I., Dijkstra BW, Von Der Osten C;
DR	WPI, 1996-485774/48.
XX	
PT	New variants of cyclo:malto:dextrin glucanotransferase (CGTase) -
PT	have altered substrate binding, useful for prodn. of cyclodextrin(s)
PT	or linear oligosaccharide(s), opt. formed in situ in e.g. baked
PT	goods
XX	
PS	Claim 40; Page -: 161pp; English.
XX	
CC	AAW17568-w17579, and AAW17592-w17605 represent mutant versions of the
CC	cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans
CC	strain 251 (see AAM06773 for wild type sequence). CGTase catalyzes the
CC	conversion of starch and similar substrates into cyclomaltodextrins
CC	(also known as cyclodextrins) via an intramolecular transglycosylation
CC	reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a
CC	hydrophobic internal cavity that form inclusion complexes with many
CC	small hydrophobic molecules. These CGTase mutants have a modified
CC	substrate binding and/or product selectivity, compared to this gene-
CC	The mutants are created using primer mutagenesis to modify the gene
CC	encoding this sequence. These sequences have greater product selectivity
CC	and/or reduced product inhibition (better yields) than wild-type CGTase.
CC	These mutant sequences are used to manufacture the 6 main CD types

CC (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides,
 CC optionally in situ, e.g. during production of baked goods, to stabilise
 CC chemicals during their manufacture and in detergents. CD are known for
 CC their usefulness in foods, e.g. as a bread-improving agent, to
 CC encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals,
 CC pesticides or fungicides, to bind/remove lipophilic compounds such as
 CC cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
 CC etc. and to make biodegradable plastics.

XX Sequence 689 AA;

Query Match 37.5%; Score 3; DB 17; Length 689;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Mismatches 0; Indels 0; Gaps 0;

OY 5 ayxg 8
 ||||
 Db 97 ayxg 100

RESULT 24

AA848523 AAR48523 standard; peptide: 3 AA.

XX AAR48523;

XX 10-AUG-1994 (first entry)

XX Lactoferrin derived peptide #17.

XX Decomposition: lactoferrin; digestion: enzyme; pepsin; trypsin;
 KW antioxi dant; oxidation; inhibitor; vitamin E; ascorbic acid;
 KM vitamin A; beta-carotene; superoxide dismutase; coenzyme Q;
 XX lipid oxidation; foodstuff; drugs; health food; toiletries; cosmetics.

XX Bos taurus.

XX W09403555-A.

XX 17-FEB-1994.

XX PF 04-AUG-1993; 93WO-JP01090.

XX PR 07-AUG-1992; 92JP-0211335.

XX (MORG) MORINAGA MILK IND CO LTD.

XX Bellamy WR, Fukuwatari Y, Kawase K, Shimamura S;

PI Takase M, Tokiday, Tomita M, Wakabayashi H, Yamauchi K;

XX WPI: 1994-065650/08.

XX Antioxi dant peptide lactoferrin decomposition product - prevents
 PT oxidation of lipid(s) in foodstuffs and drugs without affecting
 PT their taste

PS Claim 3; Page 32; 47pp; Japanese.

XX The sequences given in AAR48507-37 are peptides derived by the
 CC decomposition of lactoferrin, pref. by digestion with an enzyme, eg.
 CC pepsin or trypsin. These peptides may be used in an antioxidant
 CC composition which may also contain an oxidation inhibitor such as
 CC vitamin E, ascorbic acid, vitamin A, beta-carotene, superoxide
 CC dismutase or coenzyme Q. The antioxidant prevents lipid oxidation
 CC in foodstuffs, drugs, health foods, toiletries and cosmetics.

XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 ||
 Db 2 wr 3

RESULT 25

AA848691 AAR84691 standard; peptide: 3 AA.

XX AAR84691;

XX 13-JUN-1996 (first entry)

XX Bovine lactoferrin derived angina pectoris treating peptide.

XX Bovine lactoferrin; angina pectoris; treatment; low toxicity;
 KW no side effects; heat resistance; water solubility; stability;
 KM aqueous solution; preservative free.

XX Bos taurus.

XX JP07278011-A.

XX 24-OCT-1995.

XX PF 01-APR-1994; 94JP-0085243.

XX PR 01-APR-1994; 94JP-0085243.

XX (MORG) MORINAGA MILK IND CO LTD.

XX WPI: 1995-400916/51.

XX Peptide for treatment of angina pectoris - has low toxicity and is
 PT heat resistant and water soluble

XX Claim 1; Page 10; 12pp; Japanese.

XX The present peptide is a bovine lactoferrin derived, angina
 CC pectoris treatative agent. It has low toxicity and side effects,
 CC is heat resistant, water soluble and stable in an aq. soln.. It
 CC also requires no preservative.

XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 16; Length 3;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 ||
 Db 2 wr 3

Search completed: January 14, 2002, 07:56:32
 Job time: 727 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:57:31 ; Search time 41.59 Seconds
(without alignments)
4.329 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 8
Sequence: 1 wrxayxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2	25.0	3	1	US-08-165-545-8
2	2	25.0	3	1	US-08-305-768-27
3	2	25.0	3	1	US-08-256-771-17
4	2	25.0	3	1	US-08-381-984-17
5	2	25.0	3	2	US-08-871-163-27
6	2	25.0	3	2	US-08-767-903-27
7	2	25.0	3	5	PCT-US95-11724-27
8	2	25.0	4	1	US-08-165-545-7
9	2	25.0	4	1	US-08-190-802A-265
10	2	25.0	4	1	US-08-176-938-20
11	2	25.0	4	1	US-08-215-137-11
12	2	25.0	4	1	US-08-428-488-59
13	2	25.0	4	1	US-08-428-488-60
14	2	25.0	4	1	US-08-428-488-61
15	2	25.0	4	1	US-08-428-488-62
16	2	25.0	4	1	US-08-428-488-71
17	2	25.0	4	1	US-08-428-488-72
18	2	25.0	4	1	US-08-428-488-73
19	2	25.0	4	1	US-08-428-488-74
20	2	25.0	4	1	US-08-487-006-150
21	2	25.0	4	1	US-08-487-006-151
22	2	25.0	4	1	US-08-487-006-152
23	2	25.0	4	1	US-08-487-006-153
24	2	25.0	4	1	US-08-256-771-16
25	2	25.0	4	1	US-07-923-260A-11
26	2	25.0	4	1	US-08-222-851-22
27	2	25.0	4	1	US-08-798-897-49

28	2	25.0	4	1	US-08-381-984-16	Sequence 16, Appl
29	2	25.0	4	1	US-08-463-224-2	Sequence 2, Appl
30	2	25.0	4	2	US-08-463-377-2	Sequence 2, Appl
31	2	25.0	4	2	US-08-441-871-63	Sequence 63, Appl
32	2	25.0	4	2	US-08-441-871-66	Sequence 66, Appl
33	2	25.0	4	2	US-08-592-646A-62	Sequence 62, Appl
34	2	25.0	4	2	US-08-637-759B-108	Sequence 108, Appl
35	2	25.0	4	2	US-08-978-523-49	Sequence 49, Appl
36	2	25.0	4	2	US-08-488-659A-150	Sequence 150, Appl
37	2	25.0	4	2	US-08-488-659A-151	Sequence 151, Appl
38	2	25.0	4	2	US-08-488-659A-152	Sequence 152, Appl
39	2	25.0	4	2	US-08-488-659A-153	Sequence 153, Appl
40	2	25.0	4	2	US-08-484-905-124	Sequence 124, Appl
41	2	25.0	4	3	US-08-481-985B-124	Sequence 124, Appl
42	2	25.0	4	3	US-08-871-355A-108	Sequence 108, Appl
43	2	25.0	4	3	US-08-912-272-8	Sequence 8, Appl
44	2	25.0	4	3	US-08-981-122-24	Sequence 24, Appl
45	2	25.0	4	3	US-08-981-122-28	Sequence 28, Appl
46	2	25.0	4	4	US-08-370-476-124	Sequence 124, Appl
47	2	25.0	4	4	US-09-329-350-3	Sequence 3, Appl
48	2	25.0	4	4	US-09-051-986-26	Sequence 26, Appl
49	2	25.0	4	4	US-08-591-632-40	Sequence 40, Appl
50	2	25.0	4	4	US-08-591-632-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-165-545-8
Sequence 8, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:

FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 1 wr 2
11
Db 2 WR 3

RESULT 2
US-08-305-768-27
Sequence 27, Application US/08305768
Patent No. 5602097
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,768
FILING DATE: 12-SEPT-1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 1 wr 2
11
Db 1 WR 2

RESULT 3
US-08-256-771-17
Sequence 17, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-17

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 1 wr 2
11
Db 2 WR 3

RESULT 4
US-08-381-984-17
Sequence 17, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32

```

CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: "note" the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-17

Query Match      25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 2 wr 3

RESULT 5
US-08-871-163-27
Sequence 27, Application US/08871163
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,163
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:

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```

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-871-163-27

Query Match      25.0%; Score 2; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 1 wr 2

RESULT 6
US-08-767-903-27
Sequence 27, Application US/08767903
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,903
FILING DATE:
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-767-903-27

Query Match      25.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 1 wr 2

RESULT 7
PCT-US95-11724-27
Sequence 27, Application PC/TUS9511724
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11724
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:

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TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 25.0%; Score 2; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 1 wr 2

RESULT 8
US-08-165-545-7
Sequence 7, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE;

POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 3 wr 4

RESULT 9
US-08-190-802A-265
Sequence 265, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTA peptide
US-08-190-802A-265

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 1 wr 2

RESULT 10
US-08-176-938-20
Sequence 20, Application US/08176938
Patent No. 5602099

GENERAL INFORMATION:
APPLICANT: Schiller, Peter W.
TITLE OF INVENTION: New Peptides
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: U.S.A.
ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,938

FILING DATE: 04-JAN-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Storer Ph.D., Richard J.

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-080

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-819-8783

TELEFAX: 212-354-8113

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 2

OTHER INFORMATION: /label= TIC

OTHER INFORMATION: /note= "1,2,3,4-tetrahydroisoguanoline-3-carboxylic acid"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 3

OTHER INFORMATION: /label= Phg

OTHER INFORMATION: /note= "phenylglycine"

US-08-176-938-20

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 yxg 8
111
DB 1 yxg 3

RESULT 11
US-08-215-137-11
Sequence 11, Application US/08215137
Patent No. 5614370

GENERAL INFORMATION:

APPLICANT: Konteatis, Zenon

APPLICANT: Siciliano, Salvatore J

APPLICANT: Springer, Martin S

TITLE OF INVENTION: ASSAY TO IDENTIFY HUMAN C5A ANTAGONISTS

TITLE OF INVENTION: AND AGONISTS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 Lincoln Ave., P.O. Box 2000

CITY: Rahway

STATE: New Jersey

COUNTRY: United States of America

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/215,137

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Benzen, Gerard H

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: 19108

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3901

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: C-terminal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /label= TIC

OTHER INFORMATION: /note= "tetrahydroisoguanoline carboxylic acid"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 2

OTHER INFORMATION: /label= dcha

OTHER INFORMATION: /note= "D-cyclohexylalanine"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /label= darg

OTHER INFORMATION: /note= "D-arginine"

US-08-215-137-11

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 3 wr 4

```
RESULT 12
US-08-428-488-59
; Sequence 59, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = nicotinoyl-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = Tyr (O-tBu)."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Position 4 = Arg (jPmc)-Cholesteryl
; OTHER INFORMATION: ester."
US-08-428-488-59

Query Match      25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ay 6
      ||
Db      2 AY 3

RESULT 13
US-08-428-488-60
; Sequence 60, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = Trigonellyl-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = Tyr (O-tBu)."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Position 4 = Arg (jPmc)-Cholesteryl
; OTHER INFORMATION: ester."
US-08-428-488-60

Query Match      25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ay 6
      ||
Db      2 AY 3
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = Trigonellyl-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = Tyr (O-tBu)."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Position 4 = Arg (jPmc)-Cholesteryl
; OTHER INFORMATION: ester."
US-08-428-488-60

Query Match      25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ay 6
      ||
Db      2 AY 3

RESULT 14
US-08-428-488-61
; Sequence 61, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/428,488
: FILING DATE: 27-APR-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Mary Katherine
: REGISTRATION NUMBER: 26,254
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note="Position 1 = Trigonellyl-Ala"
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note="Position 4 = Arg-Cholesteryl ester."
: US-08-428-488-61

Query Match          25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 ay 6
   11
Db 2 Ay 3

RESULT 15
: US-08-428-488-62
: Sequence 62, Application US/08428488
: Patent No. 5624894
: GENERAL INFORMATION:
: APPLICANT: BODOR, Nicholas S.
: TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
: TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
: NUMBER OF SEQUENCES: 107
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/428,488
: FILING DATE: 27-APR-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Mary Katherine
: REGISTRATION NUMBER: 26,254
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note="Position 1 = nicotlnoyl-Pro."
: NAME/KEY: Modified-site
: LOCATION: 3
```

```

: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note="Position 1 = 1,4-Dihydrotrigonellyl-Ala."
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note="Position 4 = Arg-Cholesteryl ester."
: US-08-428-488-62

Query Match          25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 ay 6
   11
Db 2 Ay 3

RESULT 16
: US-08-428-488-71
: Sequence 71, Application US/08428488
: Patent No. 5624894
: GENERAL INFORMATION:
: APPLICANT: BODOR, Nicholas S.
: TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
: TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
: NUMBER OF SEQUENCES: 107
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/428,488
: FILING DATE: 27-APR-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Mary Katherine
: REGISTRATION NUMBER: 26,254
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note="Position 1 = nicotlnoyl-Pro."
: NAME/KEY: Modified-site
: LOCATION: 3
```

OTHER INFORMATION: /note= "Position 3 = Tyr (O-tbu)." ;
FEATURE: ;
NAME/KEY: Modified-site ;
LOCATION: 4 ;
OTHER INFORMATION: /note= "Position 4 = Arg (j-Pmc)-Cholesteryl ;
OTHER INFORMATION: ester." ;
US-08-428-488-71

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ay 6
11
Db 2 AY 3

RESULT 17
US-08-428-488-72
Sequence 72, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = trigonellyl-Pro
OTHER INFORMATION: methylsulfate."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /note= "Position 2 = Tyr (O-tbu)."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "Position 4 = Arg (j-Pmc)-Cholesteryl
OTHER INFORMATION: ester."
US-08-428-488-72

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ay 6
11
Db 2 AY 3

RESULT 18
US-08-428-488-73
Sequence 73, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = trigonellyl-Pro
OTHER INFORMATION: methylsulfate."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "Position 4 = Arg-Cholesteryl
OTHER INFORMATION: ester."
US-08-428-488-73

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ay 6
11
Db 2 AY 3

RESULT 19
US-08-428-488-74


```
Sequence 74, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BOOOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = 1,4-dihydrocrrigonellyl-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "Position 4 = Arg-Cholesteryl"
OTHER INFORMATION: ester."
US-08-428-488-74

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 ay 6
   11
Db 2 AY 3

RESULT 20
US-08-487-006-150
Sequence 150, Application US/08487006
Patent No. 5641861
GENERAL INFORMATION:
APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
Agonists and Antagonists
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
```

```
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /note= "Xaa is (D)Nve"
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Xaa is Nap."
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Amino acid is amidated at
the C-terminal."
US-08-487-006-150
```

```
Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 yxg 8
   111
Db 1 YXG 3
```

```
RESULT 21
US-08-487-006-151
Sequence 151, Application US/08487006
Patent No. 5641861
GENERAL INFORMATION:
APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
Agonists and Antagonists
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
```

```
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /note= "Xaa is (D)Nle."
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Xaa is Nap."
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Amino acid is amidated at
US-08-487-006-151
the C-terminal."
```

```
Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 6 YXG 8
111
DB 1 YXG 3
```

```
RESULT 22
US-08-487-006-152
Sequence 152, Application US/08487006
Patent No. 5641861
GENERAL INFORMATION:
APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands:
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 152:
SEQUENCE CHARACTERISTICS:
```

```
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /note= "Xaa is (D)Nle."
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Amino acid is amidated at
US-08-487-006-152
the C-terminal."
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Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 6 YXG 8
111
DB 1 YXG 3
```

```
RESULT 23
US-08-487-006-153
Sequence 153, Application US/08487006
Patent No. 5641861
GENERAL INFORMATION:
APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands:
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Peptide
LOCATION: 2
OTHER INFORMATION: /note= "Xaa is (D)Nle."
FEATURE:
NAME/KEY: Peptide
LOCATION: 4
OTHER INFORMATION: /note= "Amino acid is amidated at
US-08-487-006-153
the C-terminal."
```

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YXG 8
111
DB 1 YXG 3

RESULT 24

US-08-256-771-16
; Sequence 16, Application US/08256771

; Patent No. 5656591

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING

; TITLE OF INVENTION: PRODUCTS THEREWITH

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/256,771

; FILING DATE: July 22, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-256-771-16

OY 1 WR 2

11

DB 3 WR 4

RESULT 25

US-07-923-260A-11

; Sequence 11, Application US/07923260A

; Patent No. 5719021

; GENERAL INFORMATION:

; APPLICANT: Inouye, Masayori

; TITLE OF INVENTION: PROTEIN ACTIVATION

; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard J. Weiser
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/923,260A

FILING DATE: 31-JUL-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 377.5638P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-07-923-260A-11

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AY 6

11

DB 2 AY 3

Search completed: January 14, 2002, 07:57:31
Job time: 376 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:58:37 : Search time 45.4 Seconds
(without alignments)
13.423 Million cell updates/sec

Title: 09-185908-1G
Perfect score: 8
Sequence: 1 wrxxsfxxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : PIR_68:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	698	2	T13492	NADH dehydrogenase
2	25.0	7	2	PT0644	T-cell receptor be
3	25.0	7	2	S33245	neuroendulatory pe
4	25.0	7	2	PD0029	pev-kinin I - pena
5	25.0	8	2	A37521	R-phycocerythrin ga
6	25.0	8	2	S11078	glucose-6-phosphat
7	25.0	8	2	J50316	leucokinin VI - Ma
8	25.0	8	2	A23967	leucopyrokinin - M
9	25.0	8	2	D47393	neuropeptide calla
10	25.0	8	2	A42057	fibroblast growth
11	25.0	9	2	B57444	neuropeptide grb-A
12	25.0	9	2	C57444	neuropeptide grb-A
13	25.0	9	2	PT0315	Ig heavy chain CRD
14	25.0	10	2	JC1367	thyroloberin poten
15	25.0	10	2	JN0024	neurokinin A - chi
16	25.0	10	2	D60787	sperm-activating p
17	25.0	10	2	S23307	neurokinin A - tai
18	25.0	10	2	S23186	neurokinin A - Atl
19	25.0	10	2	B61033	ranatichykinin B -
20	25.0	10	2	C61033	ranatichykinin C -
21	25.0	10	2	S27178	neurokinin A-relat
22	25.0	10	2	I40032	type protein - Bac
23	25.0	10	2	S38305	lectin GML2 alpha
24	25.0	10	2	D28027	protein P7 - curle
25	25.0	10	2	A43977	FMRFamide-like pro
26	25.0	10	2	A37268	Ig heavy chain C r
27	25.0	10	2	PH0916	T-cell receptor be
28	25.0	10	2	T13838	cytochrome-c oxida
29	25.0	11	2	A34662	Achatina cardio-ex

30	25.0	11	2	B41946	T-cell receptor ga
31	25.0	11	2	I60434	66kDa neurofilamen
32	25.0	12	1	A53709	alpha-conotoxin Im
33	25.0	12	2	S26559	T-cell receptor be
34	25.0	12	2	S26554	T-cell receptor be
35	25.0	12	2	B61497	seed protein ws-17
36	25.0	12	2	S10626	lipovitelin - Afr
37	25.0	12	2	S74144	aggreccan - bovine
38	25.0	12	2	PH1467	T-cell receptor be
39	25.0	12	2	PH1462	T-cell receptor be
40	25.0	12	2	PH1459	T-cell receptor be
41	25.0	12	2	PH1457	T-cell receptor be
42	25.0	12	2	PH0771	T-cell receptor be
43	25.0	12	2	PH1468	T-cell receptor be
44	25.0	13	2	S08575	botulinum neurotox
45	25.0	13	2	S54344	glyceraldehyde-3-p
46	25.0	13	2	S78766	ribosomal protein
47	25.0	13	2	PC4391	cysteine proteinas
48	25.0	14	1	LFEBCW	tip operon leader
49	25.0	14	1	LFEBWC	tip operon leader
50	25.0	14	1	LFEBWT	tip operon leader

ALIGNMENTS

```

RESULT 1
T13492
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Nicotiana glauca chlorop
C:Species: chloroplast Nicotiana glauca chloroplast
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
C:Accession: T13492
R:Olstead, R.G.; Reeves, P.A.
Ann. Mo. Bot. Gard. 82, 176-193, 1995
A:Title: Evidence for the polyphyly of the Scrophulariaceae based on chloroplast rbcL
A:Reference number: Z17559
A:Accession: T13492
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-698 <OLM>
A:Cross-references: EMBL:L36405; NID:g703196; PID:g703197; PIDN:AAA84496.1
C:Genetics:
A:Genome: chloroplast
A:Note: ndhf
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 37.5% Score 3; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 sfxx 8
DB 664 SFXX 667

RESULT 2
PT0644
T-cell receptor beta chain V-D-J region (111-16) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0644
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0644
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

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Query Match 25.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 3 SF 4

RESULT 3

S33245

neuromodulatory peptide Wwamide-2 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33245

R:Minakat, H.; Ikeda, T.; Munesoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 1 WR 2

RESULT 4

PD0029

pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment)

C:Species: Penaeus vannamei

C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000

C:Accession: PD0029

R:Nieto, J.; Veelaert, D.; Dervu, R.; Waalkens, E.; Cersliens, A.; Coast, G.; Devreese,

Biochem. Biophys. Res. Commun. 248, 406-411, 1998

A:Title: Identification of one tachykinin- and two kinin-related peptides in the brain c

A:Reference number: PD0027; MUID:98342103

A:Accession: PD0029

A:Molecule type: protein

A:Residues: 1-7 <NTE>

C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 2 SF 3

RESULT 5

A37521

R-phycoerythrin gamma-E chain - red alga (Gastrocionium coulteri) (fragment)

C:Species: Gastrocionium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: A37521; J22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A37521

A:Molecule type: protein

A:Residues: 1-8 <KLO>

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 2 SF 3

RESULT 6

S11078

glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)

C:Species: Pichia jadinii, Candida utilis

C:Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #text_change 05-Aug-1994

C:Accession: S11078

R:Egsted, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.;

FEBS Lett. 269, 194-196, 1990

A:Title: Fast atom bombardment mass spectrometry and chemical analysis in determinati

A:Reference number: S11074; MUID:90353571

A:Accession: S11078

A:Molecule type: protein

A:Residues: 1-8 <ECG>

A:Note: the source is designated as Pichia jadinii

C:Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway

F:1/Modified site: acetylated amino end (Ser) #status experimental

OY 5 sf 6
||
Db 4 SF 5

RESULT 7

JS0316

leucokinin VI - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0316

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropi

A:Reference number: JS0315

A:Accession: JS0316

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyrogutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

OY 5 sf 6
||
Db 3 SF 4

RESULT 8

A23967

leucopyrokinin - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 11-Jul-1997

C:Accession: A23967

R.Nachman, R.J.; Holman, G.M.; Cook, B.J.
Biochem. Biophys. Res. Commun. 137, 936-942, 1986
A:Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure
A:Reference number: A23967; MUID:86269041
A:Accession: A23967

A:Molecule type: protein
A:Residues: 1-8 <NAC>

C:Keywords: amidated carboxyl end: neuropeptide; pyroglutamic acid
F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental
F8/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 3 SF 4

RESULT 9

D47393 neuropeptide callatostactin 4 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria

C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C:Accession: D47393

R:Dive, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A:Title: Callatostactins: neuropeptides from the blowfly Calliphora vomitoria with sequen

A:Reference number: A47393; MUID:93211980

A:Accession: D47393

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <DUV>

A:Experimental source: thoracic ganglia

A:Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 5 SF 6

RESULT 10
A42057 fibroblast growth factor receptor 1, secreted - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999

C:Accession: A42057

R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.

Mol. Cell. Biol. 12, 82-88, 1992

A:Title: Differential splicing in the extracellular region of fibroblast growth factor r

A:Reference number: A42057; MUID:92107200

A:Accession: A42057

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <MER>

A:Cross-references: GB:M80363

C:Keywords: growth factor receptor

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 5 SF 6

RESULT 11

B57444 neuropeptide Grb-AST B2 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)

C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996

C:Accession: B57444

R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the

A:Reference number: A57444; MUID:95403341

A:Accession: B57444

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 2 WR 3

RESULT 12

C57444 neuropeptide Grb-AST B3 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)

C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996

C:Accession: C57444

R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the

A:Reference number: A57444; MUID:95403341

A:Accession: C57444

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 2 WR 3

RESULT 13

PT0315 Ig heavy chain CRD3 region (clone 6-109) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0315

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0315

A:Molecule type: DNA

A:Residues: 1-9 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 7 sf 8

RESULT 14

JC1367
thyroiberin potentiating neuropeptide - bovine
N/Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating
C/Species: Bos primigenius taurus (cattle)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1997
C/Accession: JC1367
R/Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.
Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992
A/Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine
A/Reference number: JC1367; MUID:93111999
A/Accession: JC1367
A/Molecule type: protein
A/Residues: 1-10 <BUL>
A/Experimental source: hypothalamus
C/Comment: This neuropeptide corresponds to a region of the rat thyroiberin precursor
C/Function:
A/Description: potentiates thyroiberin-induced thyrotropin secretion
C/Superfamily: thyroiberin precursor
C/Keywords: hypothalamus; neuropeptide

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 1 sf 2

RESULT 15

JN0024
neurokinin A - chicken
C/Species: Gallus gallus (chicken)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000
C/Accession: JN0024
R/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A/Reference number: JN0023; MUID:88204263
A/Accession: JN0024
A/Molecule type: protein
A/Residues: 1-10 <CON>
C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
F/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 5 sf 6

RESULT 16

D60787
sperm-activating peptide (Ser-1, Ala-3, Gly-5 speract) - sea urchin (Hemacentrotus pulch
C/Species: Hemacentrotus pulcherrimus
C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C/Accession: D60787
R/Suzuki, N.; Kajitani, H.; Nomura, K.; Gabbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H
Comp. Biochem. Physiol. B 89, 687-693, 1988
A/Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentro
A/Reference number: A60787; MUID:88242184

A/Accession: D60787
A/Molecule type: protein
A/Residues: 1-10 <SU>
C/Comment: This oligopeptide from egg jelly is one of several from this species, all
at shows some, but not absolute, species restriction.
C/Superfamily: unassigned animal peptides

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 1 sf 2

RESULT 17

S23307
neurokinin A - rainbow trout
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C/Accession: S23307
R/Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A/Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A/Reference number: S23186; MUID:92298992
A/Accession: S23307
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <JEN>
C/Superfamily: unassigned animal peptides

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 5 sf 6

RESULT 18

S23186
neurokinin A - Atlantic cod
C/Species: Gadus morhua (Atlantic cod)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C/Accession: S23186
R/Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A/Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A/Reference number: S23186; MUID:92298992
A/Accession: S23186
A/Molecule type: protein
A/Residues: 1-10 <JEN>
A/Experimental source: brain
C/Function:
A/Description: may play a physiological role in the regulation of cardiovascular and
A/Note: neurokinin A is derived by post-translational processing of preprotachykinin
C/Superfamily: unassigned animal peptides
C/Keywords: neuropeptide; amidated carboxyl end; tachykinin
F/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 5 sf 6

RESULT 19
B61033
ranatachykinin B - bullfrog
C:/Species: Rana catesbeiana (bullfrog)
C:/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:/Accession: B61033; JE0427
R:/Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A:/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine
A:/Reference number: A61033
A:/Accession: B61033
A:/Molecule type: protein
A:/Residues: 1-10 <KAN>
R:/Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A:/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine
A:/Reference number: JE0426; MUID:91254337
A:/Accession: JE0427
A:/Molecule type: protein
A:/Residues: 1-10 <KOZ>
C:/Superfamily: unassigned animal peptides
C:/Keywords: amidated carboxyl end; neuropeptide
F:/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
II
Db 5 sf 6

RESULT 20
C61033
ranatachykinin C - bullfrog
C:/Species: Rana catesbeiana (bullfrog)
C:/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:/Accession: C61033; JE0428
R:/Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A:/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine
A:/Reference number: A61033
A:/Accession: C61033
A:/Molecule type: protein
A:/Residues: 1-10 <KAN>
R:/Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A:/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine
C:/Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:/Accession: S38305
R:/Kamemura, K.; Furutachi, Y.; Umekawa, H.; Takahashi, T.
Biochim. Biophys. Acta 1158, 181-188, 1993
A:/Title: Purification and characterization of novel lectins from Great Northern bean, C:/Keywords: amidated carboxyl end; neuropeptide
F:/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
II
Db 5 sf 6

RESULT 21
S27178
neurokinin A-related peptide - laughing frog
C:/Species: Rana ridibunda (laughing frog)

C:/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:/Accession: S27178
R:/Wang, Y.; Badgery-Parker, T.; Lovas, S.; Chartrel, N.; Vaudry, H.; Burcher, E.; Con Biochem. J. 287, 827-832, 1992
A:/Title: Primary structure and receptor-binding properties of a neurokinin A-related A:/Reference number: S27178; MUID:93075037
A:/Accession: S27178
A:/Status: preliminary
A:/Molecule type: protein
A:/Residues: 1-10 <KAN>
C:/Superfamily: unassigned animal peptides

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
II
Db 5 sf 6

RESULT 22
I40032
type protein - Bacillus amyloliquefaciens (fragment)
C:/Species: Bacillus amyloliquefaciens
C:/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 15-Oct-1999
C:/Accession: I40032
R:/Yoshimura, K.; Uemura, J.; Seki, T.; Oshima, Y.
J. Bacteriol. 159, 905-912, 1984
A:/Title: Construction of a promoter-probe vector for Bacillus subtilis host by using A:/Reference number: I40032; MUID:8506754
A:/Accession: I40032
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: DNA
A:/Residues: 1-10 <RES>
A:/Cross-references: GB:K02661; MID:g143775; PIDN:AB05353.1; PID:g143776

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
II
Db 5 sf 6

RESULT 23
S38305
lectin GNL2 alpha chain - kidney bean (fragment)
C:/Species: Phaseolus vulgaris (kidney bean)
C:/Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:/Accession: S38305
R:/Kamemura, K.; Furutachi, Y.; Umekawa, H.; Takahashi, T.
Biochim. Biophys. Acta 1158, 181-188, 1993
A:/Title: Purification and characterization of novel lectins from Great Northern bean, A:/Reference number: S38304; MUID:94002183
A:/Accession: S38305
A:/Status: preliminary
A:/Molecule type: protein
A:/Residues: 1-10 <KAN>

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
II
Db 5 sf 6

RESULT 24

D28027

Protein P7 - curled-leaved tobacco (fragment)

C:Species: Nicotiana glumabaginifolia (curled-leaved tobacco)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C:Accession: D28027

R:Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-

A:Reference number: A94167

A:Accession: D28027

A:Molecule type: protein

A:Residues: 1-10 <BAU>

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 5 SF 6

RESULT 25

A43977

FMRFamide-like protein - tobacco hornworm

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 17-Mar-1999

C:Accession: A43977

R:Kingan, T.G.; Teplov, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;

Peptides 11, 849-856, 1990

A:Title: A new peptide in the FMRFamide family isolated from the CNS of the hawkmoth, M.

A:Reference number: A43977; MUID:91045350

A:Accession: A43977

A:Molecule type: protein

A:Residues: 1-10 <KIN>

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
||
Db 6 SF 7

Search completed: January 14, 2002, 07:58:37
Job time: 387 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:08:23 : Search time 30.66 Seconds
(without alignments)
9.567 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 8
Sequence: 1 wrxsflxg 8

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	25.0	5	1	AL14-CARMA	P81817 carcinus ma
2	25.0	7	1	MSCL-SALTY	P39446 salmonella
3	25.0	7	1	WMA1-ACHFU	P35919 achatinia fu
4	25.0	8	1	AL15-CARMA	P81818 carcinus ma
5	25.0	8	1	AL17-CARMA	P81820 carcinus ma
6	25.0	8	1	AL18-CARMA	P81821 carcinus ma
7	25.0	8	1	AL13-CYDPO	P82154 cydia pomon
8	25.0	8	1	AL14-CALVO	P41840 calliphora
9	25.0	8	1	AL14-CYDPO	P82155 cydia pomon
10	25.0	8	1	ICK4-LEUMA	P21143 leucophaea
11	25.0	8	1	ICK6-LEUMA	P19988 leucophaea
12	25.0	9	1	LPK-LEUMA	P13049 leucophaea
13	25.0	9	1	FARP-CALSI	P8495 callinectes
14	25.0	10	1	AL19-CARMA	P81822 carcinus ma
15	25.0	10	1	FARP-MANSE	P18523 manduca sex
16	25.0	10	1	RCA-PINPS	P81084 pinus pinas
17	25.0	10	1	TKNB-CHICK	P19851 gallus gall
18	25.0	10	1	TKNB-ONCMY	P28500 oncorhynch
19	25.0	10	1	TKNB-RANCA	P22689 rana catesb
20	25.0	10	1	TKNB-RANRI	P29135 rana ridibu
21	25.0	10	1	TKNB-RANCA	P22690 rana catesb
22	25.0	11	1	CEPI-ACHFU	P22790 achatinia fu
23	25.0	11	1	MHB1-KLEPN	P80580 klebsiella
24	25.0	12	1	CXAL-CONIM	P50983 conus imper
25	25.0	12	1	V25K-MSSV	P82004 white spot
26	25.0	12	1	CALI-CALGI	P22584 caltropops
27	25.0	14	1	LECB-PSOSC	P22584 psophocarp
28	25.0	14	1	LPW-CITFR	P30366 citrobacter
29	25.0	14	1	LPW-ECOLI	P30353 escherichia
30	25.0	14	1	LPW-ECOLI	P30354 salmonella
31	25.0	15	1	ASPI-LACSN	P82648 lactobacill
32	25.0	15	1	ATP2-PINPS	P81663 pinus pinas
33	25.0	15	1	CBPB-PROAT	P19628 protopteris

ALIGNMENTS

RESULT 1									
ID	AL14-CARMA	STANDARD;	PRT;	5 AA.					
AC	P81817;								
DT	30-MAY-2000 (Rel. 39, Created)								P19920 pseudomonas
DT	30-MAY-2000 (Rel. 39, Last sequence update)								P12801 anas platyr
DT	30-MAY-2000 (Rel. 39, Last annotation update)								P3536 HS11-PINPS
DE	CARCINUSSTATIN 14.								P3737 LEC1-PSOSC
OS	Carcinus maenas (Common shore crab) (Green crab).								P3838 LEC2-PSOSC
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;								P3939 LEC3-PSOSC
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;								P4040 MLT-ONCKE
OC	Eubrachyura; Portunoidae; Portunidae; Carcinus.								P4141 UC08-MA1ZE
OX	NCBI_TaxID=6759;								P4242 CAT9-FASHE
RN	[1]								P4343 HTPG-ACICA
RP	SEQUENCE.								P4444 R1PK-TRIKI
RC	TISSUE=Cerebral ganglion, and Thoracic ganglion;								P4545 VPR-HVIC4
RX	MEDLINE=98121193; PubMed=9461295;								P4646 VPR-HVIC4
RA	Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,								P4747 LPW-HV1S3
RT	Thorppe A.;								P4848 LPW-CORGL
RT	Isolation and identification of multiple neuropeptides of the								P4949 UP41-UP41N
RL	allatostatin superfamily in the shore crab Carcinus maenas.;								P5050 GAL5-SALTY
RL	Eur. J. Biochem. 250:727-734(1997).								
CC	-1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.								
CC	-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.								
KW	Neuropeptide; Amidation; Multigene family.								
FT	MOD.RES 5								
FT	AMIDATION (POTENTIAL).								
SEQ	SEQUENCE 5 AA: 586 MW: 672879D5AB300000 CRC64;								
Query Match 25.0%; Score 2; DB 1; Length 5;									
Best local similarity 100.0%; Pred. No. 1e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	5 sf 6								
DB	2 SF 3								
RESULT 2									
ID	MSCL-SALTY	STANDARD;	PRT;	7 AA.					
AC	P39446;								
DT	01-FEB-1995 (Rel. 31, Created)								
DT	01-FEB-1995 (Rel. 31, Last sequence update)								
DT	20-AUG-2001 (Rel. 40, Last annotation update)								
DE	LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL (FRAGMENT).								
GN	MSCL.								
OS	Salmonella typhimurium.								
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;								
OC	Salmonella.								
OX	NCBI_TaxID=602;								

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94357168; PubMed=8076592;
 RA Parra-Lopez C., Lin R., Aspedon A., Groisman E.A.;
 RT "A Salmonella protein that is required for resistance to
 RT antimicrobial peptides and transport of potassium."
 RL EMBL J. 13:3964-3972(1994).
 CC -1- FUNCTION: CHANNEL THAT OPENS IN RESPONSE TO STRETCH FORCES IN THE
 CC MEMBRANE LIPID BILAYER. MAY PARTICIPATE IN THE REGULATION OF
 CC OSMOTIC PRESSURE CHANGES WITHIN THE CELL (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOPENTAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MSCL FAMILY.
 CC -----
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 DR EMBL: X80501; CA556664.1; -.
 DR StyGene; SG10531; mscL.
 DR InterPro; IPR001185; MSCL.
 DR PROSITE; PS01327; MSCL; PARTIAL.
 KM Transmembrane; Inner membrane; Ionic channel.
 FT NON_TER
 SQ SEQUENCE 7 AA; 901 MW; 69CB133059D5B6F0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 Db 2 sf 3
 RESULT 3
 ID WWAL_ACHFU STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WWAMIDE-1.
 OS Achatina fulica (giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxId=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Muneeoka Y., Kobayashi M., Nomoto K.;
 RT "Wwamide-1, -2 and -3, novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica."
 RL FEBS Lett. 323:104-108(1993).
 CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
 CC PIR: S33245; S33245.
 CC DR Neuuropeptide; Amidation.
 KW MOD.RES 7
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 Db 1 wr 2

RESULT 4
 ID AL15_CARMA STANDARD; PRT; 8 AA.
 AC P81818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 15.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OX Eubrachyura; Portunoidae; Portunidae; Carcinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuuropeptide; Amidation; Multigene family.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 Db 5 sf 6
 RESULT 5
 ID AL17_CARMA STANDARD; PRT; 8 AA.
 AC P81820;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 17.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OX Eubrachyura; Portunoidae; Portunidae; Carcinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuuropeptide; Amidation; Multigene family.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 5 sf 6

RESULT 6

ALL3_CARMA STANDARD: PRT: 8 AA.
ID ALL3_CARMA
AC P81821;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTATIN 18.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxId=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
RT -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 5 sf 6

RESULT 7

ALL3_CYPDPO STANDARD: PRT: 8 AA.
ID ALL3_CYPDPO
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATIN 3.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxId=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Duvéy M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 926 MW; C82879D5AB477415 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 5 sf 6

RESULT 8

ALL4_CALVO STANDARD: PRT: 8 AA.
ID ALL4_CALVO
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxId=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duvé H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
Thorpé A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatin."
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duvé H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatin in
the blowfly Calliphora vomitoria."
RL Cell Tissue Res. 276:367-379(1994).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEREBRAL
COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
SYSTEM AND INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR: D47393; D47393.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 5 sf 6

RESULT 9

ALL4_CYPDPO STANDARD: PRT: 8 AA.
ID ALL4_CYPDPO
AC P82155;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATIN 4.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pterygota: Neoptera: Endopterygota: Lepidoptera: Glossata: Ditrysia:
OC Tortricidae: Tortricidae: Olethreutinae: Cydia.
OX NCBI_TaxID=82600;
RN
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RT "Lepidopteran peptides of the allatostatin superfamily.";
RT Peptides 18:1301-1309(1997).
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 910 MW: 922879D5AB47740D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
DB 5 SF 6

RESULT 10
LCK4_LEUMA STANDARD; PRT; 8 AA.
ID LCK4_LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RT Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 906 MW: DC6365B1E9D5BD4A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
DB 3 SF 4

RESULT 11
LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).

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OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RT Comp. Biochem. Physiol. 88C:27-30(1987).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOTHIS ZEAE ADIPOKINETIC HORMONE.
DR PIR: JS0316; JS0316.
KW Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 8
SQ SEQUENCE 8 AA: 935 MW: 9D6365B1E9D5A5A6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
DB 3 SF 4

RESULT 12
LPR_LEUMA STANDARD; PRT; 8 AA.
ID LPR_LEUMA
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE LEUCOPYROKININ (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RT Leucopyrokinin: structure-function studies.";
RT Comp. Biochem. Physiol. 85C:219-224(1986).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RT neuropeptide isolated from the cockroach, Leucophaea maderae.";
RT Comp. Biochem. Physiol. 85C:219-224(1986).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
CC PENTAPEPTIDE FRAGMENT FTPTPL.
CC -I- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 1
FT MOD_RES 1
PYROLIDONE CARBOXYLIC ACID.

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FT MOD_RES 8 AA: 8 MW: 92341771A9D5A1B6 CRC64;
SQ SEQUENCE

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
Db 3 SF 4

RESULT 13
FARP_CALSI STANDARD; PRT: 9 AA.
ID FARP_CALSI
AC P38495;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxId=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krajinak K.G.;
RT "The identification and structure-activity relations of a
cardiacactive FMRFamide-related peptide from the blue crab Callinectes
sapidus.";
RT Peptides 12:1295-1302(1991).
CC -1- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA: 1159 MW: 134F0729D5A4045B CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
Db 5 SF 6

RESULT 14
AL19_CARMA STANDARD; PRT: 10 AA.
ID AL19_CARMA
AC P81822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 19.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxId=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Dure H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RT Eur. J. Biochem. 250:727-734(1997).

CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 10
SQ SEQUENCE 10 AA: 1101 MW: 96687CD5AB569AB1 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
Db 7 SF 8

RESULT 15
FARP_MANSE STANDARD; PRT: 10 AA.
ID FARP_MANSE
AC P18523;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxId=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045350; PubMed=2235684;
RA Kingan T.G., Teplov D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
RA Hunt D.F.;
RT "A new peptide in the FMRFamide family isolated from the CNS of the
hawkmoth, Manduca sexta.";
RT Peptides 11:849-856(1990).
CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
FLIGHT BEHAVIOR PATTERNS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
CC PIR: A43977; A43977.
DR Amidation; Neuropeptide.
KW MOD_RES 1
FT MOD_RES 10
SQ SEQUENCE 10 AA: 1247 MW: D3C45229D5B1F2D2 CRC64;

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
Db 6 SF 7

RESULT 16
RCA_PINPS STANDARD; PRT: 10 AA.
ID RCA_PINPS
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE RIBULOSE BIPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE (RUBISCO
ACTIVASE) (RA) (WATER STRESS RESPONSIVE PROTEIN 4) (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxId=71647;

RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrmann N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrmann N., Kremer A.,
RT Frigerio J.-M., Plomion C.;
RT Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CARBOXYLASE/OXGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBOXYMATE STRUCTURE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA (BY SIMILARITY).
CC -1- INDUCTION: BY WATER-STRESS.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KM Chloroplast; ATP-binding.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 1 SF 2

RESULT 17
TKNB_CHICK STANDARD; PRT; 10 AA.
AC P19851;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ A (SUBSTANCE K) (NEUROMEDIN L).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: JN0024; JN0024.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ-1.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5BAB1 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 sf 6
||
Db 5 SF 6

RESULT 18
TKNB_ONCMY STANDARD; PRT; 10 AA.
AC P28500;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ A (SUBSTANCE K) (NEUROMEDIN L).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022, 8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: S23186; S23186.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ-1.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 5 SF 6

RESULT 19
TKNB_RANCA STANDARD; PRT; 10 AA.
AC P22689;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RANATACHYKININ B (RTK B).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.

RC TISSUE=Intestine; PubMed:8210506;
RX MEDLINE=94023216; Kozawa H., Hino J., Minamino N., Matsuo H.;
RA "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT Intestine.";
RL Regul. Pept. 46:81-88(1993).
-1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
-1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: JE0427; JE0427.
DR PIR: B61033; B61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA: 1210 MW: 917E556B59D5BAA5 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
DB 5 sf 6

RESULT 20
TKNB_RANRI STANDARD; PRT; 10 AA.
AC P29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NEUROKININ A.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=93075037; PubMed=1332683;
RA Wang Y., Badger-Parker T., Lovas S., Chitrel N., Vaudry H.,
RA Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-
related peptide from frog gut.";
RL Biochem. J. 287:827-832(1992).
-1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
-1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: S27178; S27178.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA: 1160 MW: 526B407059D5BAA7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
DB 5 sf 6

RESULT 21

TKNC_RANCA STANDARD; PRT; 10 AA.
ID TKNC_RANCA
AC P22690;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RANATACHYKININ C (RTK C).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=8210506;
RX MEDLINE=94023216; Kozawa H., Hino J., Minamino N., Matsuo H.;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT Intestine.";
RL Regul. Pept. 46:81-88(1993).

-1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
-1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: JE0428; JE0428.
DR PIR: C61033; C61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA: 1086 MW: 3A3A407059D5BDC7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
DB 5 sf 6

RESULT 22
CEP1_ACHFU STANDARD; PRT; 11 AA.
ID CEP1_ACHFU
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
-1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE

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CC      MOVEMENT OF ACHATINA.
CC      -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR      PIR: A34662; A34662.
KM      Hormone: Amidation.
FT      MOD_RES      11
SQ      SEQUENCE      11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match      25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 wr 2
        11
        5 WR 6
        6

RESULT 23
MHBI_KLEPN      STANDARD;      PRT;      11 AA.
ID MHBI_KLEPN
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MALEYLPYRVUATE ISOMERASE (EC 5.2.1.4) (FRAGMENT).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; Pubmed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;
RT "In vitro formation of a catabolic plasmid carrying Klebsiella
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
RT hydroxybenzoate."
RL Microbiology 142:2115-2120(1996).
CC -1- CATALYTIC ACTIVITY: 3-MALEYLPYRVUATE = 3-FUMARYLPYRVUATE.
KM Isomerase.
FT NON_TER      11
SQ SEQUENCE      11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match      25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      5 sf 6
        11
        5 sf 6
        6

RESULT 24
CXAL_CONIM      STANDARD;      PRT;      12 AA.
ID CXAL_CONIM
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA-CONOTOXIN IMI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_Taxid=35631;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RP TISSUE=Venom;
RX MEDLINE=9426689; Pubmed=8206995;
RA McGrath J.M., Yoshikami D., Mabe E., Nielsen D.B., Rivier J.E.,
RA Gray W.R., Olivera B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin ImI."

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RL      J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; Pubmed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
RA McGrath J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors."
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; Pubmed=10194298;
RA Rogers J.P., Luglinbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
RA Wemmer D.E.;
RT "NMR solution structure of alpha-conotoxin ImI and comparison to
RT other conotoxins specific for neuronal nicotinic acetylcholine
RT receptors."
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; Pubmed=10050774;
RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
RA Mehlhess C., Tselin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
RT scaffold in snail and snake toxins recognizing neuronal nicotinic
RT acetylcholine receptors."
RL FEBS Lett. 444:275-280(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; Pubmed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin ImI by 1H nuclear magnetic
RT resonance."
RL J. Med. Chem. 42:2364-2372(1999).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
CC RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
CC WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGET NEURONAL
CC NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
CC WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
CC WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
CC ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-7/BETA-4,
CC ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
CC PDB: 1IM1, 15-JUN-99.
DR PDB: 1IM1, 23-APR-99.
DR PDB: 1CNI, 27-MAY-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT DISULFID      2
FT DISULFID      3
FT MOD_RES      12
SQ SEQUENCE      12 AA; 1357 MW; 9C29CEA545A4176A CRC64;

Query Match      25.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 wr 2
        11
        10 WR 11
        11

RESULT 25
V25K_WSSV      STANDARD;      PRT;      12 AA.
ID V25K_WSSV
AC P82004;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 25 KDA STRUCTURAL POLYPROTEIN (FRAGMENT).

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OS White spot syndrome virus (WSSV).
 OC Viruses; Unassigned viruses.
 OX NCBI_TaxID:92652;
 RN [1]
 RP SEQUENCE:
 RC STRAIN-South Carolina;
 RX MEDLINE:20214217; PubMed:10752552;
 RA Wang Q., Poulos B.T., Lightner D.V.;
 RT "Protein analysis of geographic isolates of shrimp white spot syndrome
 virus.";
 RL Arch. Virol. 145:263-274(2000).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA: 1283 MW: C5409AD9ECB731A9 CRC64:

Query Match 25.0%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 11
 DB 4 sf 5

Search completed: January 14, 2002, 08:08:23
 Job time: 708 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:07:35 ; Search time 81.98 Seconds
(without alignments)
14.274 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 8
Sequence: 1 wrxsfxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

1: SPTRMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_organella:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	23	6	Q9TRC6	Q9TRC6 canis famli
2	37.5	56	2	Q51622	Q51622 escherichia
3	37.5	144	8	Q9G8X4	Q9G8X4 toxosoma c
4	37.5	153	8	Q9T5K3	Q9T5K3 haemochus
5	37.5	271	5	Q9N7P2	Q9N7P2 leishmania
6	37.5	290	8	Q9Z2G6	Q9Z2G6 phyllotis d
7	37.5	297	8	Q9TDB9	Q9TDB9 agelatus ru
8	37.5	347	8	Q63418	Q63418 habia rubic
9	37.5	353	5	Q9NNI3	Q9NNI3 leishmania
10	37.5	379	8	Q9TF74	Q9TF74 spermophila
11	37.5	385	5	Q9GWR8	Q9GWR8 leishmania
12	37.5	413	5	Q44100	Q44100 drosophila
13	37.5	475	8	Q9TID6	Q9TID6 pieris flori
14	37.5	510	8	Q9BAX6	Q9BAX6 gongora gra
15	37.5	510	8	Q9BAX0	Q9BAX0 gongora sph
16	37.5	698	8	Q32665	Q32665 nicodemia d
17	25.0	7	2	Q07354	Q07354 synchococc
18	25.0	8	4	P87225	P87225 saccharomyc
19	25.0	8	4	Q9HCQ0	Q9HCQ0 homo sapien

20	2	25.0	8	5	P82685	P82685 periplaneta
21	2	25.0	8	5	P82686	P82686 periplaneta
22	2	25.0	8	5	P82687	P82687 periplaneta
23	2	25.0	8	11	Q62721	Q62721 rattus norv
24	2	25.0	9	2	P72345	P72345 pseudomona
25	2	25.0	9	4	P78484	P78484 homo sapien
26	2	25.0	9	4	Q9BQ74	Q9BQ74 homo sapien
27	2	25.0	9	11	P97889	P97889 rattus norv
28	2	25.0	9	12	Q67605	Q67605 squash leaf
29	2	25.0	9	12	Q67606	Q67606 squash leaf
30	2	25.0	10	2	Q44693	Q44693 bacillus am
31	2	25.0	10	2	Q9L5W6	Q9L5W6 liberibacte
32	2	25.0	10	6	Q9TRC1	Q9TRC1 bos taurus
33	2	25.0	10	8	P92576	P92576 bipes bipor
34	2	25.0	10	12	Q66190	Q66190 avian intest
35	2	25.0	10	12	Q84140	Q84140 influenza a
36	2	25.0	11	2	Q56972	Q56972 yersinia pe
37	2	25.0	11	8	Q9G649	Q9G649 otocryptis
38	2	25.0	11	8	Q9G646	Q9G646 sitana pont
39	2	25.0	11	8	Q9G643	Q9G643 calotes cal
40	2	25.0	11	8	Q9G640	Q9G640 calotes ce
41	2	25.0	11	8	Q9G634	Q9G634 calotes nig
42	2	25.0	11	8	Q9G631	Q9G631 calotes mys
43	2	25.0	11	8	Q9G628	Q9G628 calotes ver
44	2	25.0	11	8	Q9G625	Q9G625 calotes bronchocela
45	2	25.0	11	8	Q9G601	Q9G601 bronchocela
46	2	25.0	11	8	Q9G522	Q9G522 pseudocalc
47	2	25.0	11	8	Q9G5Y9	Q9G5Y9 pseudocalic
48	2	25.0	11	8	Q9G368	Q9G368 draco blati
49	2	25.0	11	8	Q9G365	Q9G365 calotes emm
50	2	25.0	12	4	Q9UMZ8	Q9UMZ8 homo sapien

ALIGNMENTS

RESULT 1
ID Q9TRC6 PRELIMINARY: PRT: 23 AA.
AC Q9TRC6; 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE CYTOCHROME P450 DBP-1 ISOFORM (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=94198820; PubMed=8185738;
RA Shiraga T., Iwasaki K., Nozaki K., Tamura T., Yamazoe Y., Kato R.,
RA Takanaoka A.;
RT "Isolation and characterization of four cytochrome P450 isozymes from
untreated and phenobarbital-treated beagle dogs.";
RL Biol. Pharm. Bull. 17:22-28(1994).
SQ SEQUENCE 23 AA: 2638 MW: AF8688BFF8029F8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
DB 6 SFXG 9
RESULT 2
ID Q51622 PRELIMINARY: PRT: 56 AA.
AC Q51622;
DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE MOB9 ORF.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85261261; PubMed=2991225;
 RA Chan P.T., Ohmori H., Tomizawa J., Lebowitz J.;
 RT "Nucleotide sequence and gene organization of ColE1 DNA."
 RL J. Biol. Chem. 260:8925-8935(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89210827; PubMed=3149585;
 RA Stirling C.J., Szatmari G., Stewart G., Smith M.C., Sherratt D.J.;
 RT "The arginine repressor is essential for plasmid-stabilizing site-
 specific recombination at the ColE1 *cer* locus."
 RL EMBO J. 7:4389-4395(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91123196; PubMed=1846858;
 RA Inoue N., Uchida H.;
 RT "Transcription and initiation of ColE1 DNA replication in Escherichia
 coli K-12."
 RL J. Bacteriol. 173:1208-1214(1991).
 DR EMBL: J01566; AAB59139.1; -.
 KW Plasmid.
 SQ SEQUENCE 56 AA; 6254 MW; 35ABA84389978EF8 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 ||||
 Db 26 SFXG 29

RESULT 3
 O968X4 PRELIMINARY; PRT; 144 AA.
 AC O968X4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN CYTB.
 OS Toxostoma curvirostre.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.
 OX NCBI_TaxID=99878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBTH52NM;
 RA Zink R.M., Blackwell-Rago R.C.;
 RT "Species limits and recent population history of the Curve-billed
 Thrasher."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX) WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
 DR EMBL: AF287539; AAG31529.1; -.

DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF00033; Cytochrome_b_N; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA; 15972 MW; 4B0320E8A892724D CRC64;

Query Match 37.5%; Score 3; DB 8; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 ||||
 Db 107 SFXG 110

RESULT 4
 O975K3 PRELIMINARY; PRT; 153 AA.
 AC O975K3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT 4 (FRAGMENT).
 GN NDA.
 OS Haemomonchus placel.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
 OX NCBI_TaxID=6290;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083438; PubMed=9866206;
 RA Blouin M.S., Yowell C.A., Courtney C.H., Dame J.B.;
 RT "Substitution bias, rapid saturation, and the use of mtDNA for
 nematode systematics."
 RL Mol. Biol. Evol. 15:1719-1727(1998).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CHAINS.
 DR EMBL: AF070801; AAC98219.1; -.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1; 1.
 KW Mitochondrion; NAD; Oxidoreductase; ubiquinone.
 FT NON_TER 1
 SQ SEQUENCE 153 AA; 18040 MW; 726825467487DB8F CRC64;

Query Match 37.5%; Score 3; DB 8; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 ||||
 Db 119 SFXG 122

RESULT 5
 O9N7P2 PRELIMINARY; PRT; 271 AA.
 AC O9N7P2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE POSSIBLE PROBABLE ECF-FAMILY SIGMA FACTOR (FRAGMENT).
 GN IM28.157.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]

RC SEQUENCE FROM N.A.
RA STRAIN-FRIEDLIN;
RL Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
DR Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL390935; CAC00895.1; -
FT NON_TER 1
FT NON_TER 271 1
SQ SEQUENCE 271 AA; 30356 MW; B59E63D0D321EFF4 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 271;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
||||
DB 154 SFXG 157

RESULT 6
ID 09ZG6 PRELIMINARY; PRT; 290 AA.
AC 09ZG6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS *Phyllotis darwini* (Darwin's leaf-eared mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Phyllotis.
OX NCBI_TaxID=56232;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-JNM NK27558;
RC Stepan S.J.;
RT "Phylogenetic relationships and species limits within *Phyllotis*
RT (Rodentia: Sigmodontinae): concordance between mtDNA sequence and
RT morphology.";
RL J. Mammal. 79:0-0(1998).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U86819; AD12338.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1.1.
DR Pfam: PF00033; cytochrome_b_n.1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME.1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN.1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 290 1
SQ SEQUENCE 290 AA; 32572 MW; BCEAF9D0DBED2771 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 290;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
||||
DB 136 SFXG 139

RESULT 7
ID 09TDH9 PRELIMINARY; PRT; 297 AA.
AC 09TDH9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS *Agelaius ruficapillus*.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Icteridae; Agelaius.
OX NCBI_TaxID=84775;
RN [1]
RP SEQUENCE FROM N.A.
RA Lanyon S.M., Omland K.E.;
RT "A molecular phylogeny of the blackbirds (Icteridae): five lineages
RT revealed by cytochrome-b sequence data.";
RL Auk 116:629-639(1999).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF089009; AAF02229.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1.1.
DR Pfam: PF00033; cytochrome_b_n.1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME.1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN.1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 297 1
SQ SEQUENCE 297 AA; 33128 MW; 8B62C22882EE2ED5 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
||||
DB 100 SFXG 103

RESULT 8
ID 063418 PRELIMINARY; PRT; 347 AA.
AC 063418;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS *Habia rubica*.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
OC Emberizinae; Habia.
OX NCBI_TaxID=62201;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98086775; PubMed=9417892;
RA Burns K.J.;
RT "Molecular systematics of tanagers (Thraupinae): evolution and
RT biogeography of a diverse radiation of neotropical birds.";
RL Mol. Phylogenet. Evol. 8:334-348(1997).

CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: O₂(2) + 2 FERRICYTOCHROME C = O + 2
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF006233; AAC05054.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR InterPro: IPR001600; Galanin.
DR Pfam: PF00032; cytochrome_b_c_1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PRINTS: PR00273; GALANIN.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
SO SEQUENCE 347 AA; 38616 MW; 81208E4E94D37A8E CRC64;

Query Match 37.5%; Score 3; DB 8; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
|||
DB 107 SFXG 110

RESULT 9
O9NNI3 PRELIMINARY; PRT; 353 AA.
AC O9NNI3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POSSIBLE 75 KDA INVARIANT SURFACE GLYCOPROTEIN (FRAGMENT).
GN IM15.181.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL160371; CAC00227.1; -
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38247 MW; 3E427E2171CC7F24 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
|||
DB 258 SFXG 261

RESULT 10
O9TF74 PRELIMINARY; PRT; 379 AA.
AC O9TF74;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE CYTOCHROME B.
GN CYTB.
OS Spermophilus erythrogenys (red-cheeked ground squirrel).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=99840;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S136;
RA Harrison R.G., Sherman P.W., Jensen E., Hoffmann R.S.,
RA Bogdanowicz S.M.;
RT "A molecular phylogeny of ground squirrels and prairie dogs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF157875; AAD50159.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c_1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
SO SEQUENCE 379 AA; 42795 MW; B0C35BAFE3118854 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 379;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
|||
DB 139 SFXG 142

RESULT 11
O9GWR8 PRELIMINARY; PRT; 385 AA.
AC O9GWR8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 43.0 KDA PROTEIN (FRAGMENT).
GN IM12.753.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL390114; CAC02470.1; -
DR InterPro: IPR001522; Desaturase.
DR PRINTS: PR00075; FACDSDSATRASE.
DR ProDom: PD002221; Desaturase; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 385
SQ SEQUENCE 385 AA; 43000 MW; A79EF6194CFA960A CRC64;

Query Match 37.5%; Score 3; DB 5; Length 385;

Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 sfxg 8
DB 247 SFXG 250

RESULT 12
ID 044100 PRELIMINARY; PRT: 413 AA.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
GN ENO.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RL Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
RA Genetica 0:0-0(1997).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COPACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF025805; AAB87890.1; -.
DR HSSP: P56252; 1PZ.
DR FlyBase: FBgn0023296; Dpse\Eno.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1 1
FT ACT_SITE 322 322 BY SIMILARITY.
FT METAL 334 334 MAGNESIUM (BY SIMILARITY).
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 44404 MW; 11414BCC18644A94 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 413;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 sfxg 8
DB 360 SFXG 363

RESULT 13
ID 0971D6 PRELIMINARY; PRT: 475 AA.
AC 0971D6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT).
GN RBCL.
OS Pteris floribunda.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Pteris.
OX NCBI_TaxID=49157;
RN [1]
RP SEQUENCE FROM N.A.
RA Kron K.A., Judd W.S., Crayn D.M.;
RT "Phylogenetic analyses of Andromedeae (Ericaceae subfam. Vaccinioideae).";
RL Am. J. Bot. 0:0-0(2000).
CC -1- FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE. (BY SIMILARITY).
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
DR EMBL: AF124577; AAF16882.1; -.
DR InterPro: IPR000685; Rubisco_large.
DR Pfam: PF00016; Rubisco_large_1.
DR PROSITE: PS00157; RUBISCO_LARGE; 1.
KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photorespiration.
SQ SEQUENCE 475 AA; 52495 MW; 76F3CA08A36481C1 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 sfxg 8
DB 61 SFXG 64

RESULT 14
ID 09BAX6 PRELIMINARY; PRT: 510 AA.
AC 09BAX6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MATURASE (FRAGMENT).
GN MATK.
OS Gongora gratulabunda.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Maxillarieae; Stanhopeinae;
OC Gongora.
OX NCBI_TaxID=125123;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitten M., Williams N.H., Chase M.W.;
RT "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinae: Combined molecular evidence.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF239478; AAK31875.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 510 510
SQ SEQUENCE 510 AA; 61288 MW; C70C056BA4F26B8E CRC64;

Query Match 37.5%; Score 3; DB 8; Length 510;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
 ||||
 Db 346 SFXG 349

RESULT 15

Q9BAX0 PRELIMINARY; PRT; 510 AA.
 AC O9BAX0; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE MATURASE (FRAGMENT).
 GN MATK.
 OS Gongora sphaerica.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 OC Epidendroideae; higher Epidendroideae; Maxillarieae; Stanhopeinae;
 OC Gongora.
 NCBI_TaxID=125126;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Whitten M., Williams N.H., Chase M.W.;
 RT "Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
 RT special emphasis on Stanhopeinae: Combined molecular evidence.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF239484; AAK31881.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT SEQUENCE 510 AA; 61361 MW; B03CD0D32738AAB3 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 510;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
 ||||
 Db 346 SFXG 349

RESULT 16

O32665 PRELIMINARY; PRT; 698 AA.
 AC O32665;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE NADH DEHYDROGENASE SUBUNIT (FRAGMENT).
 GN NDHF.
 OS Nicotiana glauca.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Scrophulariaceae; Nicotemia.
 NCBI_TaxID=28500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olmstead R.G., Reeves P.A.;
 RL Ann. Mo. Bot. Gard. 82:176-193(1995).
 CC -I- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
 CC -I- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CC CHAINS.
 DR EMBL; L36405; AAA84496.1; -.
 DR Mendel, 2471; Nicotiana glauca; 2471.
 DR InterPro; IPR001064; Crystalin.
 DR InterPro; IPR001750; Oxidored_q1.
 DR InterPro; IPR002128; Oxidored_q1.C.
 DR InterPro; IPR001516; Oxidored_q1.N.
 DR Pfam; PF00361; oxidored_q1; 1.
 DR Pfam; PF01010; oxidored_q1c; 1.

DR Pfam; PF00662; oxidored_q1.N; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Chloroplast; NAD; Oxidoreductase; Plastoquinone.
 FT NON_TER 1 1
 FT SEQUENCE 698 AA; 79217 MW; F4B4EBE4E7440A3D CRC64;

Query Match 37.5%; Score 3; DB 8; Length 698;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
 ||||
 Db 664 SFXG 667

RESULT 17

O07354 PRELIMINARY; PRT; 7 AA.
 AC O07354;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE NIFK (FRAGMENT).
 GN NIFK.
 OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothecae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen H.M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003700; AAC35193.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 7 AA; 849 MW; 7412C72A9D5B030 CRC64;

Query Match 25.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
 ||
 Db 2 SF 3

RESULT 18

P87225 PRELIMINARY; PRT; 8 AA.
 AC P87225;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE GIN11 PROTEIN (FRAGMENT).
 GN GIN11 OR YL065W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wedler H., Wedler E., Scharfe M., Wandt R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z73169; CAA97518.2; -.
 DR SGD; S0003988; GIN11.
 FT NON_TER 1 1
 FT SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 25.0%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 3 SF 4

RESULT 19
O9HCOO PRELIMINARY; PRT; 8 AA.
AC O9HCOO:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE 10A7 (PDE10A7) (FRAGMENT).
HSPDE10A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10998054;
RA Fujishige K., Kotera J., Yuasa K., Omori K.;
RT "The human phosphodiesterase PDE10A gene. Genomic organization and evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 267:5943-5951(2000).
DR EMBL; AB041779; BAB16368.1; -.
FT NOI TER 8 8
SQ SEQUENCE 8 AA; 966 MW; FDA819D5A6C76446 CRC64;

Query Match 25.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 5 SF 6

RESULT 20
P82685 PRELIMINARY; PRT; 8 AA.
ID P82685;
AC P82685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RT Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 25.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 3 SF 4

RESULT 21
P82686 PRELIMINARY; PRT; 8 AA.
ID P82686
AC P82686;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RT Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

Query Match 25.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 3 SF 4

RESULT 22
P82687 PRELIMINARY; PRT; 8 AA.
ID P82687
AC P82687;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RT Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 25.0%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 ||
 Db 3 sf 4

RESULT 23
 ID 062721 PRELIMINARY; PRT; 8 AA.
 AC 062721;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROHIBITIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FISHER;
 RX MEDLINE=95331633; PubMed=7607556;
 RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
 RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
 RA McCullung J.K.;
 RT "Regions of evolutionary conservation between the rat and human
 RT prohibitin-encoding genes.";
 RL Gene 158:291-294(1995).
 DR EMBL; U17178; AAA86692.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A1376 CRC64;

Query Match 25.0%; Score 2; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 ||
 Db 2 wr 3

RESULT 24
 ID P72345 PRELIMINARY; PRT; 9 AA.
 AC P72345;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
 GN TABA.
 OS Pseudomonas syringae.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=317;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93167809; PubMed=7679566;
 RA Barta T.M., Kinschert T.G., Uchytil T.F., Willis D.K.;
 RT "DNA sequence and transcriptional analysis of the tbaA gene required
 RT for tabtoxin biosynthesis by Pseudomonas syringae.";
 RL Appl. Environ. Microbiol. 59:458-466(1993).
 DR EMBL; S54909; AAB25381.2; -.

KM Hypothetical protein.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5B05B047 CRC64;

Query Match 25.0%; Score 2; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 ||
 Db 6 sf 7

RESULT 25
 ID P78484 PRELIMINARY; PRT; 9 AA.
 AC P78484;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE FYNC ONCOGENE, 3' END, CLONE PFYN-C-11. (FRAGMENT).
 GN FYN.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 90-98 FROM N.A.
 RX MEDLINE=88234523; PubMed=3287380;
 RA Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
 RT "Acquisition of transforming properties by FYN, a normal SRC-related
 RT human gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874(1988).
 DR EMBL; M20284; AAA52491.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1143 MW; 12BA1729D5A6D73B CRC64;

Query Match 25.0%; Score 2; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
 ||
 Db 5 sf 6

Search completed: January 14, 2002, 08:07:35
 Job time: 765 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:56:32 ; Search time 81.39 Seconds
(without alignments)
7.281 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 8
Sequence: 1 wrxxsfxxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :
1: A.Geneseq_1101.*
2: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqp/AA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseqp/AA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT.*
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11: /SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqp/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	7	19	AAW65247	Peptide containing
2	37.5	31	19	AAW62083	Hypocytoma sp. stra
3	37.5	40	20	AAV410039	Peptide sequence d
4	37.5	42	19	AAW77559	Staphylococcus aur
5	37.5	84	22	AAAG76222	Human colon cancer
6	37.5	114	22	AAAM40785	Human polypeptide
7	37.5	115	21	AAAB21195	Exol8 partial prot
8	37.5	129	18	AAW20281	H. pylori cytoplasm
9	37.5	129	18	AAW24625	H. pylori cytoplasm
10	37.5	149	21	AAAB53916	Human colon cancer
11	37.5	156	19	AAW56254	Interleukin-13 b1n

12	37.5	174	22	AAW63508	Human gastric canc
13	37.5	194	18	AAW28289	Amino acid sequenc
14	37.5	217	22	AAW63791	Human prostate can
15	37.5	229	22	AAAG72280	Human olfactory re
16	37.5	297	22	AAW41776	Human polypeptide
17	37.5	312	22	AAAG72750	Human olfactory re
18	37.5	312	22	AAAG72752	Human olfactory re
19	37.5	354	21	AAV76127	Human secreted pro
20	37.5	552	22	AAW48242	Amino acid sequenc
21	37.5	908	16	AAW85443	Rat brevic acid core
22	37.5	2466	20	AAV05842	Banana ripening fr
23	25.0	3	15	AAW48523	Lactoferrin derive
24	25.0	3	16	AAW84691	Bovine lactoferrin
25	25.0	3	17	AAW98547	Peptide for anti-u
26	25.0	3	17	AAW90601	Lactoferrin derive
27	25.0	3	19	AAW56219	Anti-inflammatory
28	25.0	3	19	AAW41282	Apoptosis inducer
29	25.0	3	21	AAW37940	Trypsin modulating
30	25.0	3	22	AAW92005	FMRF neuropeptide
31	25.0	4	7	AAW60801	Peptide with neur
32	25.0	4	8	AAW71285	Opilate binding pep
33	25.0	4	8	AAW71288	Opilate binding pep
34	25.0	4	10	AAW91630	Motif useful in to
35	25.0	4	11	AAW07103	Melanocyte-stimula
36	25.0	4	13	AAW24950	Conformationally c
37	25.0	4	13	AAW30195	Des-Tyr(1)-beta-ca
38	25.0	4	13	AAW30202	Des-Tyr(1)-beta-ca
39	25.0	4	13	AAW30206	Des-Tyr(1)-beta-ca
40	25.0	4	13	AAW27863	Antimicrobial pept
41	25.0	4	14	AAW38135	Protease-non-lab1l
42	25.0	4	14	AAW38130	Protease-non-lab1l
43	25.0	4	14	AAW38132	Protease-non-lab1l
44	25.0	4	14	AAW38113	Protease-non-lab1l
45	25.0	4	15	AAW38115	Protease-non-lab1l
46	25.0	4	15	AAW57101	Epitope p2 of anti
47	25.0	4	15	AAW48522	Lactoferrin derive
48	25.0	4	15	AAW57453	Lactoferrin derive
49	25.0	4	16	AAW11946	Dimeric peptide.
50	25.0	4	16	AAW95572	Scfv anti-GAP fusi

ALIGNMENTS

RESULT 1
ID AAW65247 standard: peptide; 7 AA.
XX AAW65247;
XX
XX 02-OCT-1998 (first entry)
DT
XX
XX Peptide containing 6-peptidylamino-1-naphthylenesulphonamide moiety.
XX
XX
XX Aminoaphthylenesulphonamide; activated protein C; blood coagulation;
XX APC; substrate; peptidomimetic.
XX
XX Synthetic.

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	7	19	AAW65247	Peptide containing
2	37.5	31	19	AAW62083	Hypocytoma sp. stra
3	37.5	40	20	AAV410039	Peptide sequence d
4	37.5	42	19	AAW77559	Staphylococcus aur
5	37.5	84	22	AAAG76222	Human colon cancer
6	37.5	114	22	AAAM40785	Human polypeptide
7	37.5	115	21	AAAB21195	Exol8 partial prot
8	37.5	129	18	AAW20281	H. pylori cytoplasm
9	37.5	129	18	AAW24625	H. pylori cytoplasm
10	37.5	149	21	AAAB53916	Human colon cancer
11	37.5	156	19	AAW56254	Interleukin-13 b1n

PF 18-NOV-1997; 97WO-US21075.
 XX
 PR 19-NOV-1996; 96US-0031359.
 XX
 PA (BUTE/) BUTENAS S.
 PA (MANN/) MANN K G.
 XX
 PI Butenas S, Mann KG;
 XX
 DR WPI: 1998-312167/27.
 XX
 PR Peptidyl-amino-1-naphthalene-sulphonamide compounds - are
 PT peptidomimetics of natural substrates for activated protein C,
 PT useful as promoters of the blood coagulation process
 XX
 PS Claim 6: Page 38; 50pp; English.
 CC
 CC The invention relates to peptidomimetics containing 6-peptidylamino-1-
 CC naphthalenesulphonamide moieties. They are peptidomimetics of natural
 CC substrates for activated protein C (APC), whose substrates are promoters
 CC of the blood coagulation process. The present sequence represents a
 CC specifically claimed peptidomimetic.
 CC
 SO Sequence 7 AA;

Query Match 37.5%; Score 3; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wrxs 5
 |||||
 Db 2 wrxs 6

RESULT 2
 AAW62083
 ID AAW62083 standard; peptide; 31 AA.
 XX
 AC AAW62083;
 XX
 DT 15-SEP-1998 (first entry)
 XX
 DE Hypochozma sp. strain CBS 648.91 phospholipase fragment #8.
 XX
 KW Hypochozma sp. strains CBS 648.91; phospholipase; fatty acyl; hydrolyse;
 KW oil degumming; wheat starch hydrolysate; breadmaking; dough.
 XX
 OS Hypochozma sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note="believed to be a glycosylated Asn residue"
 XX
 PN W09818912-A1.
 XX
 PD 07-MAY-1998.
 XX
 PE 30-OCT-1997; 97WO-DK00490.
 XX
 PR 31-OCT-1996; 96DK-0001215.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Halkier T, Hasida M, Stringer MA, Tsutsumi N;
 XX
 DR WPI: 1998-272208/24.
 XX

• New phospholipase from Hypochozma strain and related DNA - hydrolyses
 PT both acyl residues in phospholipid. useful for degumming edible
 PT oils, and to improve dough quality or filterability of carbohydrate
 PT slurries
 XX

PS Claim 3; Page 18; 46pp; English.
 XX
 CC The present sequence represents a new phospholipase peptide fragment,
 CC from strain CBS 648.91 of a Hypochozma. The phospholipase can hydrolyse
 CC both fatty acyl groups in a phospholipid (PL), has an optimum temperature
 CC about 50 degrees Celsius (measured for 10 min at pH 3-4) and optimum pH
 CC about 3 (measured at 40 degrees Celsius for 10 min). The phospholipase is
 CC used to hydrolyse acyl groups in (lyso)PL, particularly (lyso)lecithin.
 CC Specifically it is used: (a) to improve filterability of aqueous
 CC solutions or slurries of carbohydrate origin (especially wheat starch
 CC hydrolysate) containing PL; (b) in breadmaking (added to the dough) to
 CC improve elasticity; and (c) to reduce PL content (degum) in edible oils.
 CC The phospholipase lacks lipase activity and is effective at very low pH.
 CC so does not cause enzymatic/alkaline hydrolysis of triglycerides. It is
 CC not membrane bound so can be produced and purified on a commercial
 CC scale.
 CC
 SO Sequence 31 AA;

Query Match 37.5%; Score 3; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 |||||
 Db 3 sfxg 6

RESULT 3
 AAY40039
 ID AAY40039 standard; peptide; 40 AA.
 XX
 AC AAY40039;
 XX
 DT 18-NOV-1999 (first entry)
 XX
 DE Peptide sequence derived from a human secreted protein.
 XX
 KW Secreted protein; gene therapy; cancer; tumor; fetal deficiency;
 KW neurodegenerative disorder; developmental abnormality; blood disorder;
 KW immune system disease; autoimmune disease; leukemia; inflammation;
 KW allergy; Alzheimer's disease; cognitive disorder; schizophrenia;
 KW obesity; osteoporosis; arthritis; infection; AIDS; diabetes; asthma;
 KW connective tissue disorder; transplant rejection; sepsis; acne;
 KW psoriasis; cardiovascular disorder; reproductive disorder;
 KW food additive; food preservative; storage capability.
 XX
 OS Homo sapiens.
 XX
 PN W09943693-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 24-FEB-1999; 99WO-US03939.
 XX
 PR 26-FEB-1998; 98US-0076051.
 PR 26-FEB-1998; 98US-0076052.
 PR 26-FEB-1998; 98US-0076053.
 PR 26-FEB-1998; 98US-0076054.
 PR 26-FEB-1998; 98US-0076057.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen HS, Florence K, Brewer LA, Ebner R, Ruben SM, Rosen CA;
 PI Duan RD;
 XX
 DR WPI: 1999-550857/46.
 XX

New human genes and the secreted polypeptides they encode, useful for
 PT diagnosis and treatment of e.g. cancers, neurological disorders, immune
 PT diseases, inflammation or blood disorders
 XX

PS Disclosure: Page 39; 246pp; English.
XX AYA40001-92 are derived from human secreted proteins. The
CC polynucleotides and their corresponding secreted polypeptides are useful
CC for preventing, treating or ameliorating medical conditions, e.g. by
CC protein or gene therapy. Pathological conditions can also be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC uses including the presence of mutations in the polynucleotide. Specific
CC cancer, tumors, neurodegenerative disorders, developmental abnormalities
CC and fetal deficiencies, blood disorders, sepsis, diseases of the immune
CC system, autoimmune diseases, inflammation, allergies, Alzheimer's and
CC cognitive disorders, schizophrenia, obesity, osteoporosis, arthritis,
CC infections, AIDS, connective tissue disorders, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC and reproductive disorders. The polypeptides or polynucleotides can
CC also be used as food additives or preservatives, such as to increase
CC or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components.
XX
SQ Sequence 40 AA;

Query Match 37.5%; Score 3; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
| | | |
DB 7 sfxg 10

RESULT 4

AAW77559 standard; Protein: 42 AA.

AAW77559;

30-OCT-1998 (first entry)

Staphylococcus aureus protein of unknown function.

XX Staphylococcus aureus protein; Immune response induction; eye infection;
XX antibody production; T-cell immune response; gastrointestinal infection;
XX respiratory infection; inhibitor; bacterial infection; cardiac infection;
XX central nervous system; kidney infection; urinary tract infection;
XX antimicrobial compound identification; broad spectrum antibiotic;
XX therapy.
XX
OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 1..42 /note- "residues designated X are unspecified, and
FT represented as Xaa in the specification"

PN EP841394-A2.

PD 13-MAY-1998.

PF 24-SEP-1997; 97EP-0307485.

PR 24-SEP-1996; 96US-0027032.

XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Black MT, Burnham MKR, Hodgson JE, Knowles DGC;
PI Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M;
PI Ward JM;
XX WPI: 1998-252940/23.

DR N-PSDB; AAV53359.

XX New nucleic acid sequences from Staphylococcus aureus WCHU29 -
PT useful in vaccines and for treatment of bacterial infections of e.g.
PT respiratory tract and central nervous system
XX

PS Claim 11; Page 252; 390pp; English.

XX This sequence represents a Staphylococcus aureus protein of unknown
CC function, and is encoded by a DNA sequence of the invention.
CC The DNA sequences were isolated from Staphylococcus aureus WCHU29
CC (NCIMB 40771). Host cells containing the DNA sequences are used to
CC produce polypeptides or fragments. The proteins are used in the treatment
CC of disease, for inducing an immune response by administering them, to
CC produce antibody and/or T-cell immune response. Antagonists of the
CC proteins are used for the inhibition of bacterial infections, especially
CC Conditions which may be treated include bacterial infections, especially
CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
CC urinary tract, skin, bones and joints. The proteins can also be used to
CC identify antimicrobial compounds which are broad spectrum antibiotics,
CC especially useful in the treatment of H. pylori infection.
XX
SQ Sequence 42 AA;

Query Match 37.5%; Score 3; DB 19; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
| | | |
DB 34 sfxg 37

RESULT 5

AAW76222 standard; Protein: 84 AA.

AAW76222;

03-SEP-2001 (first entry)

Human colon cancer antigen protein SEQ ID NO:6986.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.
XX
OS Homo sapiens.

XX WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000MO-US26524.

PR 29-SEP-1999; 99US-0157137.

PR 03-NOV-1999; 99US-0163280.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI: 2001-235357/24.

DR N-PSDB; AAH35627.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 8423-8426; 9803pp; English.

PS AAH32943 to AAH37195 and AAH73514 to AAH77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon

CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated PS,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAM37196 to AAM37204
CC and AAM7789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.

SO Sequence 84 AA;

Query Match 37.5%; Score 3; DB 22; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
1111
Db 28 sfxg 31

RESULT 6
ID AAM40785 standard; Protein; 114 AA.

AC AAM40785;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5716.
XX
KW Human; nocrotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
KW chemokine; Thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI59941.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -
XX
PS Example 2: SEQ ID NO 5716; 10078bp; English.
XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nocrotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

SO Sequence 114 AA;

Query Match 37.5%; Score 3; DB 22; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
1111
Db 78 sfxg 81

RESULT 7
ID AAB21195 standard; Protein; 115 AA.
XX
AC AAB21195;
XX
DT 12-JAN-2001 (first entry)
XX
DE Exo18 partial protein.
XX
KW Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
KW antiallergic; antiasthmatic; nocrotropic; neuroprotective; anticonvulsant;
KW vulnerability; asthma; inflammation; allergy; Chediak-Higashi syndrome; CNS;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW digestion disorder; wound healing disorder; gene therapy.
XX
OS Mus sp.
XX
PN WO200043419-A2.
XX
PD 27-JUL-2000.
XX
PF 20-JAN-2000; 2000WO-US01431.
XX
PR 20-JAN-1999; 99US-0116534.
PR 26-JAN-1999; 99US-0117274.
PR 26-JAN-1999; 99US-0117308.
PR 26-JAN-1999; 99US-0117309.
PR 26-JAN-1999; 99US-0117312.
PR 01-FEB-1999; 99US-0118177.
PR 01-FEB-1999; 99US-0118178.
PR 01-FEB-1999; 99US-0118179.
PR 01-FEB-1999; 99US-0118179.
PR 09-FEB-1999; 99US-0119286.
PR 11-FEB-1999; 99US-0119998.
PR 11-FEB-1999; 99US-0119759.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Luo Y;
XX

DR MPI: 2000-482908/42.
DR N-PSDB: AAA89574.
XX
PT New nucleic acids encoding Exo proteins which are useful in the
PT diagnosis, treatment or prevention of exocytosis-mediated disorders
PT such as asthma, inflammation and allergies -
XX
PS Disclosure: Page 167; 305pp; English.
XX
CC The present sequence is a polypeptide which is associated with
CC the exocytosis pathway. cDNA molecules encoding proteins involved in
CC exocytosis have been isolated by yeast one-hybrid and two-hybrid
CC screening. Novel proteins, termed Exo proteins, have been identified that
CC interact with known exocytosis-associated proteins such as GS27, alpha
CC snap, unc18-1, vamps3, snap-23, and the rab family of proteins.
CC Exo proteins and their agonists and antagonists are useful in the
CC diagnosis, treatment or prevention of exocytosis-mediated disorders
CC such as asthma, inflammation, allergies, Chediak-Higashi Syndrome
CC (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC diabetes, digestion disorders and wound healing disorders.
CC The nucleic acids, antagonists or agonists of Exo proteins are useful
CC in gene therapy. The nucleic acids are also useful for generating
CC transgenic or knock-out animals which can be used in the
CC development and screening of therapeutically useful reagents.
XX
SQ Sequence 115 AA:

Query Match 37.5%; Score 3; DB 21; Length 115;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxx 8
|||
DB 107 sfxx 110

RESULT 8
AAW20281
ID AAW20281 standard; Protein: 129 AA.
XX
AC AAW20281;
XX
DT 30-JUL-1997 (first entry)
XX
DE H. pylori cytoplasmic protein 24039587.aa.
XX
KW Cytoplasmic; vaccine; prevention; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
XX
OS Helicobacter pylori.
XX
FH Key Location/Qualifiers
FT Misc-difference 115 /Label: unknown
FT /note- "encoded by AAW"
XX
XX
PN WO9640893-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09122.
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR) ASTRA AB.
XX
PI Berglindh OT, Smith D, Mellgaerd BL;
XX MPI: 1997-052306/05.
DR N-PSDB: AAT67763.
DR

XX
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
PS Claim 61; Page 482; 1481pp; English.
XX
CC This sequence is a H. pylori cytoplasmic protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
XX
SQ Sequence 129 AA:

Query Match 37.5%; Score 3; DB 18; Length 129;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxx 8
|||
DB 113 sfxx 116

RESULT 9
AAW24625
ID AAW24625 standard; Protein: 129 AA.
XX
AC AAW24625;
XX
DT 11-AUG-1997 (first entry)
XX
DE H. pylori cytoplasmic protein 24039587.aa.
XX
KW Transmembrane; cytoplasmic; cell envelope; flagella; transport;
KW secreted; periplasmic; chronic gastritis; duodenal ulcer disease;
KW activator; inhibitor; bacterial life cycle; vaccine; immunise;
KW detection; antisense; inhibition.
XX
OS Helicobacter pylori.
XX
FH Key Location/Qualifiers
FT Misc-difference 115 /note- "encoded by AAW"
FT
XX
XX
PN WO9719098-A1.
XX
PD 29-MAY-1997.
XX
PF 15-NOV-1996; 96WO-US18542.
XX
PR 17-NOV-1995; 95US-0561469.
XX
PA (ASTR) ASTRA AB.
XX
PI Smith DH;
XX
DR MPI: 1997-298052/27.
DR N-PSDB: AAT77443.
XX
PT Helicobacter pylori nucleic acid sequences and related proteins -
XX used for diagnostics and therapeutics
XX

XX 27-FEB-1997; 97AU-0005374.
PR 10-SEP-1996; 96AU-0002262.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hillon DJ, Nicola NA, Simpson RJ, Zhang J;
DR MPI; 1998-207062/18.
DR N-PSDB; AAV22697.
XX
PT New Isolated Interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX
PS Claim 7; Page 45-48; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 156 AA;

Query Match 37.5%; Score 3; DB 19; Length 156;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
|||
Db 101 sfxg 104

RESULT 12
AAB63508
ID AAB63508 standard; Protein; 174 AA.
XX
AC AAB63508;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human gastric cancer associated antigen protein sequence SEQ ID NO:870.
XX
KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine.
XX
OS Homo sapiens.
XX
PN WO200073801-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-USJ4749.
XX
PR 28-MAY-1999; 99US-0136526.
PR 10-SEP-1999; 99US-0133454.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Obata Y;
XX
XX MPI; 2001-025274/03.
XX
XX Nucleic acids encoding breast, gastric and prostate cancer associated
XX antigen precursors, useful for diagnosing and treating a condition
XX characterized by expression of an abnormal amount of a protein, e.g.
XX cancer -
XX
PS Example 1; Page 592-593; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
SQ Sequence 174 AA;

Query Match 37.5%; Score 3; DB 22; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
|||
Db 22 sfxg 25

RESULT 13
AAW28289
ID AAW28289 standard; Protein; 194 AA.
XX
AC AAW28289;
XX
DT 14-SEP-1998 (first entry)
XX
DE Amino acid sequence of an enoyl-acyl carrier protein.
XX
KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW Staphylococcal gene; regulatory element; bacterial gene expression;
KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
KW toxic shock syndrome.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 159 /note= "encoded by ANT"
FT Misc-difference 178 /note= "encoded by NTG"
FT Misc-difference 184 /note= "encoded by CNG"
XX
PN WO9730070-A1.
XX
PD 21-AUG-1997.
XX
PF 19-FEB-1997; 97WO-US02318.
XX
PR 20-FEB-1996; 96US-0011888.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;
XX
XX MPI; 1997-424969/39.
XX
XX N-PSDB; AAT84187.
XX
PT Novel polypeptide(s) from Staphylococcus aureus strain MCUH29 - used
PT to isolate antimicrobial compounds, and in vaccines against S.
PT aureus infection
XX
PS Claim 6; Page 586-587; 989pp; English.
XX
CC The present sequence represents a Staphylococcus aureus protein, that,
CC based on homology with an E. coli protein, is believed to be an

CC enoyl-acyl carrier protein. The DNA sequence was isolated from a
CC library of clones of *S. aureus* WCUN 29 in *Escherichia coli*. The DNA
CC sequence can be used in the construction of ribozymes and antisense
CC sequences to control the expression of staphylococcal genes. The DNA
CC sequence is also useful as a source of regulatory elements for the
CC control of bacterial gene expression. The present protein may be used
CC to produce vaccines to enable a host to produce specific antibodies
CC with antibacterial action. These vaccines and antibodies would protect
CC a host against invasion by *S. aureus*, and conditions relating to
CC staphylococcal infection, e.g. staphylococcal food poisoning, scaled
CC skin syndrome, and toxic shock syndrome.

SQ Sequence 194 AA;

Query Match 37.5%; Score 3; DB 18; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
||||
Db 176 sfxg 179

RESULT 14

ID AAB63791 standard; Protein; 217 AA.

XX AAB63791;

XX 26-MAR-2001 (first entry)

DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1153.

XX Human: breast cancer; gastric cancer; prostate cancer; diagnosis;

KM cancer associated antigen; cytostatic; cancer vaccine.

XX Homo sapiens.

XX WO200073801-A2.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14749.

XX PR 28-MAY-1999; 99US-0136526.

XX PR 10-SEP-1999; 99US-0153454.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX Obata Y;

XX WPI; 2001-025274/03.

XX Nucleic acids encoding breast, gastric and prostate cancer associated

XX antigen precursors, useful for diagnosing and treating a condition

XX characterized by expression of an abnormal amount of a protein, e.g.

XX cancer -

XX Example 1; Page 719; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014

XX represent nucleotide sequences encoding human breast, gastric and

XX prostate cancer associated antigen precursors (CAAP) respectively.

XX AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970

XX represent human breast, gastric and prostate CAAP protein sequence

XX respectively. CAAPs have cytosolic activity and can be used in the

XX production of cancer vaccines. The human CAAP proteins, peptides, nucleic

XX acids or anti-CAAP antibodies are useful for diagnosing and treating a

XX condition characterised by expression of an abnormal amount of a protein,

XX e.g. cancer.

SQ Sequence 217 AA;

Query Match 37.5%; Score 3; DB 22; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 5 sfxg 8
||||
Db 214 sfxg 217

RESULT 15

ID AAG72280 standard; Protein; 229 AA.

XX AAG72280;

XX 31-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1961.

XX Human: olfactory receptor; OR; primary scent determination;

KM secondary scent determination; polypeptide library; odour receptor;

XX scent profile; scent fingerprint; scent representation.

XX Homo sapiens.

XX WO200127158-A2.

XX PD 19-APR-2001.

XX PF 06-OCT-2000; 2000WO-US27582.

XX PR 08-OCT-1999; 99US-0158615.

XX PR 24-FEB-2000; 2000US-0184809.

XX PA (DIGI-) DIGISCENTS.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory

XX sensation for identifying olfactory agonists and antagonists -

XX Claim 11; Page 1311-1312; 1857pp; English.

XX The present sequence is an olfactory receptor which is encoded by

XX one of a number of novel polynucleotides. The polynucleotides can be

XX used in screening for olfactory agonists and antagonists. The methods

XX allow for the determination of primary scents and the identification

XX of the odour receptors used to detect these primary scents. The methods

XX also enable determination of secondary scents and the identification of

XX combinations of odour receptors that are involved in detecting such

XX secondary scents. This enables the construction of a scent representation

XX (also called a scent fingerprint or scent profile), which may be used to

XX re-create and edit scents. Libraries of olfactory receptors are useful

XX for determining the interaction pattern of a composition with the

XX receptors, and can be used for determining differences in the olfactory

XX faculties of different individuals.

SQ Sequence 229 AA;

Query Match 37.5%; Score 3; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 5 sfxg 8
||||
Db 183 sfxg 186

RESULT 16
 AAM41776
 ID AAM41776 standard; Protein: 297 AA.
 XX AAM41776;
 AC
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 6707.
 XX
 KW Human; nocutropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 XX
 DR N-PSDB: AAI60932.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 2: SEQ ID NO 6707; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nocutropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 297 AA;

QY 5 sfxg 8
 ||||
 Db 256 sfxg 259
 RESULT 17
 AAG72750
 ID AAG72750 standard; Protein: 312 AA.
 XX
 AC AAG72750;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor data exploratorium sequence. SEQ ID NO: 2432.
 DE Human olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation;
 KW human olfactory receptor data exploratorium; HORDE.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000MO-US27582.
 XX
 PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI: 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Example 6: Page 1652; 1857bp; English.
 XX
 CC The present sequence is a polypeptide from the human olfactory receptor
 CC data exploratorium (HORDE). It was used as a query sequence in a database
 CC search of olfactory receptor (OR)-like sequences. The invention relates
 CC to isolated polynucleotides encoding polypeptides involved in olfactory
 CC sensation. The polynucleotides can be used in screening for olfactory
 CC agonists and antagonists. The methods allow for the determination of
 CC primary scents and the identification of the odour receptors used to
 CC detect these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents. This
 CC enables the construction of a scent representation (also called a scent
 CC fingerprint or scent profile), which may be used to re-create and edit
 CC scents. Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals.
 XX
 SQ Sequence 312 AA;

Query Match 37.5%; Score 3; DB 22; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxg 8
 ||||
 Db 167 sfxg 170
 RESULT 18

AAG72752	
ID AAG72752 standard; Protein; 312 AA.	
XX AAG72752;	
DT 31-JUL-2001 (first entry)	
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2434.	
XX	
KW Human; olfactory receptor; OR; primary scent determination;	
KM secondary scent determination; polypeptide library; odour receptor;	
RK scent profile; scent fingerprint; scent representation;	
KW human olfactory receptor data exploratorium; HORDE.	
XX Homo sapiens.	
OS WO200127158-A2.	
PN 19-APR-2001.	
PD 06-OCT-2000; 2000WO-US27582.	
PF 08-OCT-1999; 99US-0158615.	
PR 24-FEB-2000; 2000US-0184809.	
PX (DIGIT-) DIGISCENTS.	
PA (YEDA) YEDA RES & DEV CO LTD.	
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;	
PT WPI: 2001-290713/30.	
PS New polynucleotides which encode polypeptides involved in olfactory	
PT sensation for identifying olfactory agonists and antagonists -	
XX Example 6: Page 1653-1654; 1857pp; English.	
CC The present sequence is a polypeptide from the human olfactory receptor	
CC data exploratorium (HORDE). It was used as a query sequence in a database	
CC search of olfactory receptor (OR)-like sequences. The invention relates	
CC to isolated polynucleotides encoding polypeptides involved in olfactory	
CC sensation. The polynucleotides can be used in screening for olfactory	
CC agonists and antagonists. The methods allow for the determination of	
CC primary scents and the identification of the odour receptors used to	
CC detect these primary scents. The methods also enable determination of	
CC secondary scents and the identification of combinations of odour	
CC receptors that are involved in detecting such secondary scents. This	
CC enables the construction of a scent representation (also called a scent	
CC fingerprint or scent profile), which may be used to re-create and edit	
CC scents. Libraries of olfactory receptors are useful for determining the	
CC interaction pattern of a composition with the receptors, and can be	
CC used for determining differences in the olfactory faculties of different	
XX individuals.	
XX Sequence 312 AA:	
OY Query Match 37.5%; Score 3; DB 22; Length 312;	
DB Best Local Similarity 100.0%; Pred. No. 1.5e+03;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY 5 sfxg 8	
DB 167 sfxg 170	
RESULT 19	
AAY76127	
ID , AAY76127 standard; Protein; 354 AA.	
XX AAY76127;	
DT 23-MAR-2000 (first entry)	

XX	Human secreted protein encoded by gene 4.
DE	
XX	
XX	Human; secreted protein; cancer; tumour; developmental abnormality;
KW	foetal deficiency; blood disorder; immune system disorder; inflammation;
KW	autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW	schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW	atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW	digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
therapy.	
XX	
OS	Homo sapiens.
XX	
XX	W09958660-A1.
PN	
PD	18-NOV-1999.
XX	
XX	
PE	06-MAY-1999; 99WO-US09847.
PR	
PR	12-MAY-1998; 98US-0085093.
PR	12-MAY-1998; 98US-0085094.
PR	12-MAY-1998; 98US-0085105.
PR	12-MAY-1998; 98US-0085180.
PR	18-MAY-1998; 98US-0085906.
PR	18-MAY-1998; 98US-0085920.
PR	18-MAY-1998; 98US-0085921.
PR	18-MAY-1998; 98US-0085922.
PR	18-MAY-1998; 98US-0085923.
PR	18-MAY-1998; 98US-0085924.
PR	18-MAY-1998; 98US-0085928.
PR	18-MAY-1998; 98US-0085925.
PR	18-MAY-1998; 98US-0085927.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI	Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
PI	Lalleur DW, Endress GA, Ebner R;
DR	WPI: 2000-062296/05.
DR	N-PSDB; AA265253.
XX	
PT	New isolated human genes and the secreted polypeptides they encode,
PT	useful for diagnosis and treatment of e.g. cancers, neurological
PT	disorders, immune diseases, inflammation or blood disorders -
XX	
PS	Claim 11; Page 358-359; 475pp; English.
XX	
CC	AA265350 to AA265350 represent 97 isolated human secreted protein genes.
CC	AA276124 to AA276223 represent the secreted proteins encoded by the 97
CC	human genes. The genes and their corresponding secreted polypeptides are
CC	useful for preventing, treating or ameliorating medical conditions,
CC	e.g. by protein or gene therapy. Also pathological conditions can be
CC	diagnosed by determining the amount of the new polypeptides in a sample
CC	or by determining the presence of mutations in the new genes. Specific
CC	uses are described for each of the 97 genes, based on which tissues they
CC	are most highly expressed in, and include developing products for the
CC	diagnosis or treatment of cancer, tumours, developmental abnormalities
CC	and foetal deficiencies; blood disorders, diseases of the immune system,
CC	autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC	disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
CC	disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC	disorders, digestive/endocrine disorders, infections and AIDS. The
CC	polypeptides are also useful for identifying their binding partners.
CC	The sequences shown in AA276224 to AA276424 represent fragments of the
CC	secreted proteins.
XX	
SQ	Sequence 354 AA;
XX	
Query Match	37.5%; Score 3; DB 21; Length 354;
Best Local Similarity	100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;


```
OY      5 sfxg 8
      ||||
Db      173 sfxg 176

RESULT  20
AAB48242
AAB48242 standard; Protein; 552 AA.
AC
AC      AAB48242;
DE
DE      02-APR-2001 (first entry)
DE
DE      Amino acid sequence of bz1p2 ORF2 protein.
KW
KW      Transcription factor; seed storage protein; lectin; oil-body protein;
KW      Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin;
KW      phaseolin; PHA-L; bean; nuclear protein; promoter; ORF; bz1p;
KW      basic leucine zipper.
XX
XX      Phaseolus vulgaris.
OS
PH      Key      Location/Qualifiers
PT      Misc-difference 1..552
      /note= "Xaa are residues encoded by internal stop codons"
XX
XX      US6160202-A.
XX
XX      12-DEC-2000.
PD
PD      06-FEB-1997; 97US-0796899.
XX
XX      07-OCT-1994; 94US-0319544.
XX
XX      (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.
PA
PA      Chern M, Bustos MM;
PT
PT      MPI: 2001-079619/09.
DR
DR      N-PSDB; ANC84565.
XX
XX      Novel transcription factor gene which encodes transcription factor
PT      protein that targets promoters of genes encoding seed storage proteins
PT      are useful for modulating seed storage protein expression in dicot seed
PT      crops
XX
XX      Disclosure: Columns 35-38; 67pp; English.
PS
PS      The invention relates to an isolated transcription factor gene which is
CC      expressed in a recombinant maturing dicot seed and which encodes a
CC      transcription factor protein which targets a promoter of a gene encoding
CC      seed storage proteins, lectins or oil-body proteins. The transcription
CC      factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding
CC      protein-1 (ROM2). These factors bind to 7S-globulin (b-phaseolin) or
CC      lectin (PHA-L) promoters. The transcription factor gene is useful for
CC      enhancing or reducing expression of seed storage protein, lectin or
CC      oil-protein genes in dicot seed crops. The present sequence represents
CC      the amino acid sequence of bz1p2 (basic leucine zipper) ORF2 protein.
XX
XX      Sequence 552 AA:
SO

Query Match      37.5%; Score 3; DB 22; Length 552;
Best Local Similarity 100.0%; Pred. No. 2,1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      5 sfxg 8
      ||||
Db      278 sfxg 281

RESULT  21
```

```
AAR85443
ID      AAR85443 standard; Protein; 908 AA.
XX
XX      AAR85443;
AC
AC      19-FEB-1996 (first entry)
DE
DE      Rat brevican core protein.
XX
XX      Brevican; Chondroitin sulphate proteoglycan; glial cell; axon;
KW      neurofibromatosis; gliosis.
XX
XX      Rattus sp.
OS
PH      Key      Location/Qualifiers
PT      Misc-difference 41..50
      /note= "unidentified amino acids"
FT      Misc-difference 72
      /note= "unidentified amino acid"
FT      Misc-difference 74..75
      /note= "unidentified amino acids"
FT      Misc-difference 93..109
      /note= "unidentified amino acids"
FT      Misc-difference 115
      /note= "unidentified amino acid"
FT      Misc-difference 117..120
      /note= "unidentified amino acids"
FT      Misc-difference 138
      /note= "unidentified amino acid"
FT      Misc-difference 150
      /note= "unidentified amino acid"
FT      Misc-difference 155
      /note= "unidentified amino acid"
FT      Misc-difference 162..166
      /note= "unidentified amino acids"
FT      Misc-difference 173
      /note= "unidentified amino acid"
FT      Misc-difference 201..222
      /note= "unidentified amino acids"
FT      Misc-difference 290
      /note= "unidentified amino acid"
FT      Misc-difference 300
      /note= "unidentified amino acid"
FT      Misc-difference 324
      /note= "unidentified amino acid"
FT      Misc-difference 395
      /note= "unidentified amino acid"
FT      Misc-difference 413
      /note= "unidentified amino acid"
FT      Misc-difference 439..440
      /note= "unidentified amino acids"
FT      Misc-difference 447..490
      /note= "unidentified amino acids"
FT      Misc-difference 524..530
      /note= "unidentified amino acids"
FT      Misc-difference 561..581
      /note= "unidentified amino acids"
FT      Misc-difference 603
      /note= "unidentified amino acid"
FT      Misc-difference 638..641
      /note= "unidentified amino acids"
FT      Misc-difference 718..720
      /note= "unidentified amino acids"
FT      Misc-difference 751..800
      /note= "unidentified amino acids"
FT      Misc-difference 835..836
      /note= "unidentified amino acids"
FT      Misc-difference 866..867
      /note= "unidentified amino acids"
FT      Misc-difference 897..898
      /note= "unidentified amino acids"
FT      /note= "unidentified amino acids"
XX
XX      WO9526201-A1.
PN
```

XX 05-OCT-1995.
 PD
 XX
 PF 27-MAR-1995; 95WO-US03747.
 XX
 PR 28-MAR-1994; 94US-0219642.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Shimonaka M, Watanabe K, Yamada H, Yamaguchi Y;
 XX WPI; 1995-351200/45.
 DR
 XX Mammalian brevican protein - directs/inhibits axonal growth, used in
 PT treatment of neuro-fibromatosis and in detection of gliosis
 CC
 PS Claim 6; Page 45-47; 73pp; English.
 XX
 CC Brevican was isolated from the proteoglycan soluble fraction of
 CC rat brain. The fraction containing the core protein was
 CC purified and the sequences of the N-terminus and internal tryptic
 CC peptides were detd., giving the sequence shown in AAR85443.
 CC Brevican is used to modulate axonal growth and to raise antibodies
 CC useful for detecting gliosis.
 XX
 SQ Sequence 908 AA;

Query Match 37.5%; Score 3; DB 16; Length 908;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 ||||
 Db 171 sfxg 174

RESULT 22
 AAY05842
 ID AAY05842 standard; Protein; 2466 AA.
 XX
 AC AAY05842;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Banana ripening fruit ENDO. translated polypeptide.
 XX
 KW Banana; fruit ripening; glucanase; differential expression;
 KM fruit development; transgenic plant.
 XX
 OS Musa acuminata.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..2466 /note="the X residues in this sequence correspond
 FT to in-frame stop codons or degenerate
 FT codons in reading frame 1 of ENDO. DNA"
 FT
 XX
 PN W09915668-A2.
 XX
 PD 01-APR-1999.
 PD
 XX
 PF 23-SEP-1998; 98WO-US03343.
 XX
 PR 25-SEP-1997; 97US-0060062.
 XX
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 XX
 PI Clendennen S, May G;
 XX
 DR WPI; 1999-244425/20.
 DR N-PSDB; AAX25613.
 XX

PT New isolated banana DNA molecules
 XX
 PS Claim 14; Fig 16A-J; 143pp; English.
 XX
 CC The present sequence represents the protein encoded by reading
 CC frame 1 of a DNA sequence termed ENDO. (see AAX25613) of the
 CC invention. Amino acid sequences deduced from reading frames 2 and
 CC 3 are given in AAY05843 and AAY05844, respectively. The identity of
 CC ENDO. and the coding region of ENDO. DNA are not indicated. The
 CC invention provides isolated DNA molecules which are differentially
 CC expressed during banana fruit development, and the protein products
 CC of these genes. The DNA is selected from a group comprising starch
 CC synthase, chitinase, endochitinase, beta-1,3-glucanase,
 CC thaumatin-like protein, ascorbate peroxidase, metallothionein,
 CC lectin and senescence-related protein. The regulatory elements of
 CC the genes can be used to produce chimeric genes for transformation
 CC of plants to provide controlled expression of heterologous DNA
 CC during fruit development, or in response to exogenous developmental
 CC signals, such as ethylene signals. The heterologous protein, e.g.
 CC a therapeutic protein, can be isolated from the fruit or consumed
 CC directly in the transformed fruit.
 XX
 SQ Sequence 2466 AA;

Query Match 37.5%; Score 3; DB 20; Length 2466;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sfxg 8
 ||||
 Db 1912 sfxg 1915

RESULT 23
 AAR48523
 ID AAR48523 standard; peptide; 3 AA.
 XX
 AC AAR48523;
 XX
 DT 10-AUG-1994 (first entry)
 XX
 DE Lactoferrin derived peptide #17.
 XX
 KW Decomposition; lactoferrin; digestion; enzyme; pepsin; trypsin;
 KM antioxidant; oxidation; inhibitor; vitamin E; ascorbic acid;
 KW vitamin A; beta-carotene; superoxidase dismutase; coenzyme Q;
 XX lipid oxidation; foodstuff; drugs; health food; toiletries; cosmetics.
 XX
 OS Bos taurus.
 OS
 XX
 PN W09403555-A.
 PN
 XX
 PD 17-FEB-1994.
 PD
 XX
 PF 04-AUG-1993; 93WO-JP01090.
 XX
 PR 07-AUG-1992; 92JP-0211335.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 PI Bellamy WR, Fukuwatari Y, Kawase K, Shimamura S;
 PI Takase M, Tokiday, Tomita M, Wakabayashi H, Yamauchi K;
 XX
 DR WPI; 1994-065650/08.
 DR
 XX
 PT Antioxidant peptide lactoferrin decomposition product - prevents
 PT oxidation of lipid(s) in foodstuffs and drugs without affecting
 PT their taste
 XX
 PS Claim 3; Page 32; 47pp; Japanese.
 PS
 XX
 CC The sequences given in AAR48507-37 are peptides derived by the

CC Decomposition of lactoferrin, pref. by digestion with an enzyme, eg.
CC pepsin or trypsin. These peptides may be used in an antioxidant
CC composition which may also contain an oxidation inhibitor such as
CC vitamin E, ascorbic acid, vitamin A, beta-carotene, superoxide
CC dismutase or coenzyme Q. The antioxidant prevents lipid oxidation
CC in foodstuffs, drugs, health foods, toiletries and cosmetics.
XX
SQ

Sequence 3 AA:

Query Match 25.0%; Score 2; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

OY 1 wr 2
11

DB 2 wr 3

RESULT 24

AA84691
ID AAR84691 standard; peptide; 3 AA.

AC AAR84691;

DT 13-JUN-1996 (first entry)

XX Bovine lactoferrin derived angina pectoris treating peptide.

DE Bovine lactoferrin; angina pectoris; treatment; low toxicity;

KM no side effects; heat resistance; water solubility; stability;

KW aqueous solution; preservative free.

XX Bos taurus.

OS JP07278011-A.

XX 24-OCT-1995.

XX 01-APR-1994; 94JP-0085243.

XX 01-APR-1994; 94JP-0085243.

XX (MORG) MORINAGA MILK IND CO LTD.

XX WPI; 1995-400916/51.

XX Peptide for treatment of angina pectoris - has low toxicity and is

XX heat resistant and water soluble

XX Claim 1; Page 10; 12pp; Japanese.

XX The present peptide is a bovine lactoferrin derived, angina

XX pectoris treatative agent. It has low toxicity and side effects,

XX is heat resistant, water soluble and stable in an aq. soln.. It

XX also requires no preservative.

XX Sequence 3 AA:

OY 1 wr 2
11

DB 2 wr 3

RESULT 25

AA84691
ID AAR84691 standard; peptide; 3 AA.

AC AAR8547;

XX 12-NOV-1996 (first entry)

XX Peptide for anti-ulcer agent.

XX anti-ulcer agent; low toxicity; stable; heat-resistant.

XX Synthetic.

XX JP08143468-A.

XX 04-JUN-1996.

XX 17-NOV-1994; 94JP-0283869.

XX 17-NOV-1994; 94JP-0283869.

XX (MORG) MORINAGA MILK IND CO LTD.

XX WPI; 1996-31857/32.

XX Anti-ulcer agent contg. peptide - has low toxicity, is

XX heat-resistant and water-soluble

XX Claim 1; Page 9; 11pp; Japanese.

XX AAR8531-54 are peptides used in an anti-ulcer agent. The agent is low

XX in toxicity, is heat-resistant and stable in aqueous soln.. It can be

XX administered orally and be produced in large amounts.

XX Sequence 3 AA:

Query Match 25.0%; Score 2; DB 17; Length 3;

Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

OY 1 wr 2
11

DB 2 wr 3

Search completed: January 14, 2002, 07:56:32

Job time: 727 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:57:31 ; Search time 41.59 Seconds
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4.329 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 8
Sequence: 1 wrxsfxg 8

Scoring table:
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Searched: 212252 seqs, 22503292 residues

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6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	37.5	7	2	US-08-764-157-8
2	3	37.5	31	3	US-09-295-186-8
3	3	37.5	552	4	US-08-796-899-28
4	3	37.5	908	5	PCT-US95-03747-3
5	2	25.0	2	3	US-08-889-841B-3
6	2	25.0	2	3	US-08-889-841B-6
7	2	25.0	2	3	US-08-889-841B-13
8	2	25.0	2	3	US-08-889-841B-17
9	2	25.0	2	3	US-08-889-841B-20
10	2	25.0	2	3	US-08-889-841B-34
11	2	25.0	2	3	US-08-889-841B-37
12	2	25.0	2	3	US-08-889-841B-40
13	2	25.0	3	1	US-08-165-545-8
14	2	25.0	3	1	US-08-305-768-27
15	2	25.0	3	1	US-08-256-771-17
16	2	25.0	3	1	US-08-381-984-17
17	2	25.0	3	2	US-08-871-163-27
18	2	25.0	3	3	US-08-767-903-27
19	2	25.0	3	5	PCT-US95-11724-27
20	2	25.0	4	1	US-07-657-769B-14
21	2	25.0	4	1	US-07-714-540-11
22	2	25.0	4	1	US-07-714-540-12
23	2	25.0	4	1	US-08-165-545-7
24	2	25.0	4	1	US-07-828-450-38
25	2	25.0	4	1	US-08-127-904-11
26	2	25.0	4	1	US-08-127-904-12
27	2	25.0	4	1	US-08-405-933-14

28	2	25.0	4	1	US-08-190-802A-265	Sequence 265, App
29	2	25.0	4	1	US-08-215-137-11	Sequence 11, Appl
30	2	25.0	4	1	US-08-461-611-12	Sequence 12, Appl
31	2	25.0	4	1	US-08-256-771-16	Sequence 16, Appl
32	2	25.0	4	1	US-07-789-184-109	Sequence 109, App
33	2	25.0	4	1	US-07-789-184-117	Sequence 117, App
34	2	25.0	4	1	US-08-222-851-22	Sequence 22, Appl
35	2	25.0	4	1	US-08-475-263-109	Sequence 109, App
36	2	25.0	4	1	US-08-475-263-117	Sequence 117, App
37	2	25.0	4	1	US-08-485-886-109	Sequence 109, App
38	2	25.0	4	1	US-08-485-886-117	Sequence 117, App
39	2	25.0	4	1	US-08-381-984-16	Sequence 16, Appl
40	2	25.0	4	2	US-08-441-871-62	Sequence 62, Appl
41	2	25.0	4	2	US-08-441-871-72	Sequence 72, Appl
42	2	25.0	4	2	US-08-477-362-109	Sequence 109, App
43	2	25.0	4	2	US-08-477-362-117	Sequence 117, App
44	2	25.0	4	2	US-08-592-646A-62	Sequence 62, Appl
45	2	25.0	4	2	US-08-477-134-109	Sequence 109, App
46	2	25.0	4	2	US-08-477-134-117	Sequence 117, App
47	2	25.0	4	2	US-08-637-759B-108	Sequence 108, App
48	2	25.0	4	2	US-08-350-260A-408	Sequence 408, App
49	2	25.0	4	2	US-09-195-049-4	Sequence 4, Appl
50	2	25.0	4	3	US-08-467-580-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-08-764-157-8
; Sequence 8, Application US/08764157
; Patent No. 5830863
; GENERAL INFORMATION:
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; APPLICANT: Kristiansky, John L
; APPLICANT: Hassman III, Chester F
; APPLICANT: McCarthy, James Ray
; TITLE OF INVENTION: Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marion Merrell Dow Inc.
; STREET: 2110 East Galbraith Rd.
; CITY: Cincinnati P. O. Box 156300
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,157
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/686,593
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Nesbitt, Stephen L
; REGISTRATION NUMBER: 28981
; REFERENCE/DOCKET NUMBER: M01352C US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 948-7965
; TELEFAX: (513) 948-7961
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note="Xaa is a Valine analog
; OTHER INFORMATION: having a 1-methylene group, in place of a
; OTHER INFORMATION: 1-carbonyl group, bonded to the alpha nitrogen"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note="(cont'd) of the subsequent
; OTHER INFORMATION: amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note="Xaa is Leucin-1-amide
; OTHER INFORMATION: (Leu-NH2)"
US-08-764-157-8

Query Match
Best Local Similarity 100.0%; Score 3; DB 2; Length 7;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxx 8
   ||||
Db 2 sfxx 5

RESULT 2
US-09-295-186-8
; Sequence 8, Application US/09295186B
; Patent No. 6127137
; GENERAL INFORMATION:
; APPLICANT: Hasida, Miyoko
; APPLICANT: Tsutsumi, No. 6127137iko
; APPLICANT: Halkier, Torben
; APPLICANT: Stringer, Mary Ann
; TITLE OF INVENTION: An Acidic Phospholipase, Production, and
; FILE REFERENCE: 4953.204-US
; CURRENT APPLICATION NUMBER: US/09/295,186B
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 1215/96
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: PCT/DK97/00490
; PRIOR FILING DATE: 1997-10-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Hypchozoma sp. CBS 648.91
; FEATURE:
; OTHER INFORMATION: Xaa at position 5 is any amino acid
US-09-295-186-8

Query Match
Best Local Similarity 100.0%; Score 3; DB 3; Length 31;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxx 8
   ||||
Db 3 sfxx 6

RESULT 3
US-08-796-899-28
; Sequence 28, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
```

```
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22133-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Neuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-796-899-28

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 552;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sfxx 8
   ||||
Db 278 sfxx 281

RESULT 4
PCT-US95-03747-3
; Sequence 3, Application PC/TUS9503747
; GENERAL INFORMATION:
; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
; TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03747
; FILING DATE: 27-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Imbra, Richard J.
; REGISTRATION NUMBER: 37,643
```

REFERENCE/DOCKET NUMBER: PP-LJ 1453
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-03747-3

Query Match 37.5%; Score 3; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 8
|||
Db 171 SFXG 174

RESULT 5
US-08-889-841B-3
Sequence 3, Application US/08889841B
GENERAL INFORMATION:

APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-3

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 1 SF 2

RESULT 6
US-08-889-841B-6
Sequence 6, Application US/08889841B
GENERAL INFORMATION:

APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-6

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 1 SF 2

RESULT 7
US-08-889-841B-13
Sequence 13, Application US/08889841B
GENERAL INFORMATION:

APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 2
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-13

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 1 SF 2

RESULT 8
US-08-889-841B-17
Sequence 17, Application US/08889841B
GENERAL INFORMATION:

APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 2
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-17

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
||
Db 1 SF 2

RESULT 9
US-08-889-841B-20
Sequence 20, Application US/08889841B
GENERAL INFORMATION:

APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08

;; PRIOR APPLICATION NUMBER: US 60/676,737
;; PRIOR FILING DATE: 1996-07-08
;; NUMBER OF SEQ ID NOS: 57
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 20
;; LENGTH: 2
;; TYPE: PRT
;; ORGANISM: HIV
US-08-889-841B-20

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
Db 1 sf 2

RESULT 10
US-08-889-841B-34
; Sequence 34, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-34

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
Db 1 sf 2

RESULT 11
US-08-889-841B-37
; Sequence 37, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-37

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
Db 1 sf 2

RESULT 12
US-08-889-841B-40
; Sequence 40, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-40

Query Match 25.0%; Score 2; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
Db 1 sf 2

RESULT 13
US-08-165-545-8
; Sequence 8, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,545
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,981
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
2 wr 3

Db 2 wr 3

RESULT 14
US-08-305-768-27
Sequence 27, Application US/08305768
Patent No. 5602097
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,768
FILING DATE: 12-SEPT-1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
2 wr 3

Db 2 wr 3

RESULT 15
US-08-256-771-17
Sequence 17, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 5.25 inch, 500 kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-17

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
2 wr 3

Db 2 wr 3

RESULT 16
US-08-381-984-17

```
; Sequence 17, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note="the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-17

Query Match      25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 2 wr 3

RESULT 17
US-08-871-163-27
; Sequence 27, Application US/08871163
; Patent No. 5885782
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,163
```

```
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-871-163-27

Query Match      25.0%; Score 2; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 1 wr 2

RESULT 18
US-08-767-903-27
; Sequence 27, Application US/08767903
; Patent No. 6020312
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,903
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-767-903-27

Query Match      25.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
   11
Db 1 wr 2

RESULT 19
PCT-US95-11724-27
; Sequence 27, Application PC/TUS9511724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11724
; FILING DATE:
```

CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 25.0%; Score 2; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 1 wr 2

RESULT 20
US-07-657-769B-14
Sequence 14, Application US/07657769B
Patent No. 5236766

GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0502.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-657-769B-14

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 1 sf 2

RESULT 21
US-07-714-540-11

Sequence 11, Application US/07714540
Patent No. 5262521
GENERAL INFORMATION:
APPLICANT: Almqvist, Ronald G.
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Irell & Manella
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,540
FILING DATE: 19910607
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Dianne E.
REGISTRATION NUMBER: 31,292
REFERENCE/DOCKET NUMBER: 8500-0135.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-714-540-11

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sf 6
11
DB 2 sf 3

RESULT 22
US-07-714-540-12
Sequence 12, Application US/07714540
Patent No. 5262521
GENERAL INFORMATION:
APPLICANT: Almqvist, Ronald G.
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Irell & Manella
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/714,540
;; FILING DATE: 19910607
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Reed, Dianne E.
;; REGISTRATION NUMBER: 31,292
;; REFERENCE/DOCKET NUMBER: 8500-0135.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-327-7250
;; TELEFAX: 415-327-2951
;;
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-714-540-12

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sf 6
11
DB 1 sf 2

RESULT 23
US-08-165-545-7
; Sequence 7, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial peptide and
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,545
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,981
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE:
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HARLOTTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 3 wr 4

RESULT 24
US-07-828-450-38
; Sequence 38, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-38

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 5 sf 6
11
Db 2 Sf 3

RESULT 25
US-08-127-904-11
Sequence 11, Application US/08127904
Patent No. 5470951
GENERAL INFORMATION:
APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method For Antagonizing
TITLE OF INVENTION: Amnesic Effects of Amyloid n
TITLE OF INVENTION: Protein and Improving the
TITLE OF INVENTION: Quality of Life In Individuals
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte
STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 5470951e
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: NO. 5470951e
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEX: NO. 5470951e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: Amino Acid

STRANDEDNESS:
TOPOLOGY: Unknown
US-08-127-904-11

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 5 sf 6
11
Db 1 Sf 2

Search completed: January 14, 2002, 07:57:31
Job time: 376 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:58:37 ; Search time 45.4 Seconds
(without alignments)
13.423 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 8
Sequence: 1 wrxxafxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : PIR-68:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37.5	31	2	B18955	class II histocomp	
2	37.5	41	2	A60753	beta-lactamase (EC	
3	37.5	122	2	A85797	hypothetical prote	
4	37.5	260	2	F85630	hypothetical prote	
5	37.5	691	2	E86025	hypothetical prote	
6	37.5	879	2	G85739	hypothetical prote	
7	25.0	3	2	S68328	blood cell protein	
8	25.0	6	2	A61068	locustakinin - mig	
9	25.0	7	1	A61324	dermorphin - Rohde	
10	25.0	7	2	S36662	dermorphin (Lys-7)	
11	25.0	7	2	S21230	dermorphin (Trp-4,	
12	25.0	7	2	S33245	neuromodulatory pe	
13	25.0	7	2	S68004	hucolin, 75K chain	
14	25.0	8	2	S37141	rp5a protein - Erw	
15	25.0	8	2	A46306	spasmodic toxin	
16	25.0	8	2	J50317	leucokinin VII - M	
17	25.0	8	2	S66646	cardioacceleratory	
18	25.0	9	2	S66607	guinoline 2-oxidor	
19	25.0	9	2	S63491	dissimilatory sulf	
20	25.0	9	2	S36898	ribosomal protein	
21	25.0	9	2	A26363	cardioactive pepti	
22	25.0	9	2	B57444	neuropeptide Grb-A	
23	25.0	9	2	C57444	neuropeptide Grb-A	
24	25.0	9	2	S39766	cardioactive pepti	
25	25.0	9	2	S27233	cardioactive pepti	
26	25.0	9	2	JN0027	[Phe-6]-mosact - s	
27	25.0	9	2	S39767	cardioactive pepti	
28	25.0	10	2	S66458	ferredoxin - Rhizo	
29	25.0	10	2	S70251	nitrogenase (EC I,	

30	25.0	10	2	C61440	polylacturonase
31	25.0	11	1	E00CC	eledoisin - curled
32	25.0	11	1	E00CC	eledoisin - musky
33	25.0	11	2	S07203	uperolein - frog (
34	25.0	11	2	A35594	buccalin - Callfor
35	25.0	11	2	A34662	Acharina cardio-ex
36	25.0	11	2	E57789	gallbladder stone
37	25.0	11	2	B41946	T-cell receptor ga
38	25.0	11	4	S52252	hypothetical prote
39	25.0	12	1	A53709	alpha-conotoxin Im
40	25.0	12	2	S29479	hypothetical prote
41	25.0	12	2	S01122	photosystem II 3.7
42	25.0	12	2	A35585	cytokinin-binding
43	25.0	12	2	S47393	T-cell antigen rec
44	25.0	13	2	S01119	photosystem II pro
45	25.0	13	2	PC1008	40K extracellular
46	25.0	13	2	S63492	dissimilatory sulf
47	25.0	13	2	G22565	R-phycocerythrin ga
48	25.0	13	2	S32471	lymadfamide 1 - 9
49	25.0	13	2	S32472	lymadfamide 2 - 9
50	25.0	13	2	S32473	lymadfamide 3 - 9

ALIGNMENTS

RESULT 1
B18955
Class II histocompatibility antigen HLA-DR beta chain - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-May-1997
C:Accession: B18955
R:Wiman, K.; Claesson, L.; Raek, L.; Tragarth, L.; Peterson, P.A.
Biochemistry 21, 5351-5358, 1982
A:Title: Purification and partial amino acid sequence of papain-solubilized class II
A:Reference number: A90463; MUID:83075335
A:Accession: B18955
A:Molecule type: protein
A:Residues: 1-31 <MIM>
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 37.5%; Score 3; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 atfg 8
DB 17 AFXG 20

RESULT 2
A60753
beta-lactamase (EC 3.5.2.6) - Lysobacter enzymogenes (fragment)
C:Species: Lysobacter enzymogenes
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A60753
R:von Tigsterrom, R.G.; Boras, G.J.
J. Gen. Microbiol. 136, 521-527, 1990
A:Title: beta-lactamase of Lysobacter enzymogenes: induction, purification and charac
A:Reference number: A60753; MUID:90362037
A:Accession: A60753
A:Molecule type: protein
A:Residues: 1-41 <VON>
C:Keywords: antibiotic resistance; hydrolase; monomer

Query Match 37.5%; Score 3; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 atfg 8
||||

Db 36 AFXG 39

RESULT 3
A:Accession: A85797
hypothetical protein yebf [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: A85797
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobecek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85797
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <STO>
A:Cross-references: GB:AE005174; NID:g12515900; PIDN:AAG56837.1; GSPDB:GN00145; UWGP:228
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yebf

Query Match 37.5%; Score 3; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 10 AFXG 13

RESULT 4
F85630
hypothetical protein Z1373 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85630
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobecek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85630
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005174; NID:g12514217; PIDN:AAG55506.1; GSPDB:GN00145; UWGP:213
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1373

Query Match 37.5%; Score 3; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 4 AFXG 7

RESULT 5
E86025
hypothetical protein yhjg [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: E86025
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobecek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E86025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-691 <STO>
A:Cross-references: GB:AE005174; NID:g12518239; PIDN:AAG58665.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yhjg
C:Superfamily: Escherichia coli hypothetical 75.1K protein (tref-ksgk region)

Query Match 37.5%; Score 3; DB 2; Length 691;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 268 AFXG 271

RESULT 6
G85739
hypothetical protein ydbH [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: G85739
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobecek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85739
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-879 <STO>
A:Cross-references: GB:AE005174; NID:g12515319; PIDN:AAG56379.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ydbH
C:Superfamily: Escherichia coli membrane protein ydbH

Query Match 37.5%; Score 3; DB 2; Length 879;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 739 AFXG 742

RESULT 7
S68328
blood cell protein A - Molgula manhattensis (fragment)
C:Species: Molgula manhattensis
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
C:Accession: S68328
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from
A:Reference number: S68325; MUID:96132650
A:Accession: S68328
A:Molecule type: protein
A:Residues: 1-3 <TAI>

Query Match 25.0%; Score 2; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||

Db 1 AF 2

RESULT 8
Locustakinin - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C:Accession: A61068
R:Schneefs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri
A:Reference number: A61068; MUID:92262851
A:Accession: A61068
A:Molecule type: protein
A:Residues: 1-6 <SCH>
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 1 AF 2

RESULT 9
A61324
dermorphin - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61324
R:Montecuchi, P.C.; De Castiglione, R.; Erspamer, V.
Int. J. Pept. Protein Res. 17, 316-321, 1981
A:Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz
A:Reference number: A61324; MUID:82029915
A:Accession: A61324
A:Molecule type: protein
A:Residues: 1-7 <MON>
C:Superfamily: dermorphin precursor: dermorphin precursor amino-terminal homology
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin
F:2/Modified site: D-alanine (Ala) #status experimental
F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 2 AF 3

RESULT 10
S36662
dermorphin (Lys-7) [validated] - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C:Accession: S36662
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502
A:Accession: S36662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MG>
C:Superfamily: dermorphin precursor: dermorphin precursor amino-terminal homology

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 2 AF 3

RESULT 11
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C:Accession: S21230
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of
A:Reference number: S21152; MUID:92339502
A:Accession: S21230
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MG>
C:Superfamily: dermorphin precursor: dermorphin precursor amino-terminal homology

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 2 AF 3

RESULT 12
S33245
neuromodulatory peptide Wamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minkata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 333, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
||
Db 1 WR 2

RESULT 13
S68004
hucollin, 75k chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68004
R:Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A:Title: Hucollin, a new corticosteroid-binding protein from human plasma with structu
A:Reference number: S68004; MUID:96087107
A:Accession: S68004

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <EDC>

Query Match 25.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 af 6
DB 2 AF 3

RESULT 14
S37141
rpas protein - Erwinia chrysanthemi
C:Species: Erwinia chrysanthemi
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C:Accession: S37141
R:Doullie, A.; Toussaint, A.; Faelen, M.
submitted to the EMBL Data Library, August 1993
A:Description: Identification of the integration host factor genes of E. chrysanthemi.
A:Reference number: S37139
A:Accession: S37141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <DCU>
A:Cross-references: EMBL:X74750; NID:g399669; PIDN:CAAS2769.1; PID:g581108

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 af 6
DB 1 AF 2

RESULT 15
A46306
spasmogenic toxin PNVI - spider (Phonetrilia nigriyenter) (fragment)
C:Species: Phonetrilia nigriyenter
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A46306
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicon 31, 377-384, 1993
A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A:Reference number: A46306; MUID:93276438
A:Accession: A46306
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
DB 2 AF 3

RESULT 16
JS0317
leucokinin VII - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0317
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the
A:Reference number: JS0317
A:Accession: JS0317
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
DB 3 AF 4

RESULT 17
S6646
cardioacceleratory protein 2b - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S6646
R:Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderik, K.M.; Tuditatz, N.J.
FEBS Lett. 371, 311-314, 1995
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from th
A:Reference number: S6646; MUID:96013159
A:Accession: S6646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HUE>

Query Match 25.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
DB 4 AF 5

RESULT 18
S6607
guinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S6607
R:Schach, S.; Tshisnaka, B.; Feltzer, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A:Title: Guinoline 2-oxidoreductase and 2-oxo-1,2-dihydroguinoline 5,6-dioxygenase fr
A:Reference number: S6606; MUID:96035889
A:Accession: S6607
A:Molecule type: protein
A:Residues: 1-9 <SCH>
A:Experimental source: strain 63

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
DB 5 AF 6

RESULT 19
S63491
disulfidatory sulfite reductase beta chain, membrane-bound - Desulfovibrio desulfuric
C:Species: Desulfovibrio desulfuricans

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63491
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from *Desulfovibrio*
A:Reference number: S63489; MUID:96085152
A:Accession: S63491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <STR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
DB 1 Af 2

RESULT 20
S36898
ribosomal protein S8 - *Mycobacterium bovis* (fragment)
C:Species: *Mycobacterium bovis*
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36898
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycobac*
A:Reference number: S36887; MUID:94009653
A:Accession: S36898
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <OH>
C:Keywords: protein biosynthesis; ribosome

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
DB 8 Af 9

RESULT 21
A26363
cardioactive peptide - green crab (fragment)
C:Species: *Cardinus maenas* (green crab, common shore crab)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: A26363
R:Standler, J.; Hilbich, C.; Beyreuther, K.; Keller, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987
A:Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crab *C*
A:Reference number: A26363
A:Accession: A26363
A:Molecule type: protein
A:Residues: 1-9 <STA>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
DB 5 Af 6

RESULT 22
B57444

neuropeptide Grb-AST B2 - two-spotted cricket
C:Species: *Gryllus bimaculatus* (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: B57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 2103-2108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
A:Reference number: A57444; MUID:95403341
A:Accession: B57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 2 WR 3

RESULT 23
C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C:Species: *Gryllus bimaculatus* (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: C57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 2103-2108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
A:Reference number: A57444; MUID:95403341
A:Accession: C57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 2 WR 3

RESULT 24
S39766
cardioactive peptide CCAP - yellow mealworm
C:Species: *Tenebrio molitor* (yellow mealworm)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C:Accession: S39766
R:Furuya, K.; Iiao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A.
Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993
A:Title: Isolation and identification of a cardioactive peptide from *Tenebrio molitor*
A:Reference number: S39766; MUID:94176032
A:Accession: S39766
A:Molecule type: protein
A:Residues: 1-9 <FUR>
C:Keywords: neuropeptide

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
DB 5 Af 6

RESULT 25
S27233
cardioactive peptide CCAP - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 09-Jun-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C:Accession: S27233
R:Cheung, C.C.; Lo1, P.K.; Sylwester, A.W.; Lee, T.D.; Tublitz, N.J.
FEBS Lett. 313, 165-168, 1992
A:Title: Primary structure of a cardioactive neuropeptide from the tobacco hawkmoth, Manduca sexta
A:Reference number: S27233; MUID:93050243
A:Accession: S27233
A:Molecule type: Protein
A:Residues: 1-9 <CHE>
C:Keywords: neuropeptide

Query Match 25.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 5 AF 6

Search completed: January 14, 2002, 07:58:38
Job time: 388 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:08:23 ; Search time 30.66 Seconds
(without alignments)
9.567 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 8
Sequence: 1 wxxxxfxg 8

Scoring table:
OLIGO
Gapop 60.0 , Capext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries
Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25.0	6	1	LOK1_LOCM1	P41491 locusta mig
2	25.0	7	1	ALL2_CARMA	P81805 carcinus ma
3	25.0	7	1	ALL3_CARMA	P81806 carcinus ma
4	25.0	7	1	ALL4_CARMA	P81807 carcinus ma
5	25.0	7	1	ALL5_CARMA	P81808 carcinus ma
6	25.0	7	1	WMA1_ACHFU	P35919 achalina fu
7	25.0	8	1	ALL2_CARMA	P81815 carcinus ma
8	25.0	8	1	ALL7_CARMA	P81809 carcinus ma
9	25.0	8	1	ALL8_CARMA	P81811 carcinus ma
10	25.0	8	1	ALL9_CARMA	P81812 carcinus ma
11	25.0	8	1	LCK1_LEUMA	P21440 leucophaea
12	25.0	8	1	LCK7_LEUMA	P19989 leucophaea
13	25.0	8	1	NS3_MYCTU	P81152 mycobacteri
14	25.0	8	1	ORMY_ORCLI	P82455 orconectes
15	25.0	8	1	RS1_ERMCH	P37985 erwinhia chr
16	25.0	9	1	AL10_CARMA	P81813 carcinus ma
17	25.0	9	1	AL11_CARMA	P81814 carcinus ma
18	25.0	9	1	CCAP_CARMA	P38556 carcinus ma
19	25.0	9	1	MOSE_CLYJA	P19853 clypeaster
20	25.0	9	1	TKC1_CALYO	P41517 calliphora
21	25.0	10	1	Q2OB_COMTE	P80465 comanonas t
22	25.0	10	1	UP11_CAEEL	P55956 caenorthabdi
23	25.0	11	1	CEP1_ACHFU	P22790 achalina fu
24	25.0	11	1	TKC2_CALYO	P41518 calliphora
25	25.0	11	1	TKN1_UPEIN	P82026 uperoleia i
26	25.0	11	1	TKN1_UPEIU	P08612 uperoleia r
27	25.0	11	1	TKN1_UPEIU	P01293 eledone mos
28	25.0	12	1	TKN1_UPEIU	P50993 conus imper
29	25.0	13	1	NP1_LYMST	P80178 lymnaea sta
30	25.0	13	1	NP2_LYMST	P80179 lymnaea sta
31	25.0	13	1	NP3_LYMST	P80180 lymnaea sta
32	25.0	13	1	NP4_LYMST	P80181 lymnaea sta
33	25.0	13	1	NP5_LYMST	P80182 lymnaea sta

ALIGNMENTS

RESULT 1		LOC1_LOCM1		STANDARD:		PRT:		6 AA.	
ID	LOC1_LOCM1								
AC	P41491:								
DT	01-NOV-1995 (Rel. 32, Created)								
DT	01-NOV-1995 (Rel. 32, Last sequence update)								
DT	15-JUL-1998 (Rel. 36, Last annotation update)								
DE	LOCUSTAKININ I.								
OS	Locusta migratoria (Migratory Locust).								
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;								P20728 calotropis
OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;								P03056 citrobacter
OC	Acridomorpha; Acridoidea; Acrididae; Locusta.								P03053 escherichia
OX	NCBI_TaxID=7004;								P03054 salmonella
RN	[1]								P30039 homo sapien
RP	SEQUENCE.								P55936 didelphis m
RC	TISSUE=Corpora cardiaca;								P03057 escherichia
RX	MEDLINE=92262851; PubMed=1585017;								P81359 oncorhynchu
RA	Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,								P80614 zea mays (m
RA	de Loof A.;								P80622 zea mays (m
RT	"Locustakinin, a novel myotropic peptide from Locusta migratoria,								P80631 zea mays (m
RT	isolation, primary structure and synthesis.";								P80634 zea mays (m
RL	Regul. Pept. 37:49-57(1992).								P80533 fasciola he
CC	-I- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION								P23436 rattus norv
CC	OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN								P81087 pinus pinas
CC	TUBULES.								P06556 corynebacte
DR	PIR: A61068; A61068.								P82696 periplaneta
KW	Neuropeptide; Amidation.								
FT	MOD_RES								
SQ	SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;								
Query Match 25.0%; Score 2; DB 1; Length 6;									
Best Local Similarity 100.0%; Pred. No. 1e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY 5 af 6									
DB 1 AF 2									
RESULT 2									
ID	ALL2_CARMA								
AC	P81805;								
DT	30-MAY-2000 (Rel. 39, Created)								
DT	30-MAY-2000 (Rel. 39, Last sequence update)								
DT	30-MAY-2000 (Rel. 39, Last annotation update)								
DE	CARCINOSTATIN 2.								
OS	Carcinus menas (Common shore crab) (Green crab).								
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;								
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;								

OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 [1]
 RN Eubrachyura; Portunioidea; Portunidae; Carcinus.
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW Neuropeptide; Multigene family.
 FT MOD.RES
 SQ SEQUENCE 7 AA; 770 MW; 672879CDBC85DB870 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 [1]
 DB 4 AF 5

RESULT 3
 ALL3_CARMA STANDARD; PRT; 7 AA.
 AC P81806;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 3.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 [1]
 RN Eubrachyura; Portunioidea; Portunidae; Carcinus.
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Multigene family.
 KW Neuropeptide; Multigene family.
 FT MOD.RES
 SQ SEQUENCE 7 AA; 796 MW; 672879CDBC8476B70 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 [1]
 DB 4 AF 5

RESULT 4
 ALL4_CARMA STANDARD; PRT; 7 AA.
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 4.
 OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 [1]
 RN Eubrachyura; Portunioidea; Portunidae; Carcinus.
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Multigene family.
 KW Neuropeptide; Multigene family.
 FT MOD.RES
 SQ SEQUENCE 7 AA; 782 MW; 672879CDBC8476AC0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 [1]
 DB 4 AF 5

RESULT 5
 ALL5_CARMA STANDARD; PRT; 7 AA.
 AC P81808;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 5.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 [1]
 RN Eubrachyura; Portunioidea; Portunidae; Carcinus.
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Multigene family.
 KW Neuropeptide; Multigene family.
 FT MOD.RES
 SQ SEQUENCE 7 AA; 781 MW; 672879CDBC8476420 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 [1]
 DB 4 AF 5

RESULT 6
 MMAL_ACHFU STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE WWMIDF-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
PIR: S33245; S33245.
DR Neuropptide; Amidation.
KW MOD.RES
FT MOD.RES
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
II
DB 1 WR 2

RESULT 7
ID AL12_CARMA STANDARD; PRT; 8 AA.
AC P81815;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 12.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropptide; Multigene family.
FT MOD.RES
SQ SEQUENCE 8 AA; 913 MW; 672879CDB569AB7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 5 Af 6

RESULT 8
ID AL17_CARMA STANDARD; PRT; 8 AA.
AC P81809; P81810; P81804;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CARCINUSTATIN 7 (CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropptide; Amidation; Multigene family.
FT CHAIN 1 8 CARCINUSTATIN 7.
FT CHAIN 2 8 CARCINUSTATIN 6.
FT CHAIN 4 8 CARCINUSTATIN 1.
FT MOD.RES
SQ SEQUENCE 8 AA; 825 MW; 922879CDBA475BD CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 5 Af 6

RESULT 9
ID AL8_CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropptide; Amidation; Multigene family.
FT MOD.RES
SQ SEQUENCE 8 AA; 795 MW; 922879CDBA47687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 5 Af 6

RESULT 10
ALL9_CARMA STANDARD; PRT: 8 AA.
ID P81812;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSSTATIN 9.
OS Carcinus menas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_Taxid=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus menas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDBC476878 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 5 AF 6

RESULT 11
LCK1_LEUMA STANDARD; PRT: 8 AA.
ID LCK1_LEUMA
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_Taxid=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -I- ACTIVITY OF COCKROACH PROTEIN (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CCD76A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 5 AF 6

Db 3 AF 4
RESULT 12
LCK7_LEUMA STANDARD; PRT: 8 AA.
ID LCK7_LEUMA
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_Taxid=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -I- ACTIVITY OF COCKROACH PROTEIN (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDD76A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 3 AF 4

RESULT 13
NS3_MYCTU STANDARD; PRT: 8 AA.
ID NS3_MYCTU
AC P81152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 30 KDA NON-SECRETORY PROTEIN 3 (FRAGMENT).
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37RV;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -I- CAUTION: WE ARE UNABLE TO FIND THIS PROTEIN IN THE TRANSLATION OF
CC THE GENOME OF STRAIN H37RV.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDD22 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
||
Db 3 AF 4


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RESULT 14
ID ORMY_ORCLI STANDARD: PRT: 8 AA.
AC P82455;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ORCOMYOTROPIN (OMT).
OS Orcomyotetes limosus (Splynheek crayfish).
OC Eukariyota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacodea; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Hindgut;
RA MEDLINE=20411310; PubMed=10952880;
RA Dirksen H., Burdzik S., Sauter A., Keller R.;
RT "Two orcocklins and the novel octapeptide orcomyotropin in the hindgut
RT of the crayfish Orconectes limosus: Identified myostimulatory
RT neuropeptides originating together in neurones of the terminal
RT abdominal ganglion."
RL J. Exp. Biol. 203:2807-2818(2000).
CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
CC AMPITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
CC BY ABDOMINAL GANGLIONIC NEURONS.
KW -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAb.
KM Amidation; Neuropeptide.
FT MOD.RES 8 8
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 3 AF 4

RESULT 15
RS1_ERMCH STANDARD: PRT: 8 AA.
ID RS1_ERMCH
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S1 (FRAGMENT).
OS RPSA.
GN Rv1741a chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Douville A., Toussaint A., Paalen M.;
RT Submitted (Aug-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC -----
DR EMBL: X74750; CAA52769.1; -.
DR PIR: S37141; S37141.
KW Ribosomal protein; Repeat; RNA-binding.
FT NON_TER 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 1 AF 2

RESULT 16
AL10_CARMA STANDARD: PRT: 9 AA.
ID AL10_CARMA
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukariyota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RA MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD.RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDBA776C7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
II
DB 6 AF 7

RESULT 17
AL11_CARMA STANDARD: PRT: 9 AA.
ID AL11_CARMA
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSTATIN 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukariyota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RA MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multiene family.
FT MOD.RES 9
SQ SEQUENCE 9 AA; 927 MW; 832D79CDB46D861 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
DB 6 AF 7

RESULT 18

CCAP_CARMA

ID CCAP_CARMA STANDARD; PRT; 9 AA.

AC P38556;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE CARDIOACTIVE PEPTIDE (CCAP).

OS *Carcinus maenas* (Common shore crab) (Green crab),OS *Manduca sexta* (Tobacco hawkmoth) (Tobacco hornworm),OS *Tenebrio molitor* (Yellow mealworm), andOS *Spodoptera eridania* (Southern armyworm).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC NCB1_Taxid=6759, 7130, 7067, 37547;

RN [1]

RP SEQUENCE.

RC SPECIES=C.maenas; TISSUE=pericardial organs;

RA Stangier J., Hilbich C., Beyreuther K., Keller R.;

RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the

RL shore crab *Carcinus maenas*.";

RN [2]

RP SEQUENCE.

RC SPECIES=M.sexta;

RX MEDLINE=93050243; PubMed=1426284;

RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;

RT "Primary structure of a cardioactive neuropeptide from the tobacco

RL hawkmoth, *Manduca sexta*.";

RN [3]

RP SEQUENCE.

RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;

RX MEDLINE=94176032; PubMed=8129851;

RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackelt M.,

RA Schooley D.A.;

RT "Isolation and identification of a cardioactive peptide from *Tenebrio*RL *molitor* and *Spodoptera eridania*.";

CC Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).

CC -I- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.

CC -I- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED

CC INTO THE HEMOLYMPH.

CC PIR: A26363; A26363.

DR PIR: S27233; S27233.

KW Neuropeptide; Amidation.

FT MOD.RES 9

SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 af 6
DB 5 AF 6

RESULT 19

MOSF_CLYXA

ID MOSF_CLYXA STANDARD; PRT; 9 AA.

AC P19853;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE [PHE-6]-MOSACT.

OS *Clypeaster japonicus* (Sand dollar).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinozoa; Euechinozoa; Gnaustomata; Clypeasteroidea;

OC Clypeasteridae; Clypeaster.

OX NCB1_Taxid=7644;

RN [1]

RP SEQUENCE.

RC TISSUE=Egg jelly;

RA Suzuki N., Kurita M., Yoshino K.I., Kajiwara H., Nomura K.,

RA Yamaguchi M.;

RT "Purification and structure of mosact and its derivatives from the

RL egg jelly of the sea urchin *Clypeaster japonicus*.";

CC Zool. Sci. 4:649-656(1987).

CC -I- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.

DR PIR: JN0027; JN0027.

SQ SEQUENCE 9 AA; 924 MW; 93245729CDB5BAB5 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

TKCL_CALVO

ID TKCL_CALVO STANDARD; PRT; 9 AA.

AC P41517;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE CALITACHYKININ I.

OS *Calliphora vomitoria* (Blue blowfly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Oestroidea; Calliphoridae; Calliphora.

OX NCB1_Taxid=27454;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RX MEDLINE=95075727; PubMed=7984492;

RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,

RA Naessel D.R.;

RT "Callitachykinin I and II, two novel myotropic peptides isolated from

RL the blowfly, *Calliphora vomitoria*, that have resemblances to

CC peptides 15:761-768(1994).

CC -I- FUNCTION: MOACTIVE PEPTIDE.

CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD.RES 9

SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDB1B7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches f 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
11
DB 4 AF 5

RESULT 21
Q20B_COMTE
ID Q20B_COMTE STANDARD; PRT: 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE QUINOLINE 2-OXIDOREDUCTASE, BETA CHAIN (EC 1.3.99.17) (FRAGMENT).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCBI_TaxID:285;
RN [1]
RP SEQUENCE.
RX MEDLINE:96035889; Pubmed:7556204;
RA STRAIN=63;
RA Schach S., Tshisuka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinolone and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-1,2-DIHYDROQUINOLINE.
CC -1- CATALYTIC ACTIVITY: QUINOLINE + ACCEPTOR + H(2)O -> ISOQUINOLIN-1(2H)-ONE + REDUCED ACCEPTOR.
CC -1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND (3-METHYL-)-QUINOLINE.
CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
11
DB 5 AF 6

RESULT 22
UP11_CAEBL
ID UP11_CAEBL STANDARD; PRT: 10 AA.
AC P55956;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 11) (FRAGMENT).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID:6239;
RN [1]
RP SEQUENCE.
RX STRAIN=BRISTOL N2;
RX MEDLINE:97295299; Pubmed=9150941;
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans RT homogenates and identification of protein spots by microsequencing.";
RL Electrophoresis 18:557-562(1997).
FT NON_TER 10
SQ SEQUENCE 10 AA; 1102 MW; 15255FB5B7287B14 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
11
DB 1 AF 2

RESULT 23
CEP1_ACHFV
ID CEP1_ACHFV STANDARD; PRT: 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RX STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX MEDLINE=90211261; Pubmed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
KW PIR: A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 5 WR 6

RESULT 24
TKC2_CALVO
ID TKC2_CALVO STANDARD; PRT: 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALLITACHYKININ II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RX MEDLINE=95075727; Pubmed=7984492;
RA Lundquist C.T., Cloutens F.L., Holman G.M., Nichols R., Nachman R.J., Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from the blowfly, Calliphora vomitoria, that have resemblances to tachykinins.";
RL Peptides 15:761-768(1994).
CC -1- FUNCTION: MYOACTIVE PEPTIDE.

CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SO SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD44 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 11
 Db 6 AF 7

RESULT 25
 TKNL_UPEIN
 ID TKNL_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE UPERIN 1.1
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Uperoleia.
 OX NCBI_TaxID-104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Bradford A.M., Rattery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the Australian
 floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 MUSCLES.
 CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -I- MASS SPECTROMETRY: MW-1208; METHOD-FAB.
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC InterPro: IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Amphibian skin; Amidation; Neuropeptide.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SO SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 11
 Db 6 AF 7

Search completed: January 14, 2002, 08:08:23
 Job time: 708 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 08:07:35 ; Search time 81.98 Seconds
(without alignments)
14.274 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 8
Sequence: 1 wrxxafxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

1: SP_RMBL_17:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_MMC:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Protoct:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	40	6	Q9TRU3	O9TRU3 oryctolagus
2	37.5	65	5	Q9GXM2	Q9GXM2 leishmania
3	37.5	66	5	Q9GXQ1	Q9GXQ1 leishmania
4	37.5	82	8	Q9TC61	Q9TC61 melaniopus
5	37.5	88	5	Q9NNG8	Q9NNG8 leishmania
6	37.5	98	12	Q9QW5	Q9QW5 tt virus
7	37.5	110	8	Q34865	Q34865 lucjanus bu
8	37.5	130	8	Q9T784	Q9T784 trinomys lh
9	37.5	131	8	Q9T220	Q9T220 trinomys lh
10	37.5	149	2	Q9K4Q2	Q9K4Q2 unidentified
11	37.5	151	2	Q59551	Q59551 mycoplasma
12	37.5	180	8	Q9G578	Q9G578 xenotodon
13	37.5	185	2	Q9ZM44	Q9ZM44 wolbachia s
14	37.5	213	2	Q86976	Q86976 desulfococc
15	37.5	305	8	Q9TEJ6	Q9TEJ6 dicostonyx
16	37.5	311	8	Q95792	Q95792 emola cyanu
17	37.5	311	8	Q9Z2G1	Q9Z2G1 phyllotis o
18	37.5	326	8	Q9MRX6	Q9MRX6 rhexia mari
19	37.5	346	8	Q03302	Q03302 campephilus

20	3	37.5	347	8	Q03340	Q03340 sphyrapius
21	3	37.5	347	8	Q03341	Q03341 sphyrapius
22	3	37.5	355	8	Q9TEF8	Q9TEF8 oryctolagus
23	3	37.5	374	8	Q21210	Q21210 parachromis
24	3	37.5	379	8	Q21218	Q21218 parachromis
25	3	37.5	732	12	Q65089	Q65089 foot-and-mo
26	2	25.0	7	4	Q15903	Q15903 homo sapien
27	2	25.0	8	2	Q09258	Q09258 synecococc
28	2	25.0	8	5	P82689	P82689 periplaneta
29	2	25.0	8	11	Q62721	Q62721 ratus norv
30	2	25.0	8	11	Q9JLD7	Q9JLD7 mesocricetu
31	2	25.0	8	12	Q98YK9	Q98YK9 human immun
32	2	25.0	9	2	Q45852	Q45852 clostridium
33	2	25.0	9	2	Q46179	Q46179 clostridium
34	2	25.0	9	4	Q14277	Q14277 homo sapien
35	2	25.0	9	10	Q9AXH8	Q9AXH8 mesembryant
36	2	25.0	9	12	Q85599	Q85599 moloney mur
37	2	25.0	9	12	Q90350	Q90350 hepatitis 9
38	2	25.0	10	2	Q9R7J8	Q9R7J8 helicobacte
39	2	25.0	10	11	Q9QVK8	Q9QVK8 mus sp. mep
40	2	25.0	11	2	Q47451	Q47451 escherichia
41	2	25.0	11	2	P95518	P95518 pasteurella
42	2	25.0	11	4	Q60614	Q60614 homo sapien
43	2	25.0	11	7	Q77883	Q77883 oreochromis
44	2	25.0	11	7	Q77912	Q77912 oreochromis
45	2	25.0	11	7	Q9T0B3	Q9T0B3 homo sapien
46	2	25.0	12	2	Q53358	Q53358 escherichia
47	2	25.0	12	2	Q02128	Q02128 desulfovibr
48	2	25.0	12	2	Q9S550	Q9S550 streptococc
49	2	25.0	12	4	Q9UMZ8	Q9UMZ8 homo sapien
50	2	25.0	12	7	Q77919	Q77919 pseudotroph

ALIGNMENTS

RESULT 1
ID Q9TRU3 PRELIMINARY; PRT; 40 AA.
AC Q9TRU3;
DC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FACTOR IX HEAVY CHAIN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92132840; PubMed=1776139;
RA Rao L.V., Hoang A.D.;
RT "Purification and characterization of rabbit factor IX and its
existence as a two-chain factor IX alpha in circulating plasma.";
RL Thromb. Res. 64:57-66(1991).
CC -I- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
DR HSSP; P00761; IMCT.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00089; trypsin.1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 40 AA; 4159 MW; CBD8CCED3AC3CF92 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Oy 5 afxg 8
|||
Db 24 AFXG 27

RESULT 2

Q9GXM2 PRELIMINARY; PRT; 65 AA.
 AC Q9GXM2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROBABLE PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 (FRAGMENT).
 GN LM12.336.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL390114; CAB98464.2; -.
 KW Helicase.
 FT NON_TER 1 1
 FT SEQUENCE 65 AA; 7105 MW; 865D6D7220703391 CRC64;
 SQ

Query Match 37.5%; Score 3; DB 5; Length 65;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 Db 1 AFXG 4

RESULT 3
 Q9GX01 PRELIMINARY; PRT; 66 AA.
 ID Q9GX01;
 AC Q9GX01;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PROBABLE REXXANK (FRAGMENT).
 GN LM12.295.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RA Oliver K.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL390114; CAC02145.1; -.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 2.
 DR SMART; SM00248; ANK; 2.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 FT NON_TER 1 1
 FT SEQUENCE 66 AA; 6919 MW; 604760C6D9670F8C CRC64;
 SQ

Query Match 37.5%; Score 3; DB 5; Length 66;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 Db 14 AFXG 17

RESULT 4
 Q9TC61

ID Q9TC61 PRELIMINARY; PRT; 82 AA.
 AC Q9TC61;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN CYTB.
 OS Melanoplus flavidus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridoidea; Acrididae; Melanoplus.
 OX NCBI_TaxID=103641;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chapco W., Kuperus W.R., Litzenberger G.S.;
 RT "Molecular phylogeny of melanoptine grasshoppers (Orthoptera:
 RT Acrididae). The genus Melanoplus";
 RL Ann. Entomol. Soc. Amer. 92:617-623(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
 DR EMBL; AF145493; AAD56053.1; -.
 DR InterPro; IPR000179; Cyt_b6.
 DR Pfam; PF00033; cytochrome_b_N; 1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 FT NON_TER 1 1
 FT SEQUENCE 82 AA; 9244 MW; 4EDAD43120D5CA4 CRC64;
 SQ

Query Match 37.5%; Score 3; DB 8; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 Db 50 AFXG 53

RESULT 5
 Q9NNG8 PRELIMINARY; PRT; 88 AA.
 ID Q9NNG8;
 AC Q9NNG8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE PROBABLE HYPOTHETICAL 27.7 KDA PROTEIN (FRAGMENT).
 GN LM15.205.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL160371; CAC00242.1; -.
 FT NON_TER 1 1
 FT SEQUENCE 88 AA; 9379 MW; 878CAE746830DA9D CRC64;
 SQ

Query Match 37.5%; Score 3; DB 5; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 5 afxg 8
    ||||
Db 11 AFXG 14

RESULT 6
Q9QTW5 PRELIMINARY; PRT; 98 AA.
AC Q9QTW5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ORF2 PROTEIN (FRAGMENT).
OS TT virus.
OS Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID:68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTV WAM973;
RA Muliyanto, Hljikata M., Matsushita M., Ingkokusmo G., Widjaya A.,
RA Sumarsidi D., Kanai K., Ohta Y., Mishiro S.;
RT "TT virus (TTV) genotypes in native and non-native prostitutes of
RT Irian Jaya, Indonesia: Implication for non-occupational
RT transmission."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB031728; BAA6191.1; -.
GN NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA: 11089 MW: FD01A6D7C29C04F CRC64;

Query Match 37.5%; Score 3; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
    ||||
Db 59 AFXG 62

RESULT 7
Q34865 PRELIMINARY; PRT; 110 AA.
AC Q34865;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Lutjanus buccanella.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Lutjanidae; Lutjaninae; Lutjanus.
OX NCBI_TaxID=40504;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarver S.K., Froehwater D., Walsh P.J.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OX(2) + 2 FERRICYTOCHROME C .. Q + 2
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U26939; AAT70175.1; -.
DR
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DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
KW Election transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA: 12530 MW: 29AA811BC7EE6458 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
    ||||
Db 99 AFXG 102

RESULT 8
Q9T7B4 PRELIMINARY; PRT; 130 AA.
AC Q9T7B4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB OR CYP B.
OS Trinomys lheringi.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Echimyidae; Trinomys.
OX NCBI_TaxID=42830;
RN [1]
RP SEQUENCE FROM N.A.
RA Lara M.C., Patton J.L.;
RT "Evolutionary diversification of spiny rats (genus Trinomys, Rodentia:
RT Echimyidae) in the Atlantic Forest of Brazil."
RL Zool. J. Linn. Soc. 0:0-0(2000).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF194318; AAF16120.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00033; cytochrome_b_n; 1.
KW Election transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 130
SQ SEQUENCE 130 AA: 14687 MW: 374EFC940B9EABE9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
    ||||
Db 127 AFXG 130

RESULT 9
Q9T2Z0 PRELIMINARY; PRT; 131 AA.
AC Q9T2Z0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DR
```

DE CYTOCHROME B (FRAGMENT).
GN CYTB OR CYT B.
OS Trinomys lheringi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Echimyidae; Trinomys.
OX NCBI_TaxID=42830;
RN [1]
RP SEQUENCE FROM N.A.
RA Lara M.C., Patton J.L.;
RT "Evolutionary diversification of spiny rats (genus Trinomys, Rodentia;
RT Echimyidae) in the Atlantic Forest of Brazil."
RL Zool. J. Linn. Soc. 0:0-0(2000).
CC -I- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -I- CORFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -I- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RISKE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF194320; AAF16122.1; -.
DR EMBL: AF194319; AAF16121.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF000033; cytochrome_b_n; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane
FT NON_TER 131
SQ SEQUENCE 131 AA; 14850 MW; F5374EFC940B9EAB CRC64;

Query Match 37.5%; Score 3; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 127 AFXG 130

RESULT 10
O9K402 PRELIMINARY; PRT; 149 AA.
AC O9K402;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMOA PROTEIN (FRAGMENT).
GN AMOA.
OS unidentified proteobacterium.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=2722;
RN [1]
RP SEQUENCE FROM N.A.
RA Speksnijder A.G.C.L., Kowalchuk G.A., Jong de S., Jaanbroek H.J.;
RT "Recovery of a Nitrosomonas-like amoA sequence group from freshwater
RT habitats".
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ388566; CAB96453.1; -.
DR InterPro: IPR003393; AMO.
DR Pfam: PF02461; AMO; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16673 MW; A35D0692633C6BE6 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 afxg 8
||||

Db 104 AFXG 107

RESULT 11
O59551 PRELIMINARY; PRT; 151 AA.
AC O59551;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADENOSINETRIPHOSPHATASE (EC 3.6.1.3) (ADENYLPHOSPHATASE) (ATP
DE MONOPHOSPHATASE) (ATPase) (FRAGMENT).
GN ATPA.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M129;
RX MEDLINE=93054343; Pubmed=1429453;
RA Wenzel R., Pirkl E., Herrmann R.;
RT "Construction of an EcoRI restriction map of Mycoplasma pneumoniae and
RT localization of selected genes."
RL J. Bacteriol. 174:7289-7296(1992).
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
CC -I- SIMILARITY: TO ATPASE ALPHA/BETA CHAINS FAMILY.
DR EMBL: X67653; CAA47895.1; -.
DR InterPro: IPR000194; ATPase_alpha_beta.
DR Pfam: PF00006; ATP_syn_ab; 1.
KW Hydrogen ion transport; Hydrolase.
FT NON_TER 1
FT NON_TER 151
SQ SEQUENCE 151 AA; 16671 MW; A7FD19618264466 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
Db 84 AFXG 87

RESULT 12
O9G578 PRELIMINARY; PRT; 180 AA.
AC O9G578;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Xenentodon cancila.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Belontiidae; Xenentodon.
OX NCBI_TaxID=129108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N26;
RX MEDLINE=20458311; Pubmed=11005301;
RA Lovejoy N.R.;
RT "Reinterpreting recapitulation: systematics of needlefishes and their
RT allies".
RL Evolution 54:1349-1362(2000).
CC -I- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).


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CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF243891; AAC24985.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 180 180
SQ SEQUENCE 180 AA; 20032 MW; 01B64BB7C00C58D6 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
| | | |
DB 86 AFXG 89

RESULT 13
O9ZH44 PRELIMINARY; PRT; 185 AA.
AC O9ZH44:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OUTER SURFACE PROTEIN PRECURSOR (FRAGMENT).
GN WSP.
OS Wolbachia sp. wKayLC.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=77833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:MKAYLC;
RA van Meer M.M.M., Witteveldt J., Stoutamer R.;
RT "Phylogeny of the arthropod endosymbiont Wolbachia based on the wsp
RT gene.";
RL Insect MOL. Biol. 0:0-0(1999).
DR EMBL: AF071927; AAC77407.1; -.
DR InterPro: IPR002566; Surface_Ag_msp4.
DR Pfam: PF01617; Surface_Ag_2; 1.
FT NON_TER 1 1
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 19990 MW; 1F1D66A2B72F4E62 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
| | | |
DB 83 AFXG 86

RESULT 14
O86976 PRELIMINARY; PRT; 213 AA.
AC O86976:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DISSIMILATORY SULFITE REDUCTASE ALPHA SUBUNIT (FRAGMENT).
OS Desulfococcus multivorans.
OC Bacteria; Proteobacteria; delta subdivision; Desulfococcus.
OX NCBI_TaxID=897;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33890;
RX MEDLINE=98269016; PubMed=9603890;
RA Wagner M., Roger A.J., Flax J.L., Brusseau G.A., Stahl D.A.;
RT "Phylogeny of dissimilatory sulfite reductases supports an early
RT origin of sulfate respiration.";
RL J. Bacteriol. 180:2975-2982(1998).
DR EMBL: U58126; AAC24101.1; -.
DR InterPro: IPR000660; Nlr_Sir.
DR Pfam: PF01077; Nlr_Sir; 1.
DR PRINTS: PR00397; SIROHAEM.
FT NON_TER 1 1
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 23637 MW; 49EF93808F46AACA CRC64;

Query Match 37.5%; Score 3; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
| | | |
DB 22 AFXG 25

RESULT 15
O9TEJ6 PRELIMINARY; PRT; 305 AA.
AC O9TEJ6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Dicrostonyx torquatus (Arctic lemming).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
OC Dicrostonyx.
OX NCBI_TaxID=85952;
RN [1]
RP SEQUENCE FROM N.A.
RA Fedorov V.B., Goropashnaya A.V.;
RT "The importance of ice ages in diversification of Arctic collared
RT lemmings (Dicrostonyx): evidence from the mitochondrial cytochrome b
RT region.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AJ238425; CAB53232.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1; 1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 305 305
SQ SEQUENCE 305 AA; 34456 MW; 1F4CA31BA50A7239 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 5 afxg 8
|||||
Db 98 AFXG 101

RESULT 16
Q95792 PRELIMINARY; PRT; 311 AA.
AC Q95792;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CYTOCHROME C (FRAGMENT).
GN CYTB.
OS Emoia cyanura (blue-tailed skink).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
OC Scincidae; Emoia.
OX NCBI_TaxID=38244;
RN [1]
RP SEQUENCE FROM N.A.
RA Bruna E.M., Fisher R.N., Case T.J.;
RL Proc. R. Soc. Lond., B, Biol. Sci. 263:681-688(1996).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C = O + 2
FEROXYCYTOCHROME C.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U49347; AAB0601.1; -;
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1; 1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
KM Transmembrane.
FT NON_TER 1 1
FT NON_TER 311 311
SQ SEQUENCE 311 AA; 34962 MW; 2CE6D105C11CF0C5 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
|||||
Db 101 AFXG 104

RESULT 17
Q92ZG1 PRELIMINARY; PRT; 311 AA.
AC Q92ZG1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Phyllotis osgoodi (Osgood's leaf-eared mouse).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;
OC Phyllotis.
OX NCBI_TaxID=59938;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1CM 638;
RA Steppan S.J.;
RT "Phylogenetic relationships and species limits within Phyllotis
(Rodentia: Sigmodontinae): concordance between mtDNA sequence and
morphology.";
RL J. Mammal. 79:0-0(1998).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: U86825; AAD12350.1; -;
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1; 1.
DR Pfam: PF00033; cytochrome_b_n; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
KM Transmembrane.
FT NON_TER 1 1
FT NON_TER 311 311
SQ SEQUENCE 311 AA; 34708 MW; 3E91294031F728BD CRC64;

Query Match 37.5%; Score 3; DB 8; Length 311;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
|||||
Db 117 AFXG 120

RESULT 18
Q9MRX6 PRELIMINARY; PRT; 326 AA.
AC Q9MRX6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE NADH DEHYDROGENASE (FRAGMENT).
GN NDHF.
OS Rhexia mariana.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Myrtales; Melastomataceae; Rhexia.
OX NCBI_TaxID=130523;
RN [1]
RP SEQUENCE FROM N.A.
RA Renner S.S., Meyer K.;
RT "Melastomeae come full circle: biogeographic reconstruction and
molecular clock dating.";
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Renner S.S., Meyer K.;
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Clausen G., Renner S.S.;
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CHAINS.
DR EMBL: AF272819; AAF81819.2; -;
DR InterPro: IPR000916; Bet_v_1.

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DR InterPro: IPR001750; Oxidored_g1.
DR InterPro: IPR002128; Oxidored_g1_c.
DR Pfam: PF00361; Oxidored_g1. 1.
DR Pfam: PF01010; Oxidored_g1_c. 1.
DR Prodom: PD000531; Bel_v_1.1.
KM Chltoplast; MAD; Oxidoreductase; Plastocuinone.
FT NON_TER 1 1
PT NON_TER 326 326
SQ SEQUENCE 326 AA; 37082 MW; 9B42F1A1B32BB906 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 8; Length 326;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
    ||||
Db 275 AFXG 278

RESULT 19
003302 PRELIMINARY; PRT; 346 AA.
DT 01-JUL-1997 (TRFMBLrel. 04, Created)
DT 01-JUL-1997 (TRFMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TRFMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Camphillius haematogaster.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauilia; Aves; Neognathae; Piciformes; Picidae; Campephilus.
OX NCBI_TaxID=56085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSU11786;
RA Moore W.S.; DeFilippis V.R.;
RL (In) Mindell D.P. (eds.);
RL Avian molecular evolution and systematics, pp.81-116, Academic Press,
RL New York (1997).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC EMBL: U83284; AAB53600.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1. 1.
DR Pfam: PF00033; cytochrome_b_n. 1.
DR PROSITE: PS00193; CYTOCHROME_B_QQ. 1.
KM Electron transport; Heme; Mitochondrion; Respiratory chain;
KM Transmembrane. 1
FT NON_TER 1 1
PT NON_TER 346 AA; 38424 MW; 442E8ABF45EAA2E CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 8; Length 346;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
    ||||
Db 94 AFXG 97

RESULT 20
003340 PRELIMINARY; PRT; 347 AA.

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AC 003340:
DT 01-JUL-1997 (TRFMBLrel. 04, Created)
DT 01-JUL-1997 (TRFMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TRFMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Sphyrapicus varius (Yellow-bellied sapsucker).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauilia; Aves; Neognathae; Piciformes; Picidae; Sphyrapicus.
OX NCBI_TaxID=56079;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WSU86148;
RA Moore W.S.; DeFilippis V.R.;
RL (In) Mindell D.P. (eds.);
RL Avian molecular evolution and systematics, pp.81-116, Academic Press,
RL New York (1997).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC EMBL: U83295; AAB53613.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b_c1. 1.
DR Pfam: PF00033; cytochrome_b_n. 1.
DR PROSITE: PS00193; CYTOCHROME_B_QQ; UNKNOWN.1.
KM Electron transport; Heme; Mitochondrion; Respiratory chain;
KM Transmembrane. 1
FT NON_TER 1 1
PT NON_TER 347 AA; 38763 MW; D367AF657218DDE0E CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 8; Length 347;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
    ||||
Db 95 AFXG 98

RESULT 21
003341 PRELIMINARY; PRT; 347 AA.
DT 01-JUL-1997 (TRFMBLrel. 04, Created)
DT 01-JUL-1997 (TRFMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TRFMBLrel. 17, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Sphyrapicus varius (Yellow-bellied sapsucker).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauilia; Aves; Neognathae; Piciformes; Picidae; Sphyrapicus.
OX NCBI_TaxID=56079;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WSU86149;
RA Moore W.S.; DeFilippis V.R.;
RL (In) Mindell D.P. (eds.);
RL Avian molecular evolution and systematics, pp.81-116, Academic Press,
RL New York (1997).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C O + 2

```

CC FERROCYTOCHROME C.
 CC -I COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -I SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -I SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
 DR EMBL: 083296; AAB53614.1; -.
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF000032; cytochrome_b_c1.
 DR Pfam: PF000033; cytochrome_b_n; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 DR Electron transport; Heme; Mitochondrion; Respiratory chain;
 KM Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 347 AA; 38794 MW; 50BB475A78C9E28D CRC64;

Query Match 37.5%; Score 3; DB 8; Length 347;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 DB 95 AFXG 98

RESULT 22
 Q9TEF8 PRELIMINARY; PRT; 355 AA.
 AC Q9TEF8; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN CYTB.
 OS Oryctolagus cuniculus (Rabbit).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Brancu M., Ferrand N., Monnerot M.;
 RT "Phylogeography of the European rabbit (*Oryctolagus cuniculus*) on the
 RT Iberian peninsula inferred from RFLP analysis of the cytochrome b
 RT gene."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -I FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -I COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -I SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -I SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
 DR EMBL: AJ243096; CAB45258.1; -.
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF000032; cytochrome_b_c1.
 DR Pfam: PF000033; cytochrome_b_n; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
 DR Electron transport; Heme; Mitochondrion; Respiratory chain;
 KM Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 355 AA; 40051 MW; 821F1AFA9A85E9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 355;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 DB 103 AFXG 106

RESULT 23
 ID 021210 PRELIMINARY; PRT; 374 AA.
 AC 021210; 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN CYTB.
 OS Parachromis dovli.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
 OC Cichlidae; Parachromis.
 OX NCBI_TaxId=63177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98224076; PubMed=9562979;
 RA Martin A.P., Bermingham E.;
 RT "Systematics and evolution of lower Central American cichlids inferred
 RT from analysis of cytochrome b gene sequences."
 RL Mol. phylogenet. Evol. 9:192-203(1998).
 CC -I FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -I COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -I SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -I SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
 DR EMBL: AF000924; AAB64130.2; -.
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF000032; cytochrome_b_c1.
 DR Pfam: PF000033; cytochrome_b_n; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_OO; 1.
 DR Electron transport; Heme; Mitochondrion; Respiratory chain;
 KM Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 374 AA; 41771 MW; 28E57DD28DCA24D4 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
 ||||
 DB 125 AFXG 128

RESULT 24
 ID 021218 PRELIMINARY; PRT; 379 AA.
 AC 021218; 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN CYTB.
 OS Parachromis loiseliei.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;

Qy 5 afxg 8
Db 75 AFXG 78

Search completed: January 14, 2002, 08:07:35
Job time: 765 sec

OC Cichlidae; Parachromis.
OX NCBI_Taxid 63178;
RN [1]
RP SEQUENCE FROM N.A.
RA Martin A.P., Bermingham E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUITIN-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: OH(2) + 2 FERRICYTOCHROME C + Q + 2
CC FERROCYTOCHROME C
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
DR EMBL: AF009926: AAB64132.1; -
DR InterPro: IPR000179: Cyt_b6.
DR Pfam: PF00032: cytochrome_b_c: 1.
DR Pfam: PF00033: cytochrome_b_n: 1.
DR PROSITE: PS00192: CYTOCHROME_B_HEME: 1.
DR PROSITE: PS00193: CYTOCHROME_B_OO: 1.
DR Electon transport; Heme; Mitochondrion; Respiratory chain;
KM Transmembrane.
FT NON_TER 379 379
SQ SEQUENCE 379 AA: 42399 MW: 2858955481FEBF9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 379;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 afxg 8
Db 127 AFXG 130

RESULT 25
ID 065089 PRELIMINARY: PRT: 732 AA.
AC 065089;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE P1 POLYPEPTIDE (FRAGMENT).
OS Foot-and-mouth disease virus C.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid:12116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: ARGENTINA/85 C1;
RX MEDLINE:94149827; PubMed:8107204;
RA Mateu M.G., Hernandez J., Martinez M.A., Feigeistock D., Lea S.,
RA Perez J.J., Giralt E., Stuart D., Palma E.L., Domingo E.;
RT "Antigenic heterogeneity of a foot-and-mouth disease virus serotype in
RT the field is mediated by very limited sequence variation at several
RT antigenic sites.";
RL J. Virol. 68:1407-1417(1994).
DR EMBL: L29062: AAA21017.1; -
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073: rhv; 3.
KW Polypeptidn.
FT NON_TER 1 1
FT NON_TER 732 732
SQ SEQUENCE 732 AA: 79701 MW: A5837A80F4330196 CRC64;

Query Match 37.5%; Score 3; DB 12; Length 732;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX (NITO) NITTO BOSEKI CO LTD.
 PA
 XX WPI; 1998-046962/05.
 DR
 XX
 PT New substrate for the determination of pepsin enzymatic activity -
 PT by allowing the enzyme to hydrolyse the substrate and then measuring
 PT the amount of thiol derivative formed
 XX
 PS Example 13; Page 8; 12pp; Japanese.
 XX
 CC The present sequence represents a peptide substrate for the
 CC determination of pepsin activity. The invention relates to peptides
 CC of the following formula: X-A-B-C (1); X = H, a group masking a terminal
 CC amino group irreversibly or a protective group for an amino group used
 CC usually in peptide chemistry; A = glycine, D- or L-alanine, valine,
 CC norvaline, leucine, isoleucine, norleucine, serine and threonine, or a
 CC dipeptide residue consisting of two of these amino acids; B =
 CC phenylalanine, paranthiophenylalanine or tyrosine; C = thiol derivative
 CC residue constituted by 1 to 30 C atoms which can form thioester bond and
 CC H atoms combining with them in which 1 to 10 C atoms can be substituted
 CC by O, N and/or S and 2 to 10 H atoms can be substituted by O, N and/or
 CC S, or its salt. The peptides can be used to determine the
 CC presence/activity of pepsin or pepsinogen in a sample by determining the
 CC amount of thiol derivative formed due to the action (ie. hydrolysis) of
 CC the enzyme on the peptides.
 CC
 SQ Sequence 5 AA;

Query Match 37.5%; Score 3; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 afix 8
 ||||
 Db 2 afix 5

RESULT 2
 AAR51894
 ID AAR51894 standard; peptide; 15 AA.
 XX
 AC AAR51894;
 XX
 DT 09-SEP-1994 (first entry)
 XX
 DE Chitin binding protein internal peptide.
 XX
 KW Chitin binding protein; CBP; antifungal; fungicide;
 KW beta-1,3-glucanase; transgenic plant; disease-resistance;
 KW crop improvement; tobacco.
 XX
 OS Nicotiana tabacum.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 5 /note= "probably tyrosine"
 FT
 FT Misc-difference 11 /note= "probably proline or arginine"
 FT
 PN WO9408009-A.
 XX
 PD 14-APR-1994.
 XX
 PF 05-OCT-1993; 93WO-EP02790.
 XX
 PR 05-OCT-1992; 92EP-0203071.
 PR 13-MAY-1993; 93EP-0201370.
 XX
 PA (MOGE-) MOGEN INT NV.
 XX
 PI Apothekef M, Bres-vloemans AA, Cornelissen BJC, Melchers LS;

PI Ponsstein AS, Sela-duurlage MB;
 XX
 DR WPI; 1994-135576/16.
 XX
 PT New antifungal chitin binding protein from plants - without
 PT significant chitinase activity, showing synergistic activity with
 PT 1,3-beta-glucanase, also its nucleic acid, vectors, transformed
 PT plants, etc.
 XX
 PS Disclosure; Page 31; 54pp; English.
 XX
 CC Internal peptides of tobacco cv. Samsun NN chitin binding protein
 CC were obtained by digestion with protease V8 (peptide AAR51895) and N-
 CC chlorosuccinimide/urea (peptide AAR51894). CBP can be expressed in
 CC transgenic plants to improve resistance to fungal pathogens.
 XX
 SQ Sequence 15 AA;

Query Match 37.5%; Score 3; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 afix 8
 ||||
 Db 3 afix 6

RESULT 3
 AAY18320
 ID AAY18320 standard; peptide; 45 AA.
 XX
 AC AAY18320;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Bovine prothrombin GlA domain.
 XX
 KW GlA domain; vitamin K-dependent protein; clotting disorder;
 KW therapy.
 XX
 OS Bos taurus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1.45 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 FT acid"
 FT
 PN WO9920767-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22152.
 XX
 PR 23-OCT-1997; 97US-0955636.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Nelsessten GL;
 PT
 PT WPI; 1999-288309/24.
 PT
 PT vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
 PT acid domain, useful for treating clotting disorders
 XX
 PS Disclosure; Page 44; 86pp; English.
 XX
 CC This sequence is the prothrombin GlA (gamma-carboxyglutamic acid)
 CC domain. The invention relates to a vitamin K-dependent polypeptide
 CC comprising a modified GlA domain containing an amino acid substitution
 CC which enhances membrane binding of the modified polypeptide as compared
 CC to the native polypeptide. The polypeptide is used to treat a clotting
 CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.

SO Sequence 45 AA;

Query Match 37.5%; Score 3; DB 20; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 rxxaf 6
|||||
DB 25 rxxaf 29

RESULT 4

AAB36400
ID AAB36400 standard; peptide; 45 AA.

AC AAB36400;

DT 27-FEB-2001 (first entry)

DE Bovine prothrombin gamma-carboxyglutamic acid domain SEQ ID NO:17.

XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.

OS Bos taurus.

PN MO20006753-A2.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-US11416.

PR 29-APR-1999; 99US-0302239.

PA (MINU) UNITV MINNESOTA.

PI Nelsaetuen GL;

DR WPI; 2001-007226/01.

XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity

PS Example 5; Page 42; 81pp; English.

XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a bovine prothrombin GLA domain sequence, given in the
CC exemplification of the present invention.

SO Sequence 45 AA;

Query Match 37.5%; Score 3; DB 22; Length 45;

Best Local Similarity 100.0%; Pred. NO. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 rxxaf 6
|||||
DB 25 rxxaf 29

RESULT 5

AAV36099
ID AAV36099 standard; Protein; 65 AA.

AC AAV36099;

DT 13-SEP-1999 (first entry)

DE Extended human secreted protein sequence, SEQ ID NO. 484.

XX Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease.

OS Homo sapiens.

PN WO9931236-A2.

PD 24-JUN-1999.

PF 17-DEC-1998; 98WO-1B02122.

PR 10-AUG-1998; 98US-0096116.

PR 17-DEC-1997; 97US-0069957.

PR 09-FEB-1998; 98US-0074121.

PR 13-APR-1998; 98US-0081563.

PA (GEST) GENSET.

PI Bouquelaret L, Duclert A, Dumas Milne Edwards J;

DR WPI: 1999-385906/32.

DR N-PSDB; AAX97783.

PI New isolated human secreted proteins

PS Claim 9; Page 419; 516pp; English.

XX This sequence is encoded by an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibitory activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases.

SO Sequence 65 AA;

Query Match 37.5%; Score 3; DB 20; Length 65;
Best Local Similarity 100.0%; Pred. NO. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
|||||
DB 55 afxg 58

```

RESULT      6
AAG76045
ID   AAG76045 standard; Protein; 91 AA.
XX
AC   AAG76045;
XX
DT   03-SEP-2001 (first entry)
XX
DE   Human colon cancer antigen protein SEQ ID NO:6809.
XX
KM   Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX   colorectal carcinoma; chromosome 2.
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000MO-US26524.
XX
PR   29-SEP-1999; 99US-0157137.
XX   03-NOV-1999; 99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR   WPI: 2001-235357/24.
XX   N-PSDB: AAH35450.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 11: Page 8261-8262; 9803pp; English.
XX
XX   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX   cancer-associated nucleic acid molecules (N) and proteins (P), where
XX   the proteins are collectively known as colon cancer antigens. The colon
XX   cancer antigens have cytostatic activity and can be used in gene
XX   therapy and vaccine production. N and P may be used in the prevention,
XX   diagnosis and treatment of diseases associated with inappropriate P
XX   expression. For example, N and P may be used to treat disorders
XX   associated with decreased expression by rectifying mutations or deletions
XX   in a patient's genome that affect the activity of P by expressing P,
XX   inactive proteins or to supplement the patients own production of P.
XX   Additionally, N may be used to produce the colon cancer-associated Ps,
XX   by inserting the nucleic acids into a host cell and culturing the cell
XX   to express the proteins. N and P can be used in the prevention, diagnosis
XX   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX   and AAG77789 represent sequences used in the exemplification of the
XX   present invention.
XX   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX   missing at time of publication, meaning no sequences are present for
XX   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence 91 AA;

```

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Query Match      37.5%; Score 3; DB 22; Length 91;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY   5 afxg 8
    ||||
DB   83 afxg 86

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RESULT      7
AAW27978
ID   AAW27978 standard; Protein; 105 AA.
XX

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AC   AAW27978;
XX
XX   26-AUG-1998 (first entry)
XX
DE   Amino acid sequence of branched amino acid transport system protein.
XX
XX   Staphylococcus aureus protein; ribozyme; antisense sequence; control;
XX   Staphylococcal gene; regulatory element; bacterial gene expression;
XX   vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
XX   toxic shock syndrome.
XX
OS   Staphylococcus aureus.
XX
XX   Key Location/Qualifiers
XX   FT Misc-difference 1..105
XX   FT /note= "residues designated X are not defined in
XX   FT the specification"
XX
XX   WO9730070-A1.
XX
XX   21-AUG-1997.
XX
XX   19-FEB-1997; 97WO-US02318.
XX
XX   20-FEB-1996; 96US-0011888.
XX
XX   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX   Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
XX   Pratt JM, Reichard RW, Rosenberg M, Ward JM;
XX
XX   WPI: 1997-424969/39.
XX   N-PSDB: AAT83937.
XX
XX   Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
XX   PT to isolate antimicrobial compounds, and in vaccines against S.
XX   aureus infection
XX
XX   Claim 6; Page 385-386; 989pp; English.
XX
XX   The present sequence represents a Staphylococcus aureus protein, that,
XX   based on homology is believed to be a membrane-associated component of a
XX   branched amino acid transport system. The DNA sequence was isolated from
XX   a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA
XX   sequence can be used in the construction of ribozymes and antisense
XX   sequences to control the expression of Staphylococcal genes. The DNA
XX   sequence is also useful as a source of regulatory elements for the
XX   control of bacterial gene expression. The present protein may be used
XX   CC to produce vaccines to enable a host to produce specific antibodies
XX   CC with antibacterial action. These vaccines and antibodies would protect
XX   CC a host against invasion by S. aureus, and conditions relating to
XX   CC Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
XX   CC skin syndrome, and toxic shock syndrome.
XX
XX   Sequence 105 AA;

```

```

Query Match      37.5%; Score 3; DB 18; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY   5 afxg 8
    ||||
DB   47 afxg 50

```

```

RESULT      8
AAV13018
ID   AAV13018 standard; Protein; 112 AA.
XX
XX   AAV13018;
XX
XX   22-JUN-1999 (first entry)
XX

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```
XX Human secreted protein encoded by 5' EST SEQ ID NO: 32.
DE
XX
KM Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
KM upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
KM reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN MO9906552-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-1B01236.
XX
PR 01-AUG-1997; 97US-0905223.
XX
XX (GEST ) GENSET.
XX
PI Ducleert A, Dumae Milne Edwards J, Lacroix B;
XX
DR WPI: 1999-153782/13.
XX
DR N-PSDB; AAX51818.
XX
PT New isolated brain-derived nucleic acids - used to develop products
XX which may have cytokine, immune, regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
XX
XX Claim 34; Page 454; 577pp; English.
XX
CC AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AAY12987 to
CC AAY133219, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ Sequence 112 AA:

Query Match 37.5%; Score 3; DB 20; Length 112;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
   ||||
DB 64 afxg 67

RESULT 9
AAY27139
ID AAY27139 standard; protein: 127 AA.
XX
AC AAY27139;
XX
XX 15-SEP-1999 (first entry)
XX
DE Vertebrate slit protein (Seq ID No: 3 of JP11164690).
XX
```

```
KM Vertebrate-derived protein; slit protein; diagnosis; cancer; nerve;
XX muscle; endocrine system.
XX
OS Vertebrata.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..150
FT /note= "residues Xaa can be any amino acid"
XX
XX JP11164690-A.
XX
PN 22-JUN-1999.
XX
PD 05-DEC-1997; 97JP-0335435.
XX
PF 05-DEC-1997; 97JP-0335435.
XX
PR 05-DEC-1997; 97JP-0335435.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
PA WPI: 1999-411830/35.
XX
DR
XX
XX New vertebrate slit protein - useful for diagnosis and treatment of
XX cancers in nerves, muscle and endocrine system
XX
PS Claim 1; Page 38-39; 102pp; Japanese.
XX
XX The invention relates to a vertebrate-derived protein containing an
CC amino acid sequence shown in AAY27137 and AAY27139. The
CC vertebrate-derived protein has at least 55 % homology to one of sequences
CC shown in AAY27141-Y27143, and has slit protein-like activity. The
CC vertebrate slit proteins encoding nucleic acid sequences have at least
CC 60% homology to nucleic acid sequences AAX89161-163. The
CC vertebrate-derived proteins can be produced recombinantly by transforming
CC host cells with expression vectors comprising the encoding nucleic acids.
CC The proteins of the invention are for diagnosing and treating cancer of
CC the nerves, muscle and/or endocrine system.
XX
SQ Sequence 127 AA:

Query Match 37.5%; Score 3; DB 20; Length 127;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
   ||||
DB 40 afxg 43

RESULT 10
AAB63955
ID AAB63955 standard; protein: 162 AA.
XX
AC AAB63955;
XX
XX 26-MAR-2001 (first entry)
XX
DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1317.
XX
XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KM cancer associated antigen; cytosolic; cancer vaccine.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200073801-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14749.
XX
PR 28-MAY-1999; 99US-0136526.
XX
PR 10-SEP-1999; 99US-0153454.
XX
```

PA (LUDW-) LUDWIG INST CANCER RES.
PI Odata Y;
XX
XX WPI: 2001-025274/03.
DR
PT Nucleic acids encoding breast, gastric and prostate cancer associated
PT anticancer precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer -
PS Example 1; Page 792; 799pp; English.
XX
XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB62332 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63770
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
XX Sequence 162 AA;
SQ

Query Match 37.5%; Score 3; DB 22; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 afxg 8
| | | |
Db 128 afxg 131

RESULT 11
AAG73946
ID AAG73946 standard; Protein: 172 AA.
XX
XX AAG73946;
AC
XX
XX 03-SEP-2001 (first entry)
DT
XX
XX Human colon cancer antigen protein SEQ ID NO:4710.
DE
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KM colorectal carcinoma; chromosome 11.
XX
XX Homo sapiens.
OS
XX
XX WO200122920-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000WO-US26524.
PF
XX
XX 29-SEP-1999; 99US-0157137.
PR
XX 03-NOV-1999; 99US-0163280.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Barash SC, Blirze CE, Rosen CA;
PI
XX WPI: 2001-235357/24.
DR
XX N-PSDB; AAB33377.
DR
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
PT
XX Claim 11; Page 6511-6512; 9803pp; English.
PS
XX AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon

CC Cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated P,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAB37196 to AAB37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
XX
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX Sequence 172 AA;
SQ

Query Match 37.5%; Score 3; DB 22; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 afxg 8
| | | |
Db 77 afxg 80

RESULT 12
AAG80899
ID AAG80899 standard; Protein: 181 AA.
XX
XX AAG80899;
AC
XX
XX 28-AUG-2001 (first entry)
DT
XX
XX Lipid degradation protein protein sequence #14.
DE
XX
XX Moss; Physcomitrella patens; lipid metabolism related protein; LMRP;
XX lipid biosynthesis; lipid modification; lipid degradation; cofactor;
XX fatty acid transport; genetic engineering; fatty acid; enzyme; plant;
XX microorganism; polyunsaturated fatty acid; oilseed plant; maize;
XX biotic stress tolerance; abiotic stress tolerance; rye; oat; triticale;
XX rice; barley; soybean; peanut; cotton; rapeseed; canola; manihot;
XX pepper; sunflower; tagetes; potato; tobacco; eggplant; tomato; Vicia;
XX pea; alfalfa; coffee; cacao; tea; Salix; oil palm; coconut;
XX perennial grass; forage crop.
XX
XX Physcomitrella patens.
OS
XX
XX WO200138484-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-EP11615.
PF
XX
XX 25-NOV-1999; 99WO-EP09108.
PR
XX
XX (BADI) BASF PLANT SCI GMBH.
PA
XX
XX Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;
XX
XX WPI: 2001-367669/38.
DR
XX
XX Nucleic acids encoding lipid metabolism related proteins from
PT Physcomitrella patens useful to produce fine chemicals in modified
PT organisms, particularly polyunsaturated fatty acids in oilseed plants -
PT
XX Claim 31; Page 116; 120pp; English.
PS

XX The present invention describes isolated nucleic acid sequences which
CC encode lipid metabolism related proteins (LMRP). The LMRP nucleic acids
CC can be used to modify lipids and fatty acids, cofactors and enzymes in
CC microorganisms and plants, particularly to produce polyunsaturated fatty
CC acids, and are especially useful in oilseed plants. The nucleic acids
CC may also confer biotic or abiotic stress tolerance, particularly to
CC maize, wheat, rice, oat, triticale, rice, barley, soybean, peanut,
CC cotton, rapeseed, canola, sunflower, tagetes, potato,
CC tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao,
CC tea, Salix species, oil palm, coconut, perennial grasses and forage
CC crops. AAH50878 to AAH50882 represent primers used in the exemplification
CC of the present invention. AAH50883 to AAH50968 represents LMRP nucleotide
CC sequences, and AAC80843 to AAC80928 represent LMRP protein sequences,
CC given in the present invention.

XX Sequence 181 AA:

Query Match 37.5%; Score 3; DB 22; Length 181;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 afxg 8

|||||

5 afxg 8

RESULT 13

AAG83349

ID AAG83349 standard; Protein; 181 AA.

XX AAG83349;

DT 06-SEP-2001 (first entry)

DE P patens lipid metabolism related protein #67.

KW Moss; LMRP: lipid metabolism related protein; polyunsaturated fatty acid;

KM fine chemical; transgenic plant.

OS Physcomitrella patens.

PN WO200138541-A1.

PD 31-MAY-2001.

PF 25-NOV-1999; 99WO-EP09108.

PR 25-NOV-1999; 99WO-EP09108.

PA (BADI) BASF PLANT SCI GMBH.

PI Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;

PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;

DR WPI: 2001-381293/40.

PT New isolated nucleic acid molecule encoding Lipid Metabolism Related

PT Proteins useful in the production of fine chemicals -

PS Claim 31; Page 106; 113pp; English.

CC The present invention provides the protein and coding sequences of a

CC number of moss lipid metabolism related proteins (LMRPs). The moss

CC Physcomitrella patens is one of the few plants able to produce

CC polyunsaturated fatty acids, and the sequences can be used to create

CC transgenic plants also capable of producing them. They can also be used

CC to identify the presence of P. patens and in the production of fine

CC chemicals. The present sequence is one of the proteins of the invention.

XX Sequence 181 AA:

Query Match 37.5%; Score 3; DB 22; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 afxg 8

|||||

5 afxg 8

Db 5 afxg 8

|||||

5 afxg 8

RESULT 14

AAH43545

ID AAH43545 standard; Protein; 186 AA.

XX AAH43545;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 223.

KW Human; antiarthritic; antiarheumatic; antiproliferative; vasotropic;

KW cerebroprotective; nootropic; neuroprotective; antibacterial; vitrucide;

KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;

KW neuroprotective; antiallergic; hepatotropic; antidiabetic;

KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;

KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;

KW cardiovascular disorder; neurological disease; infection; human.

OS Homo sapiens.

PN WO200155308-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01309.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-020515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.

PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251038.
PR 05-DEC-2000; 2000US-0251088.
PR 05-DEC-2000; 2000US-0251619.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488781/53.
XX N-PSDB; AAI63851.
DR
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
PS Claim 11; SEQ ID NO 223; 664pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAI634497-AAI63660) useful for gene therapy. The
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, Rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 186 AA;

Query Match 37.5%; Score 3; DB 22; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 afxg 8
|||
Db 73 afxg 76

RESULT 15
AAE04176
ID AAE04176 standard; Protein: 392 AA.

XX
AC AAE04176:
XX
XX 09-AUG-2001 (first entry)
XX
DE Human gene 2 encoded secreted protein fragment, SEQ ID NO:167.
XX
XX Human: secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerability; binding partner identification;
XX gene therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 152
FT /label="Unknown
FT /note="Xaa equals any of the naturally occurring
FT L-amino acids"
FT Misc-difference 388
FT /label="Unknown
FT /note="Xaa equals any of the naturally occurring
XX L-amino acids"
XX
XX WO200134643-A1.
XX
XX 17-MAY-2001.
XX
XX 08-NOV-2000: 2000WO-US30629.
XX
XX 12-NOV-1999: 99US-0164825.
XX 03-AUG-2000: 2000US-0222904.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
XX WPI: 2001-374441/39.
XX
XX Nucleic acids encoding 24 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. Gaucher's disease.
PT Alzheimer's disease, Schmitz syndrome, Creutzfeldt-Jacob disease,
PT diabetes mellitus and multiple sclerosis -
XX
XX
XX Disclosure: Page 10: 532pp; English.
XX
XX AAD08404-AA008478 represent cDNAs corresponding to 24 human secreted
CC protein genes, and AAE04100-AAE004170 represent the proteins they encode.
CC AAE04172-AAE04197 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 24 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiotensin disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,

CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein fragment referred
CC to in the disclosure of the invention.
XX
SQ Sequence 392 AA:
XX
XX
XX Query Match 37.5%; Score 3; DB 22; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 atxg 8
XX ||||
DB 386 atxg 389
XX
XX
XX RESULT 16
XX AAE04125
XX ID AAE04125 standard; Protein; 414 AA.
XX
XX AC AAE04125;
XX
XX DT 09-AUG-2001 (first entry)
XX
XX
XX Human gene 2 encoded secreted protein HMWFE89, SEQ ID NO:112.
XX
XX DE
XX
XX KW Human: secreted protein; proliferative disorder; cancer; tumour; asthma;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW inflammation; neurological disorder; Alzheimer's disease; food additive;
KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW cell culture; chemotaxis; vulnerability; binding partner identification;
KW gene therapy.
XX
XX
XX OS Homo sapiens.
XX
XX
XX FH Key Location/Qualifiers
FH Peptide 1..26
FT /label="Signal_peptide
FT Protein 27..414
FT /label="Mature_human_secreted_protein
FT Misc-difference 174
FT /label="Unknown
FT /note="Encoded by GKT"
FT FT Misc-difference 410
FT /label="Unknown
FT /note="Encoded by CAN"
XX
XX WO200134643-A1.
XX
XX 17-MAY-2001.
XX
XX 08-NOV-2000: 2000WO-US30629.
XX
XX 12-NOV-1999: 99US-0164825.
XX 03-AUG-2000: 2000US-0222904.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
XX WPI: 2001-374441/39.
XX N-PSDB: AAD08430.
XX
XX Nucleic acids encoding 24 human secreted polypeptides, useful for

PT preventing, diagnosing and/or treating e.g. Gaucher's disease,
PT Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
PT diabetes mellitus and multiple sclerosis --
PS Claim 11: Page 480-482; 532pp; English.
XX
PS AAD08404 represent cDNAs corresponding to 24 human secreted
CC protein genes, and AAE04100-AAE04170 represent the proteins they encode.
CC AAE04172-AAE04197 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing, treating
CC or ameliorating medical conditions, e.g., by protein or gene therapy.
CC Pathological conditions can be diagnosed by determining the amount of the
CC new protein in a sample or by determining the presence of mutations in
CC the new genes. Specific uses are described for each of the 24 genes,
CC based on the tissues in which they are most highly expressed, and include
CC developing products for the diagnosis or treatment of proliferative
CC disorders, cancer, tumours, foetal and developmental abnormalities,
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
CC pregnancy-related disorders, endocrine disorders, and infections. The
CC proteins can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC The present sequence represents a human secreted protein of
CC the invention.
XX
SQ Sequence 414 AA:
XX
Query Match 37.5%; Score 3; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 afxg 8
| | | |
Db 408 afxg 411
XX
RESULT 17
AAB63190
ID AAB63190 standard; Protein; 503 AA.
XX
XX AAB63190;
AC
DT 26-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 5 SEQ ID NO:116.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KW rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
KW cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; skin aging;
KW food additive; preservative.
XX
XX Homo sapiens.
OS
XX WO200061629-A1.
PN
XX 19-OCT-2000.
PD

XX
XX 06-APR-2000; 2000WO-US09071.
PF
XX 09-APR-1999; 99US-0128694.
PR
XX 20-JAN-2000; 2000US-0176931.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Ruden SM, Komatsoulis G;
XX
DR WPI: 2000-647420/62.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
PS Disclosure; Page 489-491; 533pp; English.
XX
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
CC to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
CC and polypeptides homologous to them. Human secreted proteins have
CC activities based on the tissues and cells the genes are expressed in.
CC Examples of activities include: immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The polynucleotides and proteins can be
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are
CC also used in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular
CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
CC ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's
CC disease, infections caused by bacteria, viruses and fungi and ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. AAF22364 to
CC AAF22372 and AAB63133 represent sequences used in the exemplification of
CC the present invention.
XX
XX
SQ Sequence 503 AA;
XX
Query Match 37.5%; Score 3; DB 21; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 afxg 8
| | | |
Db 49 afxg 52
XX
RESULT 18
AAR48523
ID AAR48523 standard; peptide; 3 AA.
XX
XX AAR48523;
AC
DT 10-AUG-1994 (first entry)
XX
DE Lactoferrin derived peptide #17.
XX
XX Decomposition; lactoferrin; digestion; enzyme; pepsin; trypsin;
KW antioxidant; oxidation; inhibitor; vitamin E; ascorbic acid;
KW vitamin A; beta-carotene; superoxidase dismutase; coenzyme Q;
KW lipid oxidation; foodstuff; drugs; health food; toiletries; cosmetics.
XX
XX Bos taurus.
OS
XX

PN MO9403555-A.
XX
PD 17-FEB-1994.
XX
PF 04-AUG-1993: 93WC-JP01090.
XX
PR 07-AUG-1992: 92JP-0211335.
XX
PA (MORG) MORINAGA MILK IND CO LTD.
XX
PI Bellamy WR, Fukuwatari Y, Kawase K, Shimamura S:
XX Takase M, Tokiday, Tomita M, Makabayashi H, Yamauchi K:
XX WPI: 1994-065650/08.
DR
PT Antioxidant peptide lactoferrin decomposition product - prevents
XX oxidation of lipid(s) in foodstuffs and drugs without affecting
XX their taste
PS
PS Claim 3: Page 32: 47pp; Japanese.
XX
XX The sequences given in AAR85069-37 are peptides derived by the
CC decomposition of lactoferrin, pref. by digestion with an enzyme, eg.
CC pepsin or trypsin. These peptides may be used in an antioxidant
CC composition which may also contain an oxidation inhibitor such as
CC vitamin E, ascorbic acid, vitamin A, beta-carotene, superoxidase
CC dismutase or coenzyme Q. The antioxidant prevents lipid oxidation
CC in foodstuffs, drugs, health foods, toiletries and cosmetics.
XX
XX Sequence 3 AA:

Query Match 25.0%; Score 2; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 2 wr 3

RESULT 19
AAR85069
ID AAR85069 standard; peptide; 3 AA.
XX
XX AAR85069:
XX
DT 13-JUN-1996 (first entry)
XX
XX Calcium ion channel blocking peptide fragment #2.
DE
XX Calcium ion channel; blocking peptide; hypotensive agent; blood pressure;
KM therapy.
XX
XX Synthetic.
OS
XX JP07278185-A.
PN
XX
PD 24-OCT-1995.
XX
XX 08-APR-1994: 94JP-0070579.
PF
XX 08-APR-1994: 94JP-0070579.
PR
XX (FARH) HOECHST JAPAN KK.
PA
XX WPI: 1995-400979/51.
DR
XX
XX Peptide having calcium channel blocking activity - useful in
PT hypotensive agent
XX
PS Claim 2; Page 2; 6pp; Japanese.
XX

CC AAR85068 and AAR85069 represent calcium ion channel blocking peptides.
CC This sequence corresponds to residues 10-13 of the peptide represented
CC by AAR85068. The peptides suppress blood pressure by inhibiting the
CC calcium influx into cells. These peptides can be used in a hypotensive
CC agent.
XX
XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 16; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
11
Db 2 af 3

RESULT 20
AAR84691
ID AAR84691 standard; peptide; 3 AA.
XX
XX AAR84691:
AC
XX 13-JUN-1996 (first entry)
DT
XX Bovine lactoferrin derived angina pectoris treating peptide.
DE
XX Bovine lactoferrin; angina pectoris; treatment; low toxicity;
XX no side effects; heat resistance; water solubility; stability;
KW aqueous solution; preservative free.
XX
XX Bos taurus.
OS
XX JP07278011-A.
PN
XX 24-OCT-1995.
PD
XX 01-APR-1994: 94JP-0085243.
PF
XX 01-APR-1994: 94JP-0085243.
PR
XX (MORG) MORINAGA MILK IND CO LTD.
PA
XX WPI: 1995-400916/51.
DR
XX
XX Peptide for treatment of angina pectoris - has low toxicity and is
PT heat resistant and water soluble
XX
XX Claim 1; Page 10; 12pp; Japanese.
PS
XX The present peptide is a bovine lactoferrin derived, angina
CC pectoris treatative agent. It has low toxicity and side effects,
CC is heat resistant, water soluble and stable in an aq. soln.. It
CC also requires no preservative.
XX
XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 16; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 2 wr 3

RESULT 21
AAR98547
ID AAR98547 standard; peptide; 3 AA.
XX
XX AAR98547:
AC

XX 12-NOV-1996 (first entry)
XX Peptide for anti-ulcer agent.
DE anti-ulcer agent; low toxicity; stable; heat-resistant.
XX Synthetic.
XX JP08143468-A.
XX
XX 04-JUN-1996.
XX
XX 17-NOV-1994; 94JP-0283869.
XX
XX 17-NOV-1994; 94JP-0283869.
XX
XX (MORG) MORINAGA MILK IND CO LTD.
XX
XX WPI; 1996-31857/32.
XX
XX Anti-ulcer agent contg. peptide - has low toxicity, is
XX heat-resistant and water-soluble
XX
XX Claim 1; Page 9; 11pp; Japanese.
XX
XX AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low
XX in toxicity, is heat-resistant and stable in aqueous soln.. It can be
XX administered orally and be produced in large amounts.
XX
XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 17; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 2 wr 3

RESULT 22
AAR90601
ID AAR90601 standard; peptide; 3 AA.
XX
AC AAR90601;
XX
DT 09-JUL-1996 (first entry)
XX
DE Lactoferrin derived peptide #17.
XX
XX Lactoferrin; antitumour; therapy; tumour; parenteral administration;
XX thermostable; cytotoxic; antibacterial.
XX
XX Synthetic.
XX
XX JP07309771-A.
XX
XX 28-NOV-1995.
XX
XX 17-MAY-1994; 94JP-0103109.
XX
XX 17-MAY-1994; 94JP-0103109.
XX
XX 17-MAY-1994; 94JP-0103109.
XX
XX (MORG) MORINAGA MILK IND CO LTD.
XX
XX WPI; 1996-045317/05.
XX
XX Antitumour agent, derived from lactoferrin, for parenteral
XX administration - has few side effects and is thermally stable and
XX water soluble

PS Claim 1; Page 8; 10pp; Japanese.
XX
XX AAR90585-R90613 represent lactoferrin derived peptides. These sequences
CC can be used as antitumour agents for parenteral administration. The
CC sequences are thermally stable, water soluble and stable in water.
CC These peptide sequences are only cytotoxic to tumour cells.
CC Administration of these sequences results in few side effects. No
CC antiseptic is required for administration due to the antibacterial action
CC of the peptide. Drugs made from these peptides can be rapidly
XX metabolised.
XX
XX Sequence 3 AA;

Query Match 25.0%; Score 2; DB 17; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 2 wr 3

RESULT 23
AAW76946
ID AAW76946 standard; peptide; 3 AA.
XX
XX AAW76946;
AC
XX
XX 25-JAN-1999 (first entry)
DT
XX
XX Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #86.
DE
XX
XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IGH;
XX human immune deficiency virus; HIV; tolerance; treatment; therapy;
XX prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
XX microbial infection; autoimmune disease; antibody; apoptosis;
XX antiviral T cell immunity.
XX
XX Mus sp.
OS
XX Homo sapiens.
XX
XX WO9836087-A1.
XX
XX 20-AUG-1998.
PD
XX
XX 13-FEB-1998; 98WO-US02766.
PE
XX
XX 13-FEB-1997; 97US-0040581.
PR
XX
XX (AMNA-) AMERICAN NAT RED CROSS.
XX
XX Scott D, Zambidis E;
XX
XX WPI; 1998-506315/43.
XX

New fusion immunoglobulin heavy chain including gp120 epitopes and
PT related complete antibodies - DNA, vectors and transformed cells,
PT used to induce tolerance to the epitopes for treatment of human
PT immune deficiency virus infection
XX
XX Disclosure; Page 40; 154pp; English.
XX
XX This sequence is an epitope used in the construction of a novel fusion
CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially
CC human, IGH chain fused in frame at its N-terminus to one or more human
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
CC transfected cells are used to tolerate subjects to gp120 epitopes and to
CC maintain this tolerance, particularly for treatment of HIV infection,
CC optionally together with other therapeutic/prophylactic agents such as
CC vaccines, chemotherapeutic agents and immune response modifiers. Such
CC proteins can be used against other diseases where an immune response is
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.

CC Induction of tolerance suppresses production of antibodies against gp120,
 CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
 CC are bound to gp120 protein, maximising induction of protective antiviral
 CC T cell immunity.

SO Sequence 3 AA:

Query Match 25.0%; Score 2; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
 1 1
 Db 2 af 3

RESULT 24

AAW56219 ID AAW56219 standard; peptide: 3 AA.

AAW56219;

20-JUL-1998 (first entry)

Anti-inflammatory tripeptide.

Anti-inflammatory; macrophage inhibitory activity; fibronectin;

T-cell inhibitory activity; adherence; extracellular matrix;

up-regulation; fas receptor expression; inflammation.

Synthetic.

WO9809985-A2.

12-MAR-1998.

03-SEP-1997; 97WO-1100295.

28-MAY-1997; 97US-0864301.

03-SEP-1996; 96US-0025376.

20-NOV-1996; 96US-0753141.

(YEDA) YEDA RES & DEV CO LTD.

Beserman P, Eisenbachschwartz M, Hirschberg DL;

WPI; 1998-193550/17.

Anti-inflammatory peptides and derivatives - used for treating, e.g.

arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

shock, HIV infection, transplant rejection or Alzheimer's disease

Claim 6; Page 35; 42pp; English.

AAW56171-248 represent anti-inflammatory tripeptides of the invention.

They are derived from the formulae:

Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

Xaa = any amino acid residue.

Cyclic derivatives of the peptides also function as anti-inflammatory

agents. The peptides can be covalently linked to one another either

directly or through a spacer. The peptides and their derivatives have

macrophage inhibitory and T-cell inhibitory activity and thus,

anti-inflammatory activity. The peptides and compositions have

anti-immune activity, i.e. inhibitory effects against a cellular and

humoral immune response, including a response not associated with

inflammation. The peptides also inhibit the ability of macrophages and

T-cells to adhere to extracellular matrix components and fibronectin, as

well as up-regulated fas receptor expression in T-cells. They can be

used to inhibit unwanted immune reaction and inflammation.

Sequence 3 AA:

Query Match 25.0%; Score 2; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 1 1
 Db 1 wr 2

RESULT 25

AAW41282 ID AAW41282 standard; peptide: 3 AA.

AAW41282;

20-MAY-1998 (first entry)

Apoptosis inducer peptide.

Apoptosis inducer; hydrolysed lactoferrin.

Synthetic.

JP10045618-A.

17-FEB-1998.

26-JUL-1996; 96JP-0198196.

26-JUL-1996; 96JP-0198196.

(MORG) MORINAGA MILK IND CO LTD.

WPI; 1998-189187/17.

New inducer(s) of apoptosis - comprise active parts of peptide(s)

derived from hydrolysis of lactoferrin

Claim 3; Page 8; 11pp; Japanese.

This sequence represents an apoptosis inducer peptide of the invention.

The apoptosis inducers comprising active parts of peptides derived from

hydrolysed lactoferrin. The peptides can be used to prepare therapeutic

compositions in the form of tablets, capsules or injections. The inducers

are safe and do not cause adverse reactions.

Sequence 3 AA:

OY 1 wr 2
 1 1
 Db 2 wr 3

Search completed: January 14, 2002, 07:56:32
 Job time: 727 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:57:31 ; Search time 41.59 Seconds
(without alignments)
4.329 Million cell updates/sec

Title: 09-185908-1H
Perfect score: 8
Sequence: 1 wrxxafxg 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 segs, 22503292 residues

Word size : 0
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.5	15	2	US-08-935-886-1	Sequence 1, Appli
2	37.5	24	2	US-08-404-531B-34	Sequence 34, Appl
3	37.5	24	3	US-08-476-900A-34	Sequence 34, Appl
4	37.5	24	3	US-08-488-546A-34	Sequence 34, Appl
5	37.5	45	3	US-08-955-636-17	Sequence 17, Appl
6	37.5	112	4	US-08-905-223-302	Sequence 302, App
7	25.0	3	1	US-08-165-545-8	Sequence 8, Appli
8	25.0	3	1	US-08-305-768-27	Sequence 27, Appl
9	25.0	3	1	US-08-213-897A-13	Sequence 13, Appl
10	25.0	3	1	US-08-213-897A-14	Sequence 14, Appl
11	25.0	3	1	US-08-256-771-17	Sequence 17, Appl
12	25.0	3	1	US-08-470-837-11	Sequence 11, Appl
13	25.0	3	1	US-08-381-98A-17	Sequence 17, Appl
14	25.0	3	2	US-08-871-163-27	Sequence 27, Appl
15	25.0	3	3	US-08-767-903-27	Sequence 27, Appl
16	25.0	3	5	PCT-US95-11724-27	Sequence 27, Appl
17	25.0	4	1	US-07-719-692A-1	Sequence 1, Appli
18	25.0	4	1	US-07-719-692A-2	Sequence 2, Appli
19	25.0	4	1	US-07-719-692A-3	Sequence 3, Appli
20	25.0	4	1	US-07-805-727-8	Sequence 8, Appli
21	25.0	4	1	US-08-165-545-7	Sequence 7, Appli
22	25.0	4	1	US-07-866-018-4	Sequence 4, Appli
23	25.0	4	1	US-08-127-904-8	Sequence 8, Appli
24	25.0	4	1	US-08-390-272-8	Sequence 8, Appli
25	25.0	4	1	US-08-102-372-4	Sequence 4, Appli
26	25.0	4	1	US-08-190-802A-265	Sequence 265, App
27	25.0	4	1	US-08-206-789-5	Sequence 5, Appli

28	2	25.0	4	1	US-08-211-070A-7	Sequence 7, Appli
29	2	25.0	4	1	US-08-176-938-24	Sequence 24, Appl
30	2	25.0	4	1	US-08-176-938-35	Sequence 35, Appl
31	2	25.0	4	1	US-08-215-137-11	Sequence 11, Appl
32	2	25.0	4	1	US-08-193-977-20	Sequence 20, Appl
33	2	25.0	4	1	US-08-461-611-12	Sequence 12, Appl
34	2	25.0	4	1	US-08-340-045-18	Sequence 18, Appl
35	2	25.0	4	1	US-08-340-045-20	Sequence 20, Appl
36	2	25.0	4	1	US-08-256-771-16	Sequence 16, Appl
37	2	25.0	4	1	US-08-224-868-7	Sequence 7, Appli
38	2	25.0	4	1	US-08-561-478-4	Sequence 4, Appli
39	2	25.0	4	1	US-08-549-008-29	Sequence 29, Appl
40	2	25.0	4	1	US-08-222-851-22	Sequence 22, Appl
41	2	25.0	4	1	US-08-387-156-23	Sequence 23, Appl
42	2	25.0	4	1	US-08-425-069-18	Sequence 18, Appl
43	2	25.0	4	1	US-08-460-343B-63	Sequence 63, Appl
44	2	25.0	4	1	US-08-388-321-8	Sequence 8, Appli
45	2	25.0	4	1	US-08-466-632-8	Sequence 8, Appli
46	2	25.0	4	1	US-08-446-177-8	Sequence 8, Appli
47	2	25.0	4	1	US-08-643-709A-4	Sequence 4, Appli
48	2	25.0	4	1	US-08-398-028B-63	Sequence 63, Appl
49	2	25.0	4	1	US-08-798-897-46	Sequence 46, Appl
50	2	25.0	4	1	US-08-381-984-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-935-886-1
; Sequence 1, Application US/08935886
; Patent No. 5994625
; GENERAL INFORMATION:
; APPLICANT: Melchers, Leo S.
; APPLICANT: Sela-Bauri, Marianne B.
; APPLICANT: Bres-Vloemans, Alexandra A.
; APPLICANT: Ponstein, Anne S.
; APPLICANT: Apotheker-de Groot, Marlon
; APPLICANT: Cornelissen, Bernardus J. C.
; TITLE OF INVENTION: Antifungal Chitin Binding Proteins and DNA
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 14.4 MB storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: DOS 6.20
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,886
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,640
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: PCT/EP93/02790
; FILING DATE: 05-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mess. Clifford J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010139-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELE: 233288
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;

LENGTH: 15 Amino Acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Nicotiana tabacum
STRAIN: Samsun NN
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Leaf, wounded
US-08-935-886-1

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
1111
DB 3 AFXG 6

RESULT 2
US-08-404-531B-34
Sequence 34, Application US/08404531B
Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 5863724
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-404-531B-34

Query Match 37.5%; Score 3; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 afxg 8

DB 3 AFXG 6

RESULT 3
US-08-476-900A-34
Sequence 34, Application US/08476900A
Patent No. 6031150
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6031150
TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypogly
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,900A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-476-900A-34

Query Match 37.5%; Score 3; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
1111
DB 3 AFXG 6

RESULT 4
US-08-488-546A-34
Sequence 34, Application US/08488546A
Patent No. 6054313
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cole, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
Patent No. 6054313
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor

CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-488-546A-34

Query Match 37.5%; Score 3; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
DB 3 AFXG 6

RESULT 5
US-08-955-636-17
Sequence 17, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsesluen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 45
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: MOD.RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-17

Query Match 37.5%; Score 3; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 rxxaf 6

||||
DB 25 RXXAF 29

RESULT 6
US-08-905-223-302
Sequence 302, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Dueltz, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig-peptide
LOCATION: -52...-1
IDENTIFICATION METHOD: Von Heljne matrix
OTHER INFORMATION: score 7
OTHER INFORMATION: seq SWMLCLCYFAFP/FQ
US-08-905-223-302

Query Match 37.5%; Score 3; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 afxg 8
||||
DB 64 AFXG 67

RESULT 7
US-08-165-545-8
Sequence 8, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial peptide and
NUMBER OF SEQUENCES: 13

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Wenderoth, Lind & Ponack
;; STREET: 805 Fifteenth Street, N.W., #700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: DisplayWrite
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/165,545
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/871,981
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; HYPOTHEICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLER:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
||
Db 2 wr 3

RESULT 8
US-08-305-768-27
; Sequence 27, Application US/08305768
; Patent No. 5602097
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,768
; FILING DATE: 12-SEPT-1994
; CLASSIFICATION: 514

;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
||
Db 1 wr 2

RESULT 9
US-08-213-897A-13
; Sequence 13, Application US/08213897A
; Patent No. 5618790
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Protease Mediated Drug Delivery System
; NUMBER OF SEQUENCES: 18
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,897A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/593,867
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/833,183
; FILING DATE: 10-FEB-1992
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-213-897A-13

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 3;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
Db 1 Af 2

RESULT 10
US-08-213-897A-14
Sequence 14, Application US/08213897A
Patent No. 5618790
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Protease Mediated Drug Delivery System
NUMBER OF SEQUENCES: 18
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/213,897A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/593,867
FILING DATE: 05-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/833,183
FILING DATE: 10-FEB-1992
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-213-897A-14

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 3;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
Db 1 Af 2

RESULT 11
US-08-256-771-17
Sequence 17, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-17

Query Match
Best Local Similarity 25.0%; Score 2; DB 1; Length 3;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 WR 3

RESULT 12
US-08-470-837-11
Sequence 11, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimmi, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Ian
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30630-1US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-837-11

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
DB 2 AF 3

RESULT 13
US-08-381-984-17
; Sequence 17, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,984
; FILING DATE: April 11, 1995
; CLASSIFICATION: 252
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note="the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-17

Query Match 25.0%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 2 WR 3

RESULT 14
US-08-871-163-27
; Sequence 27, Application US/08871163
; Patent No. 5885782
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,163
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-871-163-27

Query Match 25.0%; Score 2; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 1 WR 2

RESULT 15
US-08-767-903-27
; Sequence 27, Application US/08767903
; Patent No. 6020312
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,903
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-767-903-27

Query Match 25.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 wr 2

Db 1 11
1 WR 2

RESULT 16
PCT-US95-11724-27
Sequence 27, Application PC/TUS9511724
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11724
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 25.0%; Score 2; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 11
1 WR 2

RESULT 17
US-07-719-692A-1
Sequence 1, Application US/07719692A
Patent No. 5250414
GENERAL INFORMATION:
APPLICANT: Schwab, Martin E. et al.
TITLE OF INVENTION: Neutrite Growth Regulatory Factors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/719,692A
FILING DATE: 19910624
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "amide at carboxy terminus"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "carboxybenzoxy derivatized"
OTHER INFORMATION: N-terminus"
US-07-719-692A-1

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 af 6
1 11
2 Af 3

Db 2 Af 3

RESULT 18
US-07-719-692A-2
Sequence 2, Application US/07719692A
Patent No. 5250414
GENERAL INFORMATION:
APPLICANT: Schwab, Martin E. et al.
TITLE OF INVENTION: Neutrite Growth Regulatory Factors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/719,692A
FILING DATE: 19910624
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "carboxybenzoxy derivatized"
OTHER INFORMATION: end"
FEATURE:
NAME/KEY: Modified-site

LOCATION: 4
OTHER INFORMATION: /note="Tyrosine is radiolabeled
OTHER INFORMATION: with Iodine-125."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note="amide at carboxy-terminus"
US-07-719-692A-2

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
Db 2 Af 3

RESULT 19
US-07-719-692A-3
Sequence 3, Application US/07719692A
Patent No. 5250414
GENERAL INFORMATION:
APPLICANT: Schwab, Martin E. et al.
TITLE OF INVENTION: Neurite Growth Regulatory Factors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/719,692A
FILING DATE: 19910624
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note="amide at carboxy-terminus"
US-07-719-692A-3

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
Db 2 Af 3

RESULT 20
US-07-805-727-8
Sequence 8, Application US/07805727
Patent No. 5424186
GENERAL INFORMATION:
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Strayer, Hubert
APPLICANT: Pirrung, Michael C.
APPLICANT: Read, J. Leighton
TITLE OF INVENTION: Very Large Scale Immobilized Polymer
SYNTHESIS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vernon A. No. 5424186v1el
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,727
FILING DATE: 19911206
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: No. 5424186v1el, Vernon A.
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 11509A(1)11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-805-727-8

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
Db 3 Af 4

RESULT 21
US-08-165-545-7
Sequence 7, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Check, Jr.
REGISTRATION NUMBER: 33,367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
* HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wr 2
11
3 wr 4
Db

RESULT 22
US-07-866-018-4
Sequence 4, Application US/07866018
Patent No. 5470705
GENERAL INFORMATION:
APPLICANT: Grossman, Paul D.
APPLICANT: Fung, Steven
APPLICANT: Menchen, Steven M.
APPLICANT: Woo, Sam L.
APPLICANT: Winn-Deen, Emily S.
TITLE OF INVENTION: Probe Composition and Method
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,018
FILING DATE: 19920407
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 0550-0023.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TETRAPEPTIDE, PAGE 28
US-07-866-018-4

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 af 6
11
2 af 3
Db

RESULT 23
US-08-127-904-8
Sequence 8, Application US/08127904
Patent No. 5470951
GENERAL INFORMATION:
APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method For Antagonizing
TITLE OF INVENTION: Amnestic Effects of Amyloid n
TITLE OF INVENTION: Protein and Improving the
TITLE OF INVENTION: Quality of Life in Individuals
TITLE OF INVENTION: With Alzheimer Disease
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte

STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5470951e
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: No. 5470951e
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEX: No. 5470951e
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
US-08-127-904-8

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
DB 1 AF 2

RESULT 24
US-08-390-272-8
Sequence 8, Application US/08390272
Patent No. 5489678
GENERAL INFORMATION:
APPLICANT: Fodor, Stephen P. A.
APPLICANT: Stryer, Lubert
APPLICANT: Winkler, James L.
APPLICANT: Holmes, Christopher P.
APPLICANT: Solas, Dennis W.
TITLE OF INVENTION: Very large scale Immobilized Polymer
TITLE OF INVENTION: Synthesis
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vernon A. No. 5489678v1e1
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,272
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/624,120
FILING DATE: 06-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: No. 5489678v1e1, Vernon A.

REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 11509-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-272-8

Query Match 25.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 af 6
11
DB 3 AF 4

RESULT 25
US-08-102-372-4
Sequence 4, Application US/08102372
Patent No. 5514543
GENERAL INFORMATION:
APPLICANT: Grossman, Paul D.
APPLICANT: Fung, Steven
APPLICANT: Menchen, Steven M.
APPLICANT: Woo, Sam L.
APPLICANT: Winn-Deen, Emily S.
TITLE OF INVENTION: Probe Composition and Method
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,372
FILING DATE: 04-AUG-1993
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Powers, Vincent M.
REGISTRATION NUMBER: 36,246
REFERENCE/DOCKET NUMBER: 0550-0023.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: synthetic tetrapeptide
US-08-102-372-4

Query Match 25.0%; Score 2; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0;

Indels

0;

Gaps

0;

Oy 5 af 6
11
Db 2 Af 3

Search completed: January 14, 2002, 07:57:32
Job time: 377 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:22:55 ; Search time 66.39 Seconds
(without alignments)
2.712 Million cell updates/sec

Title: US-09-185-908-34

Perfect score: 48

Sequence: 1 WKIYSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: Issued_Patents_AA: *
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	70.8	344	2	US-07-857-224B-92
2	34	70.8	344	2	US-07-857-224B-93
3	33	68.8	349	4	US-09-137-855-4
4	33	68.8	350	4	US-09-137-855-2
5	33	68.8	3672	2	US-08-822-445-12
6	33	68.8	3801	2	US-08-822-445-10
7	32	66.7	54	1	US-08-222-616-27
8	32	66.7	54	5	PCT-US95-04228-27
9	32	66.7	137	3	US-08-747-221B-11
10	32	66.7	137	4	US-09-005-051-11
11	32	66.7	563	4	US-08-714-168-1
12	32	66.7	563	2	US-09-320-721A-1
13	32	66.7	570	3	US-08-747-221B-54
14	32	66.7	570	3	US-08-747-221B-55
15	32	66.7	570	4	US-09-005-051-54
16	32	66.7	570	4	US-09-005-051-55
17	32	66.7	595	4	US-08-747-221B-31
18	32	66.7	595	4	US-09-005-051-31
19	32	66.7	596	4	US-08-747-221B-25
20	32	66.7	596	4	US-09-005-051-25
21	32	66.7	853	3	US-08-451-946B-6
22	32	66.7	853	3	US-08-446-938B-6
23	32	66.7	853	3	US-08-311-703A-6
24	32	66.7	853	3	US-08-446-939B-6
25	32	66.7	853	3	US-09-183-543-6
26	32	66.7	853	4	US-08-446-936A-6
27	32	66.7	853	5	PCT-US92-09326-2

28	31	64.6	41	4	US-08-706-344C-23	Sequence 23, Appl
29	31	64.6	278	2	US-08-569-168-2	Sequence 2, Appl
30	31	64.6	383	2	US-08-569-168-7	Sequence 7, Appl
31	31	64.6	430	1	US-08-484-105-22	Sequence 22, Appl
32	31	64.6	430	1	US-08-484-105-22	Sequence 22, Appl
33	31	64.6	500	1	US-08-117-083-69	Sequence 69, Appl
34	31	64.6	734	2	US-08-765-243-8	Sequence 8, Appl
35	31	64.6	734	5	PCT-US95-07295-8	Sequence 8, Appl
36	30	62.5	207	3	US-08-549-515-9	Sequence 9, Appl
37	30	62.5	231	1	US-08-144-121-5	Sequence 5, Appl
38	30	62.5	231	2	US-08-735-893-5	Sequence 5, Appl
39	30	62.5	258	3	US-09-035-706-3	Sequence 3, Appl
40	30	62.5	258	3	US-08-955-841-3	Sequence 3, Appl
41	30	62.5	269	2	US-08-701-191A-35	Sequence 35, Appl
42	30	62.5	304	2	US-08-701-191A-30	Sequence 30, Appl
43	30	62.5	413	2	US-08-846-762-15	Sequence 15, Appl
44	30	62.5	413	2	US-08-846-762-88	Sequence 18, Appl
45	30	62.5	438	1	US-08-111-939-17	Sequence 17, Appl
46	30	62.5	450	5	PCT-US95-05008-7	Sequence 7, Appl
47	30	62.5	458	4	US-09-223-989-9	Sequence 9, Appl
48	30	62.5	530	5	PCT-US95-08493-2	Sequence 2, Appl
49	30	62.5	860	5	PCT-US95-08493-19	Sequence 19, Appl
50	30	62.5	868	1	US-08-374-834-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-07-857-224B-92
Sequence 92, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857, 224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 344
TYPE: amino acid
MOLECULE TYPE: linear
TOPOLOGY: linear
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Scizosaccharomyces pombe
FEATURE: Alcohol dehydrogenase, Table 3 Column 15
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases

JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-92

Query Match 70.8%; Score 34; DB 2; Length 344;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
||| |||
Db 82 WKIGDYAG 89

RESULT 2
US-07-857-224B-93
Sequence 93, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 344
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Aspergillus
FEATURE: Alcohol dehydrogenase, Table 3 Column 16
PUBLICATION INFORMATION:
AUTHORS: Joernvall, H.
AUTHORS: Persson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of the National Academy of Sciences, USA
VOLUME: 78
PAGES: 4226-4230
DATE: 1981
US-07-857-224B-93

Query Match 70.8%; Score 34; DB 2; Length 344;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8

Db ||| |||
82 WKIGDYAG 89

RESULT 3
US-09-137-855-4
Sequence 4, Application US/09137855B
Patent No. 6242237
GENERAL INFORMATION:
APPLICANT: Kotof, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Andersen, Lene N.
APPLICANT: Clausen, Ib G.
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: An Enzyme With Galactanase Activity
FILE REFERENCE: 4686.204-US
CURRENT APPLICATION NUMBER: US/09/137,855B
CURRENT FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 0233/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 0235/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: PCT/DK97/00092
EARLIER FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 349
TYPE: PRT
ORGANISM: Humicola insolens
US-09-137-855-4

Query Match 68.8%; Score 33; DB 4; Length 349;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
||| |||
Db 124 WKLYNY 129

RESULT 4
US-09-137-855-2
Sequence 2, Application US/09137855B
Patent No. 6242237
GENERAL INFORMATION:
APPLICANT: Kotof, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Andersen, Lene N.
APPLICANT: Clausen, Ib G.
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: An Enzyme With Galactanase Activity
FILE REFERENCE: 4686.204-US
CURRENT APPLICATION NUMBER: US/09/137,855B
CURRENT FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 0233/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 0235/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: PCT/DK97/00092
EARLIER FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Myceliophthora thermophila
US-09-137-855-2

Query Match 68.8%; Score 33; DB 4; Length 350;
Best Local Similarity 66.7%; Pred. No. 92;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 WKIYSY 6
11:1:1
DB 125 WKLYNY 130

RESULT 5

US-08-822-445-12
; Sequence 12, Application US/08822445
; Patent No. 5952223
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Jerry
; APPLICANT: Moore, Charles
; TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION NUMBER: US/08/822,445
; APPLICATION NUMBER: US/08/822,445
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-062-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3672 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-822-445-12

Query Match 68.8%; Score 33; DB 2; Length 3672;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSY 6
11:1:1
DB 728 WKLYNY 733

RESULT 6

US-08-822-445-10
; Sequence 10, Application US/08822445
; Patent No. 5952223
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Jerry
; APPLICANT: Moore, Charles
; TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennile & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,445
FILING DATE: 21-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-062-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3801 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-822-445-10

Query Match 68.8%; Score 33; DB 2; Length 3801;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSY 6
11:1:1
DB 728 WKLYNY 733

RESULT 7
US-08-222-616-27
; Sequence 27, Application US/08222616
; Patent No. 5635177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,616
; FILING DATE: 4-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-27

Query Match 66.7%; Score 32; DB 1; Length 54;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSA 7
11111
Db 19 WKIYSGA 25

RESULT 8
PCT-US95-04228-27
Sequence 27, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Shao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
TOPOLOGY: linear

PCT-US95-04228-27

Query Match 66.7%; Score 32; DB 5; Length 54;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSA 7
11111
Db 19 WKIYSGA 25

RESULT 9
US-08-747-221B-11
Sequence 11, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747, 221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-11

Query Match 66.7%; Score 32; DB 3; Length 137;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
11111
Db 105 IYSYAG 110

RESULT 10
US-09-005-051-11
Sequence 11, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Hsaka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 62912222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-11

Query Match 66.7%; Score 32; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IYSYAG 8
|||||
DB 105 IYSYAG 110

RESULT 11
US-08-714-168-1
Sequence 1, Application US/08714168
Patent No. 5948636
GENERAL INFORMATION:
APPLICANT: Hideharu MORI et al.
TITLE OF INVENTION: CELL SURFACE POLYPEPTIDE GENE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,168
FILING DATE: September 27, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 563 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Porphyromonas (Bacteroides) gingivalis
STRAIN: OM2409
US-08-714-168-1

Query Match 66.7%; Score 32; DB 2; Length 563;
Best Local Similarity 66.7%; Pred. No. 2,2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSY 6
|||||
DB 554 WKVHSY 559

RESULT 12
US-09-320-721A-1
Sequence 1, Application US/09320721A
Patent No. 6171805
GENERAL INFORMATION:
APPLICANT: Hideharu MORI et al.
TITLE OF INVENTION: DNA AND HOST CELLS ENCODING A CELL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,721A
FILING DATE: May 27, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,168
FILING DATE: September 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 563 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:

ORGANISM: Porphyromonas (Bacteroides) gingivalis
STRAIN: OM2409
US-09-320-721A-1

Query Match 66.7%; Score 32; DB 4; Length 563;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYSYG 6
DB 554 WKVHST 559

RESULT 13
US-08-747-221B-54
Sequence 54, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-54

Query Match 66.7%; Score 32; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYG 8
DB 79 IYSYG 84

RESULT 14
US-08-747-221B-55
Sequence 55, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy

TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-55

Query Match 66.7%; Score 32; DB 3; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYG 8
DB 79 IYSYG 84

RESULT 15
US-09-005-051-54
Sequence 54, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-54

Query Match 66.7%; Score 32; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
|||||
DB 79 IYSYAG 84

RESULT 16
US-09-005-051-55
Sequence 55, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-55

Query Match 66.7%; Score 32; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 IYSYAG 8
|||||
DB 79 IYSYAG 84

RESULT 17
US-08-747-221B-31
Sequence 31, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: NO. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: PC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-31

Query Match 66.7%; Score 32; DB 3; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
|||||
DB 104 IYSYAG 109

RESULT 18
US-09-005-051-31
Sequence 31, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carol Talkington Verser, Ph.D.

```

ADDRESS: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-31

Query Match      66.7%; Score 32; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
Db 104 IYSYAG 109

RESULT 19
US-08-747-221B-25
Sequence 25, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESS: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
```

```

REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-25

Query Match      66.7%; Score 32; DB 3; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
Db 105 IYSYAG 110

RESULT 20
US-09-005-051-25
Sequence 25, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESS: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-25

Query Match      66.7%; Score 32; DB 4; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSYAG 8
```


Db 105 IYISYAG 110

RESULT 21

US-08-451-946B-6
Sequence 6, Application US/08451946B
Patent No. 6001969

GENERAL INFORMATION:

APPLICANT: Lin, Herbert Y.
APPLICANT: Wang, Xiao-Fan
APPLICANT: Weinberg, Robert A.

TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
TITLE OF INVENTION: Products and Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,946B
FILING DATE: 26-MAY-1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,703
FILING DATE: 23-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,063
FILING DATE: 31-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI91-09V

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-451-946B-6

Query Match 66.7%; Score 32; DB 3; Length 853;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8

Db 808 WYIYSHTG 815

RESULT 22

US-08-446-938B-6
Sequence 6, Application US/08446938B
Patent No. 6008011

GENERAL INFORMATION:

APPLICANT: Lin, Herbert Y.
APPLICANT: Wang, Xiao-Fan
APPLICANT: Weinberg, Robert A.

TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded

TITLE OF INVENTION: Products and Uses Therefor

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,938B
FILING DATE: 23-MAY-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,703
FILING DATE: 23-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/786,063
FILING DATE: 31-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI91-09FZ

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-446-938B-6

Query Match 66.7%; Score 32; DB 3; Length 853;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8

Db 808 WYIYSHTG 815

RESULT 23

US-08-311-703A-6
Sequence 6, Application US/08311703A
Patent No. 6010872

GENERAL INFORMATION:

APPLICANT: Lin, Herbert Y.
APPLICANT: Wang, Xiao-Fan
APPLICANT: Weinberg, Robert A.

TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
TITLE OF INVENTION: Products and Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,703A
; FILING DATE: 23-SEP-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hogle, Doreen
; REGISTRATION NUMBER: 36,361
; REFERENCE/DOCKET NUMBER: WH191-09F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-311-703A-6

Query Match          66.7%; Score 32; DB 3; Length 853;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
Db 808 WYIYSHTG 815

RESULT 24
; Sequence 6, Application US/08446939B
; Patent No. 6046157
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,939B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 23-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH191-09FX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
```

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-939B-6

Query Match          66.7%; Score 32; DB 3; Length 853;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
Db 808 WYIYSHTG 815

RESULT 25
; US-09-183-543-6
; Sequence 6, Application US/09183543A
; Patent No. 6085867
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Modulation of TGF-Beta by TGF-Beta Type III Receptor Polypepti
; FILE REFERENCE: WH191-09FXA
; CURRENT APPLICATION NUMBER: US/09/183,543A
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: US 08/446,939
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: US 08/311,703
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: US 07/786,063
; EARLIER FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 853
; TYPE: PRT
; ORGANISM: genomic
; US-09-183-543-6

Query Match          66.7%; Score 32; DB 3; Length 853;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
Db 808 WYIYSHTG 815
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Search completed: January 14, 2002, 06:22:57
Job time: 175 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:21:36 ; Search time 75.2 Seconds
(without alignments)
8.104 Million cell updates/sec

Title: US-09-185-908-34
Perfect score: 48
Sequence: 1 WKIYSTAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR.68: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	81.2	513	1 A35742	aqualysin (EC 3.4.
2	37	77.1	288	2 D75286	serine proteinase
3	37	77.1	493	2 A48457	hexokinase (EC 2.7
4	36	75.0	168	2 B25217	myosin heavy chain
5	36	75.0	168	2 A28476	myosin heavy chain
6	36	75.0	168	2 A25217	myosin heavy chain
7	36	75.0	215	2 S66521	myosin heavy chain
8	36	75.0	307	2 T22558	hypothetical prote
9	36	75.0	396	2 PS0075	myosin heavy chain
10	36	75.0	571	2 S49119	embryonic/neonatal
11	36	75.0	830	2 JX0317	myosin S-1 heavy c
12	36	75.0	1175	2 S39951	chitin synthase (E
13	36	75.0	1931	2 A59234	slow myosin heavy
14	36	75.0	1934	2 I48153	myosin heavy chain
15	36	75.0	1935	2 A37102	myosin beta heavy
16	36	75.0	1935	1 S06006	myosin beta heavy
17	36	75.0	1935	2 A58286	myosin beta heavy
18	36	75.0	1937	2 I38055	myosin heavy chain
19	36	75.0	1938	1 S06005	myosin heavy chain
20	36	75.0	1938	1 JX0178	myosin alpha heavy
21	36	75.0	1938	2 I49464	myosin heavy chain
22	36	75.0	1938	2 A59293	alpha cardiac myos
23	36	75.0	1939	2 A46762	skeletal myosin be
24	36	75.0	1939	1 A46175	myosin alpha heavy
25	36	75.0	1940	1 S04090	myosin heavy chain
26	36	75.0	1940	1 A24922	myosin heavy chain
27	36	75.0	1940	2 A29320	myosin heavy chain
28	35	72.9	664	2 T10573	probable serine/th
29	35	72.9	664	2 B85122	serine/threonine k

30	35	72.9	817	2 T21336	hypothetical prote
31	35	72.9	947	2 T03795	ornithine decarbox
32	34	70.8	42	2 I56598	aromatase - human
33	34	70.8	262	2 H64311	hypothetical prote
34	34	70.8	264	2 H85861	hypothetical prote
35	34	70.8	336	1 DEECDO	hypothetical prote
36	34	70.8	36	2 C85621	dihydro-oxotrate de
37	34	70.8	348	1 DEBYA	dihydro-oxotrate de
38	34	70.8	348	1 DEBYA2	alcohol dehydrogen
39	34	70.8	416	2 T41655	alcohol dehydrogen
40	34	70.8	459	2 B69458	probable dipeptida
41	34	70.8	549	2 H64992	sulfate adenylyl tr
42	34	70.8	660	2 A84232	hypothetical prote
43	34	70.8	685	1 A48289	spore cortex synth
44	34	70.8	1980	2 S54307	neurotrophic recep
45	34	70.8	2022	2 A59256	myosin-IXb [simila
46	34	70.8	2894	2 C64474	hypothetical prote
47	33.5	69.8	411	2 S74760	hypothetical prote
48	33	68.8	159	1 OOCV2	aphid transmission
49	33	68.8	245	2 S16033	rRNA methylase erm
50	33	68.8	245	2 B27739	erythromycin resis

ALIGNMENTS

RESULT 1
A35742
aqualysin (EC 3.4.21.-) I precursor - Thermus aquaticus
C:Species: Thermus aquaticus
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #tox_change 16-Jun-2000
C:Accession: A35742; S00620; S00324
J. Terada, I.; Kwon, S.T.; Miyata, Y.; Matsuzawa, H.; Ohta, T.
J. Biol. Chem. 265, 6576-6581, 1990
A:Title: Unique precursor structure of an extracellular protease, aqualysin I, with N
A:Reference number: A35742; MUID:90216674
A:Accession: A35742
A:Molecule type: DNA
A:Residues: 1-513 <TER>
A:Cross-references: GB:J90108; GB:D90108; GB:J05414; NID:q217171; PIDN:BAAL135.1; PI
A:Note: the authors translated the codon CTG for residue 470 as Val, and GGT for res1
R:Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T.
Eur. J. Biochem. 173, 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline ser
A:Reference number: S00620; MUID:88225062
A:Accession: S00620
A:Molecule type: DNA
A:Residues: 75-442 <KKMO>
A:Cross-references: EMBL:X07734; NID:q48069; PIDN:CA30559.1; PID:q602091
A:Note: part of this sequence, including the amino and carboxyl ends of the mature pr
R:Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; K
Eur. J. Biochem. 171, 441-447, 1988
A:Title: Purification and characterization of aqualysin I (a thermophilic alkaline se
A:Reference number: S00324; MUID:88151937
A:Accession: S00324
A:Molecule type: protein
A:Residues: 128-170 <MAVS>
C:Superfamily: subtilisin; subtilisin homology
C:Keywords: extracellular protein; hydrolase; serine proteinase
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-127/Domain: propeptide #status predicted <PRO>
F:128-408/Product: aqualysin I #status experimental <MAT>
F:157-364/Domain: subtilisin homology <SBT>
F:255-257,281-283/Region: SI specificity crevice #status predicted
F:409-513/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F:166,197,349/Active site: Asp, His, Ser #status predicted

Query Match 81.2%; Score 39; DB 1; Length 513;
Best Local Similarity 62.5%; Prod. No. 8.9;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 WKIYSTAG 8

Db 495 WRIVAYSG 502

RESULT 2

D75286
serine proteinase truncated homolog DR2322 [imported] - Deinococcus radiodurans (strain

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000

C:Accession: D75286

R:White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20336896

A:Accession: D75286

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-288 <WHI>

A:Cross-references: GB:AE002064; GB:AE000513; NID:g6460134; PIDN:AAF11870.1; PID:g646013

A:Experimental source: strain R1

A:Gene: DR2322

A:Map position: 1

Query Match 77.1%; Score 37; DB 2; Length 288;
Best Local Similarity 50.0%; Pred. No. 12;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8

Db 271 WVIYATSG 278

RESULT 3

A48457
hexokinase (EC 2.7.1.1) - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000

C:Accession: A48457

R:Olafsson, P.; Matile, H.; Certa, U.

Mol. Biochem. Parasitol. 56, 89-101, 1992

A:Title: Molecular analysis of Plasmodium falciparum hexokinase.

A:Reference number: A48457; MUID:93116809

A:Accession: A48457

A:Status: Preliminary

A:Molecule type: nucleic acid

A:Residues: 1-493 <OLA>

A:Cross-references: GB:M92054; NID:g160320; PID:g160321

A:Note: sequence extracted from NCBI backbone (NCBIN:121419, NCBI:121420)

C:Superfamily: hexokinase; hexokinase homology

C:Keywords: Phosphotransferase

F:42-482/Domain: hexokinase homology <HXK>

Query Match 77.1%; Score 37; DB 2; Length 493;
Best Local Similarity 75.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8

Db 279 WKIYATSG 286

J. Biol. Chem. 261, 6613-6618, 1986

A:Title: A canonical sequence organization at the 5'-end of the myosin heavy chain ge

A:Reference number: A92587; MUID:86196091

A:Accession: B25217

A:Molecule type: DNA

A:Residues: 1-168 <KRO>

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; muscle

F:85-168/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 75.0%; Score 36; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8

Db 113 WVIYATSG 120

RESULT 5

A28476
myosin heavy chain - chicken (clone N127) (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 13-Aug-1999

C:Accession: A28476

R:Kropp, K.E.; Gulick, J.; Robbins, J.

J. Biol. Chem. 262, 16536-16545, 1987

A:Title: Structural and transcriptional analysis of a chicken myosin heavy chain gene

A:Reference number: A28476; MUID:88059036

A:Accession: A28476

A:Molecule type: DNA

A:Residues: 1-168 <KRO>

A:Cross-references: GB:M18139; GB:J03467; NID:g212379; PIDN:AAA48973.1; PID:g555469

C:Genetics:

A:Insertions: 68/3; 116/3

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; muscle

F:89-168/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 75.0%; Score 36; DB 2; Length 168;
Best Local Similarity 62.5%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8

Db 113 WVIYATSG 120

RESULT 6

A25217
myosin heavy chain - chicken (clone N101) (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 13-Aug-1999

C:Accession: A25217

R:Kropp, K.; Gulick, J.; Robbins, J.

J. Biol. Chem. 261, 6613-6618, 1986

A:Title: A canonical sequence organization at the 5'-end of the myosin heavy chain ge

A:Reference number: A92587; MUID:86196091

A:Accession: A25217

A:Molecule type: DNA

A:Residues: 1-169 <KRO>

A:Cross-references: GB:M13513; NID:g212361; PIDN:AAA48965.1; PID:g555466

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; muscle

F:90-169/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 75.0%; Score 36; DB 2; Length 169;
Best Local Similarity 62.5%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 114 WMIITYSG 121

RESULT 7

S66521
myosin heavy chain - common carp (fragment)
C:Species: Cyprinus carpio (common carp)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
C:Accession: S66521
R:Gauvry, L.; Emilion, S.; Hansen, E.; Butterworth, P.; Goldspink, G.
Eur. J. Biochem. 236, 887-894, 1996
A:Title: The characterisation of the 5' regulatory region of a temperature-induced myosin
A:Reference number: S66521; MUID:96270741
A:Accession: S66521
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-215 <GAP>
A:Cross-references: EMBL:Z37999
C:Genetics:
A:Introns: 67/3; 115/3; 167/3; 177/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:88-215/Domain: myosin motor domain homology (fragment) <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 36; DB 2; Length 215;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 112 WMIITYSG 119

RESULT 8

T22558
hypothetical protein F53C11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22558
R:Baynes, C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z19581
A:Accession: T22558
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-307 <MIL>
A:Cross-references: EMBL:Z79756; PIDN:CA802120.1; GSPDB:GN00023; CESP:F53C11.1
A:Experimental source: clone F53C11
C:Genetics:
A:Gene: CESP:F53C11.1
A:Map position: 5
A:Introns: 53/3; 89/2

Query Match 75.0%; Score 36; DB 2; Length 307;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 175 WMIITYDG 182

RESULT 9

PS0075
myosin heavy chain, cardiac muscle - chicken (fragments)
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 10-Jun-1993 #text_change 02-Feb-2001
C:Accession: PS0075; A21173

R:Nakayama, S.
Nagasaki Igakkai Zaasshi 63, 316-343, 1988
A:Title: Primary structure of N-terminal fragment (23kDa) of chicken cardiac myosin S
A:Reference number: PS0075
A:Accession: PS0075
A:Molecule type: protein
A:Residues: 1-205 <NAK>

R:Tanaka, H.
Nagasaki Igakkai Zaasshi 62, 143-163, 1987
A:Title: Primary structure of C-terminal fragment (22kDa) of chicken cardiac myosin S
A:Reference number: A21173
A:Accession: A21173

A:Molecule type: protein
A:Residues: 206-396 <TAN>
C:Comment: Myosin is composed of two molecules of heavy chains and four molecules of
ase activity and binds to actin. The proteolytic fragment corresponding to this part
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; blocked amino end; cardiac muscle; heart; methylated amino acid; mus
F:86-333/Domain: myosin motor domain homology (fragments) <MMOT>
F:176-183/Region: nucleotide-binding motif A (P-loop)
F:1/Modified site: blocked amino end (Met) #status experimental
F:32/Modified site: N6-methyllysine (Lys) #status experimental
F:127/Modified site: N6,N6-Triethyllysine (Lys) #status experimental
F:320/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 75.0%; Score 36; DB 2; Length 396;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 110 WMIITYSG 117

RESULT 10

S49119
embryonic/neonatal myosin heavy chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 02-Feb-2001
C:Accession: S49119
R:Jaenicke, T.; Goldspink, G.
submitted to the EMBL Data Library, June 1994
A:Description: unpublished.
A:Reference number: S49119
A:Accession: S49119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-571 <JAE>
A:Cross-references: EMBL:Z34849; NID:9509377; PIDN:CA84358.1; PID:9509378
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; nucleotide binding; P-loop
F:89-571/Domain: myosin motor domain homology (fragment) <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 36; DB 2; Length 571;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 113 WMIITYSG 120

RESULT 11

JX0317
myosin S-1 heavy chain, cardiac muscle - chicken (fragment)
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Gallus gallus (chicken)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001
C:Accession: JX0317
R:Nakayama, S.; Tanaka, H.; Yajima, E.; Malta, T.

J. Blochem. 115, 909-926, 1994
A>Title: Primary structure of chicken cardiac myosin S-1 heavy chain.
A:Reference number: JX0317, MUID:95050426
A:Accession: JX0317
A:Molecule type: protein
A:Residues: 1-830 <NAK>
A:Experimental source: cardiac ventricular muscle
C:Comment: This protein acts as a transducer which converts chemical energy into work and
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; heart; hydrolase; methylated amino acid;
F:86-767/Domain: myosin motor domain homology <MMOT>
F:176-183/Region: nucleotide-binding motif A (P-loop)
F:32/Modified site: N6-methyllysine (Lys) #status predicted
F:127-549/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:754/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 75.0%; Score 36; DB 2; Length 830;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| 111111
Db 110 WMITYSG 117

RESULT 12
S39951
chitin synthase (EC 2.4.1.16) 3 - yeast (Candida albicans)
C:Species: Candida albicans
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Aug-1999
C:Accession: S39951
R:Stroh, M.; Nagaishi, S.; Dol, M.; Ohta, A.; Takagi, M.; Arita, M.
Mol. Gen. Genet. 241, 351-358, 1993
A>Title: Cloning of the chitin synthase 3 gene from Candida albicans and its expression
A:Reference number: S39951; MUID:94067017
A:Accession: S39951
A:Molecule type: DNA
A:Residues: 1-1175 <SUD>
A:Cross-references: EMBL:DL3454
C:Genetics:
A:Gene: CHS3
A:Map position: 1
C:Superfamily: chitin synthase chs4
C:Keywords: chitin biosynthesis; glycosyltransferase; hexosyltransferase; transmembrane

Query Match 75.0%; Score 36; DB 2; Length 1175;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYA 7
| 111111
Db 129 WKVYCYA 135

RESULT 13
A59234
slow myosin heavy chain 3 - quail
C:Species: Coturnix coturnix
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59234
R:Nikovits Jr., W.; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, L.; Stock
J. Biol. Chem. 271, 17047-17056, 1996
A>Title: Isolation and characterization of an avian slow myosin heavy chain gene express
A:Reference number: A59234; MUID:96291845
A:Accession: A59234
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1931 <NTK>
A:Cross-references: GB:U53862; NID:g1289513; PIDN:AAC59912.1; PID:g1289514
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:81-761/Domain: myosin motor domain homology <MMO>

Query Match 75.0%; Score 36; DB 2; Length 1931;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| 111111
Db 105 WMITYSG 112

RESULT 14
I48153
myosin heavy chain beta, cardiac muscle [similarity] - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
C:Accession: I48153; A28298
R:Wang, R.; Sole, M.J.; Cukerman, E.; Liew, C.C.
J. Mol. Cell. Cardiol. 26, 1155-1165, 1994
A>Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy c
A:Reference number: I48153; MUID:95115033
A:Accession: I48153
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1934 <RES>
A:Cross-references: GB:LI2104; NID:g402371; PIDN:AAA62313.1; PID:g402372
R:Jandreski, M.A.; Sole, M.J.; Liew, C.C.
Nucleic Acids Res. 16, 4737, 1988
A>Title: Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin heavy chain
A:Reference number: A28298; MUID:88247788
A:Accession: A28298
A:Molecule type: mRNA
A:Residues: 962-965, 'E', 967-980, 'E', 981-985, 'Q', 987-1007, 'A', 1009, 'E', 1011, 'RKT', 1015
536, 'L', 1538-1555, 'K', 1557-1934 <JAN>
A:Cross-references: GB:X07273; NID:949640; PIDN:CAA30256.1; PID:g49641
A:Note: the authors translated the codon GTG for residue 1504 as Leu
C:Genetics:
A:Introns: 66/3; 114/3; 167/1; 176/2; 212/3; 243/3; 265/1; 298/1; 332/3; 379/1; 418/3
23/3; 1389/2; 1450/3; 1506/1; 1547/3; 1650/3; 1718/3; 1760/3; 1852/3; 1884/3; 1929/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; muscle; nucleotid
F:87-765/Domain: myosin motor domain homology <MMOT>
F:177-184/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 36; DB 2; Length 1934;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| 111111
Db 111 WMITYSG 118

RESULT 15
A37102
myosin beta heavy chain, cardiac and skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A37102; S12733; A94224; B28908; A24997; A27858; I54254; S09331;
R:Jendrick, T.; Dieckrich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bac
Genomics 8, 194-206, 1990
A>Title: The complete sequence of the human beta-myosin heavy chain gene and a compar
A:Reference number: A37102; MUID:91065634
A:Accession: A37102
A:Molecule type: DNA
A:Residues: 1-1935 <JAE>
A:Cross-references: GB:M57965; GB:M30603; NID:g179507; PIDN:AAA51837.1; PID:g179508;
R:Liew, C.C.; Sole, M.J.; Yamauchi-Takahara, K.; Kellam, B.; Anderson, D.H.; Lin, L.;
Nucleic Acids Res. 18, 3647-3651, 1990
A>Title: Complete sequence and organization of the human cardiac beta-myosin heavy ch
A:Reference number: S12733; MUID:90301496

A:Accession: S12733
 A:Molecule type: DNA
 A:Residues: 1-106, 'E', 108-671, 'LYH', 675-657, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',
 A:Cross-references: EMBL:X52889; NID:929726; PIDN:CAA37068.1; PID:929727
 R.Yamuchi-Tsukihara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
 A:Title: Characterization of human cardiac myosin heavy chain genes.
 A:Reference number: A94224; MUID:89264452
 A:Accession: A94224
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-106, 'E', 108-177, 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1935
 R.Yamuchi-Tsukihara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
 A:Reference number: A94226
 A:Contents: annotation; Eretulum
 R.Kurabayashi, M.; Tsuchimoto, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
 J. Clin. Invest. 82, 524-531, 1988
 A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
 human actium.
 A:Reference number: A92770; MUID:88299163
 A:Accession: B28908
 A:Molecule type: mRNA
 A:Residues: 1412-1518, 'R', 1520-1574, 'NV', 1577-1935 <KUR>
 A:Cross-references: GB:M21655
 A:Note: the authors translated the codon AGC for residue 108 as Arg
 R.Lichter, P.; Umeda, P.K.; Levlin, J.E.; Vosberg, H.P.
 Eur. J. Biochem. 160, 419-426, 1986
 A:Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
 A:Reference number: A24997; MUID:87030293
 A:Accession: A24997
 A:Molecule type: DNA
 A:Residues: 682-721, 975-1112, 1854-1935 <LIC>
 A:Cross-references: GB:X04627
 R.Saez, L.J.; Glanville, K.M.; McNally, E.M.; Feghall, R.; Eddy, R.; Shows, T.B.; Leinwand
 Nucleic Acids Res. 15, 5443-5459, 1987
 A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
 A:Reference number: A93669; MUID:87260010
 A:Accession: A27858
 A:Molecule type: DNA
 A:Residues: 1854-1865, 'A', 1867-1935 <SAE>
 A:Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDN:CAA29119.1; PID:934644
 R.Diedrich, K.M.; Elisei, I.; Ried, T.; Jaenicke, T.; Lichter, P.; Vosberg, H.P.
 Hum. Genet. 81, 214-220, 1989
 A:Title: Isolation and characterization of the complete human beta-myosin heavy chain ge
 A:Reference number: I54254; MUID:89154425
 A:Accession: I54254
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 653-720 <RES>
 A:Cross-references: GB:M27636; NID:9179511; PIDN:AAA79019.1; PID:9601916
 R.Hober, E.
 submitted to the EMBL Data Library, January 1989
 A:Reference number: S12458
 A:Accession: S12458
 A:Molecule type: mRNA
 A:Residues: 785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>
 A:Cross-references: EMBL:X51591; NID:929467; PIDN:CAA35940.1; PID:929468
 R.Hober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedeke, H.W.; Arnold, H.H.
 Eur. J. Biochem. 189, 55-65, 1990
 A:Title: Identification of three developmentally controlled isoforms of human myosin hez
 A:Reference number: S09331; MUID:90235862
 A:Accession: S09331
 A:Molecule type: mRNA
 A:Residues: 785-830, 'X', 832-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X',
 '1602-1670, 'X', 1672-1702, 'DE', 1705-1740, 'X', 1742-1810, 'X', 1812-1935 <BOB>
 A:Cross-references: EMBL:X51591
 R.Jandroski, M.A.; Liew, C.C.
 Hum. Genet. 76, 47-53, 1987
 A:Title: Construction of a human ventricular cDNA library and characterization of a beta
 A:Reference number: S02229; MUID:87192738
 A:Accession: S02229
 A:Molecule type: mRNA
 A:Residues: 1393-1702, 'DR', 1705-1935 <AN>

A:Cross-references: EMBL:X06976; NID:934860; PIDN:CAA30039.1; PID:9825694
 R.Saez, L.; Leinwand, L.A.
 Nucleic Acids Res. 14, 2951-2969, 1986
 A:Title: Characterization of diverse forms of myosin heavy chain expressed in adult h
 A:Reference number: A93616; MUID:8616778
 A:Accession: B23767
 A:Molecule type: mRNA
 A:Residues: 'LAGVGLASG', 1311-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LO', 14
 A:Note: The first ten codons of the sequence figure show the reverse complementary st
 C:Genetics:
 A:Gene: GDB:MYH7
 A:Cross-references: GDB:120215; OMIM:160760
 A:Map position: 14q12-14q12
 A:Introns: 67/3; 115/3; 168/1; 177/2; 213/3; 244/3; 266/1; 299/1; 333/3; 380/1; 419/3
 24/3; 1390/2; 1451/3; 1507/1; 1548/3; 1651/3; 1719/3; 1761/3; 1853/3; 1885/3; 1930/3
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
 F:88-766/Domain: myosin motor domain homology <MOT>
 F:178-185/Region: nucleotide-binding motif A (P-loop)
 F:548-585/Region: actin binding #status predicted
 F:655-677/Region: actin binding #status predicted
 F:839-1935/Domain: coiled coil #status predicted <COI>
 F:1280-1935/Region: S2
 F:1280-1935/Region: Light meromyosin
 F:129/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
 F:184/Binding site: ATP (lys) #status predicted
 F:695,705/Active site: Cys #status predicted
 Query Match 75.0%; Score 36; DB 1; Length 1935;
 Best Local Similarity 62.5%; Pred. No. 1.2e+00;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WKIYSYAG 8
 | |||:|
 DB 112 WKIYYSYG 119
 RESULT 16
 S06006
 myosin beta heavy chain, cardiac muscle [similarity] - rat
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text-change 19-Jan-2001
 C:Accession: S06006; S07536; I67441; A02989
 R.Krafft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
 Nucleic Acids Res. 17, 7529-7530, 1989
 A:Title: Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin
 A:Reference number: S06006; MUID:90016823
 A:Accession: S06006
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1935 <KRA>
 A:Cross-references: EMBL:X15939; NID:956656; PIDN:CAA34065.1; PID:956657
 R.McNally, E.M.; Krafft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
 J. Mol. Biol. 210, 665-671, 1989
 A:Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Compari
 A:Reference number: S07535; MUID:90133919
 A:Accession: S07536
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-950, 'RK', 953-1935 <MCN>
 R.Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
 Eur. Heart J. 5, 181-191, 1984
 A:Title: Cardiac myosin heavy chain isozymlc transitions during development and under
 A:Reference number: I53305; MUID:85179510
 A:Accession: I67441
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1871-1935 <RES>
 A:Cross-references: GB:M32698; NID:9205598; PIDN:AAA41659.1; PID:9205599
 R.Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
 Nature 297, 659-664, 1982

A:Title: Molecular characterization of two myosin heavy chain genes expressed in the adult
A:Reference number: A02988; MUID:82220036
A:Accession: A02989
A:Molecule type: mRNA
A:Residues: 1524-1528, 'V', 1530, 'R', 1532-1730, 'H', 1732-1783, 'K', 1785-1850, 'N', 1852-1857, 'A'
A:Cross-references: GB:J00752; NID:g205577; PIDN:AAA4154.1; PID:g205578
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate
F:178-185/Region: nucleotide-binding motif A (P-loop)
F:188-766/Domain: myosin motor domain homology <MMOT>
F:548-588/Region: actin binding #status predicted
F:653-677/Region: actin binding #status predicted
F:839-1935/Domain: coiled coil #status predicted <COI>
F:839-1279/Region: S2
F:1280-1935/Region: light meromyosin
F:129/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted
F:184/Binding site: ATP (lys) #status predicted
F:695/705/Active site: Cys #status predicted

Query Match 75.0%; Score 36; DB 1; Length 1935;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
1 ||:|:|
Db 112 WMITYSYG 119

RESULT 17
A59286
myosin heavy chain beta chain, cardiac - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C:Accession: A59286
R:Ko, Y. L.
Submitted to GenBank, October 1996
A:Reference number: A59286
A:Accession: A59286
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1935 <KO>
A:Cross-references: GB:U75316; NID:g1698894; PIDN:AAB37320.1; PID:g1698895
A:Experimental source: strain domestica
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: cardiac muscle; heart
F:88-766/Domain: myosin motor domain homology <MMO>

Query Match 75.0%; Score 36; DB 2; Length 1935;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
1 ||:|:|
Db 112 WMITYSYG 119

RESULT 18
I38055
myosin heavy chain, perinatal skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 02-Feb-2001
C:Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R:Jullian, E. R.; Kelly, A. M.; Pompidou, A. J.; Hoffman, R.; Schiaffino, S.; Stedman, H. H.
Eur. J. Biochem. 230, 1001-1006, 1995
A:Title: Characterization of a human perinatal myosin heavy-chain transcript.
A:Reference number: I38055; MUID:95324556
A:Accession: I38055
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1937 <RES>

A:Cross-references: EMBL:Z38133; NID:g558668; PIDN:CAA6293.1; PID:g558669
R:Kersch-Mizrachi, I.; Peghali, R.; Shows, T. B.; Leinwand, L. A.

Gene 89, 289-294, 1990
A:Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA
A:Reference number: JH0154; MUID:90323631

A:Accession: JH0154
A:Molecule type: mRNA
A:Residues: 1-14, 'A', 16-859 <KAR>

A:Cross-references: GB:Y00821
A:Experimental source: skeletal muscle
R:Bober, E.

Submitted to the EMBL Data Library, January 1989
A:Reference number: S12458
A:Accession: S12459

A:Molecule type: mRNA
A:Residues: 502-1071, 'N', 1073-1250, 'DGC', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>

A:Cross-references: EMBL:X51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A:Experimental source: clone gTMC-F
R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H. W.; Arnold, H. H.

Eur. J. Biochem. 189, 55-65, 1990
A:Title: Identification of three developmentally controlled isoforms of human myosin
A:Reference number: S09331; MUID:90235862
A:Accession: S09332

A:Molecule type: mRNA
A:Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 8

1-376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668
A:Cross-references: EMBL:X51592
R:Peghali, R.; Leinwand, L. A.

J. Cell Biol. 108, 1791-1797, 1989
A:Title: Molecular genetic characterization of a developmentally regulated human perli
A:Reference number: A30220; MUID:89234168
A:Accession: A30220

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-

A:Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
C:Genetics:
A:Gene: GDB:MYH8

A:Cross-references: GDB:125267; OMIM:160741
A:Map position: 17pter-17p12
C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotid
F:91-769/Domain: myosin motor domain homology <MMOT>
F:181-188/Region: nucleotide-binding motif A (P-loop)

F:551-588/Region: actin binding #status predicted
F:658-680/Region: actin binding #status predicted
F:842-1282/Region: S2 #status predicted

F:698,708/Active site: Cys #status predicted

Query Match 75.0%; Score 36; DB 2; Length 1937;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
1 ||:|:|
Db 115 WMITYSYG 122

RESULT 19
S06005
myosin alpha heavy chain, cardiac muscle [similarity] - rat
N:Alternate names: alpha-myosin heavy chain
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: S06005; S07535; A20971; A02988; I53305
R:McNally, E. M.; Gianola, K. M.; Leinwand, L. A.
Nucleic Acids Res. 17, 7527-7528, 1989
A:Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosi
A:Reference number: S06005; MUID:90016822
A:Accession: S06005
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-1938 <MCN>
A:Cross-references: EMBL:X15938; NID:956654; PIDD:CAA34064.1; PID:956655
R:McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
J. Mol. Biol. 210, 665-671, 1989
A:Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison
A:Reference number: S07555; MUID:90133919
A:Accession: S07555
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1938 <MC2>
R:Mahdavi, V.; Chambers, A.P.; Nadal-Ginard, B.
Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984
A:Title: Cardiac alpha- and beta-myosin heavy chain genes are organized in tandem.
A:Reference number: A20971; MUID:84194059
A:Accession: A20971
A:Molecule type: protein
A:Residues: 1-12, 'AP', 14-45, 'A', 47-50, 'AP', 53-81, 'E', 83-86, 'Q', 88-109, 111-133, 'H', 135-16
R:Mahdavi, V.; Perlemany, M.; Nadal-Ginard, B.
Nature 297, 659-664, 1982
A:Title: Molecular characterization of two myosin heavy chain genes expressed in the ad
A:Reference number: A02988; MUID:82220036
A:Accession: A02988
A:Molecule type: mRNA
A:Residues: 1512-1574, 'S', 1576-1721, 'N', 1723-1851, 'N', 1853-1869, 'N', 1871-1933, 'I', 1935-1
A:Note: There are 10 or more myosin heavy chain genes in the rat, at least two of which
R:Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
Eur. Heart J. 5, 181-191, 1984
A:Title: Cardiac myosin heavy chain isozymic translations during development and under pa
A:Reference number: I53305; MUID:85179510
A:Accession: I53305
A>Status: translated from GR/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1872-1933, 'I', 1935-1938 <RBS>
A:Cross-references: GB:M32697; NID:9205596; PIDD:AAA41658.1; PID:9205597
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate
F:87-767/Domain: myosin motor domain homology <MMOT>
F:177-184/Region: nucleotide-binding motif A (P-loop)
F:548-585/Region: actin binding #status predicted
F:656-678/Region: actin binding #status predicted
F:840-1938/Domain: coiled coil #status predicted <COI>
F:840-1280/Region: S2
F:1281-1938/Region: light meromyosin
F:183/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:183/Binding site: ATP (Lys) #status predicted
F:696,706/Active site: Cys #status predicted

Query Match	75.0%	Score 36;	DB 1;	Length 1938;
Best Local Similarity	62.5%	Pred. No. 1.3e+02;		
Matches 5; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

Oy 1 WKIYSYG 8
Db 111:1:1
111 WMTYSG 118

RESULT 20
JX0178
myosin heavy chain, fast skeletal muscle, adult [validated] - chicken
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: PX0050; PX0051; JX0178; A26365; S02082; PW0009; S39081; S24351; S05
R:Hayashida, M.; Malta, T.; Matsuda, G.
J. Biochem. 110, 54-59, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the
A:Reference number: PX0050; MUID:92041767
A:Accession: PX0050
A:Molecule type: protein
A:Residues: 1-205 <HAY>
R:Komine, Y.; Malta, T.; Matsuda, G.

J. Biochem. 110, 60-67, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of
A:Reference number: PX0051; MUID:92041768
A:Accession: PX0051
A:Molecule type: protein
A:Residues: 206-636 <KOM>
R:Malta, T.; Miyashishi, T.; Matsuzono, K.; Tanioke, Y.; Matsuda, G.
J. Biochem. 110, 68-74, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence o
A:Reference number: PX0052; MUID:92041769
A:Accession: PX0052
A:Molecule type: protein
A:Residues: 201-213; 632-837 <MAI>
R:Malta, T.; Hayashida, E.; Nagata, S.; Miyashishi, T.; Nakayama, S.; Matsuda, G.
J. Biochem. 110, 75-87, 1991
A:Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of
A:Reference number: JX0178; MUID:92041770
A:Accession: JX0178
A:Molecule type: protein
A:Residues: 833-1938 <MA2>
R:Malta, T.; Hayashida, M.; Tanioke, Y.; Komine, Y.; Matsuda, G.
Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987
A:Title: The primary structure of the myosin head.
A:Reference number: A26365; MUID:87092420
A:Accession: A26365
A:Molecule type: protein
A:Residues: 1-129, 'X', 131-139, 141-550, 'X', 552-754, 'X', 756-784, 'QL', 787-804, 806-810 <M
R:Watanabe, B.
Biol. Chem. Hoppe-Seyler 370, 55-61, 1989
A:Title: Amino-acid sequence of the hinge region in chicken myosin subfragment-2.
A:Reference number: S02082; MUID:89228549
A:Accession: S02082
A:Molecule type: protein
A:Residues: 1144-1270 <WAT>
R:Yajima, E.
Nagasaki Igakkaï zaasshi 65, 409-430, 1990
A:Title: Study on tail region of skeletal muscle myosin: primary structure and protea
A:Reference number: PW0009
A:Accession: PW0009
A:Molecule type: protein
A:Residues: 1304-1938 <YAJ>
R:Moore, L.A.; Arrizubeta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
Submitted to the EMBL Data Library, August 1991
A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o
A:Reference number: S39081
A:Accession: S39081
A:Molecule type: mRNA
A:Residues: 1081-1203 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1795, 'HV', 1798-1829, 'S', 1
A:Cross-references: EMBL:M74084
R:Moore, L.A.; Arrizubeta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isofo
A:Reference number: S24348; MUID:92309413
A:Accession: S24351
A:Molecule type: mRNA
A:Residues: 1082-1182, 'T', 1184-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1780, 'W', 17
A:Cross-references: EMBL:M74084
R:Watanabe, B.
Biol. Chem. Hoppe-Seyler 370, 1027-1034, 1989
A:Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal musc
A:Reference number: S05515; MUID:90121764
A:Accession: S05515
A:Molecule type: protein
A:Residues: 842-906, 'Q', 908-1270 <WA3>
R:Watanabe, B.
Biol. Chem. Hoppe-Seyler 370, 549-558, 1989
A:Title: Amino-acid sequence of the short subfragment-2 in adult chicken skeletal mus
A:Reference number: S04501; MUID:89374803
A:Accession: S04501
A:Molecule type: protein
A:Residues: 852-906, 'Q', 908-1108 <WA2>
R:Matsuda, G.; Malta, T.; Miyashishi, T.; Hayashida, M.
J. Protein Chem. 6, 33-46, 1987

A:Title: Structure and function of muscle myosin.
A:Reference number: A60877
A:Accession: A60877
A:Molecule type: protein
A:Residues: 1-139,141-205 <MA1>
R:Gulick, J.; Kropp, K.; Robbins, J.
J. Biol. Chem. 260, 14513-14520, 1985
A:Title: The structure of two fast-white myosin heavy chain promoters. A comparative stu
A:Reference number: A92507; MUID:86033956
A:Accession: A24124
A:Molecule type: DNA
A:Residues: 'M',1-168 <GUL>
A:Cross-references: GB:M13512; GB:M12083; GB:M13510; NID:g212363; PIDN:AAA48966.1; PID:g
R:Kropp, K.; Gulick, J.; Robbins, J.
J. Biol. Chem. 261, 6613-6618, 1986
A:Title: A canonical sequence organization at the 5'-end of the myosin heavy chain genes
A:Reference number: A92587; MUID:86196091
A:Accession: C25217
A:Molecule type: DNA
A:Residues: 'M',1-56,'T',58-76,'T',78-168 <KRO>
A:Cross-references: GB:M13515; GB:M13511; NID:g212373; PIDN:AAA48971.1; PID:g555468
C:Comment: This is a fragment of the globular head.
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methylated
F:1-1938/Product: myosin heavy chain #status experimental <MAT>
F:89-768/Domain: myosin motor domain homology <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)
F:550-587/Region: actin binding #status predicted
F:657-679/Region: actin binding #status predicted
F:841-1938/Domain: coiled coil <COI>
F:841-1289/Region: S2
F:852-1108/Domain: short subfragment 2 <SUB2>
F:1290-1938/Region: light meromyosin
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:335/Modified site: N6-methyllysine (Lys) #status experimental
F:130,551/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental
F:1185/Binding site: ATP (Lys) #status predicted
F:697,707/Active site: Cys #status predicted
F:755/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 75.0%; Score 36; DB 1; Length 1938;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 113 WMITYSG 120

RESULT 21
149464
alpha cardiac myosin heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
C:Accession: 149464; 149463; 149462; 149461; 149604
R:Quinn-Jaguer, B.K.; Kennedy, J.E.; Wei, S.J.; Beisel, K.W.
Genomics 13, 176-188, 1992
A:Title: Characterization of the allelic differences in the mouse cardiac alpha-myosin h
A:Reference number: A36207; MUID:92250040
A:Accession: 149464
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1938 <RES>
A:Cross-references: GB:M76601; NID:g191623; PIDN:AAA37162.1; PID:g191624
A:Accession: 149463
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-193,'D',195-837,'S',839-955,'M',957-1938 <RE2>
A:Cross-references: GB:M76600; NID:g191621; PIDN:AAA37161.1; PID:g191622
A:Accession: 149462
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-1938 <RE3>
A:Cross-references: GB:M76599; NID:g191619; PIDN:AAA37160.1; PID:g191620
A:Accession: 149461
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-544,'A',546-1938 <RE4>
A:Cross-references: GB:M76598; NID:g191617; PIDN:AAA37159.1; PID:g191618
R:Gulick, J.; Subramaniam, A.; Neumann, J.; Robbins, J.
J. Biol. Chem. 266, 9180-9185, 1991
A:Title: Isolation and characterization of the mouse cardiac myosin heavy chain genes
A:Reference number: 149604; MUID:91225025
A:Accession: 149604
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-67 <RE5>
A:Cross-references: GB:M62404; NID:g192609; PIDN:AAA37424.1; PID:g192610
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop
F:88-768/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 36; DB 2; Length 1938;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 112 WMITYSG 119

RESULT 22
A59293
skeletal myosin heavy chain - domestic rabbit
C:Species: Oryctolagus cuniculus
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C:Accession: A59293
R:Maeda, K.; Hostanova, E.; Roesc, Kleinkauf, A.; Schuster, H.; Gasperik, J.; Wittingh
submitted to GenBank, July 1995
A:Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal
A:Reference number: A59293
A:Accession: A59293
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1938 <MAE>
A:Cross-references: GB:U32574; NID:g940232; PIDN:AA474199.1; PID:g940233
A:Experimental source: strain New Zealand White; cell type skeletal muscle fiber type
C:Genetics:
A:Gene: MHC
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:89-769/Domain: myosin motor domain homology <MMO>

Query Match 75.0%; Score 36; DB 2; Length 1938;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 113 WMITYSG 120

RESULT 23
A46762
myosin alpha heavy chain, cardiac muscle - human
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A46762; B46762; A49354; S18830; B32562; B3835; B27858; A28908
R:Matsuo, R.; Beisel, K.W.; Furutani, M.; Arai, S.; Takao, A.
Am. J. Med. Genet. 41, 537-547, 1991
A:Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino a
A:Reference number: A46762; MUID:92133665

A:Accession: A46762
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1939 <MAT>
 A:Cross-references: DDBJ:D00943; NID:g219523; PIDN:BAA00791.1; PID:g219524
 A:Accession: B46762
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1461 <MA2>
 R:EPP, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Llew, C.C.
 Genomics 18, 505-509, 1993
 A:Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (MYH)
 A:Reference number: A49354; MUID:94140346
 A:Accession: A49354
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-573, 'Q', 575-607, 'A', 609-743, 'T', 745-789, 'W', 791-1013, 'V', 1015-101939 <EPP>
 A:Cross-references: GB:220656; NID:9297023; PIDN:CAA79675.1; PID:9297024
 R:Brand, N.J.; Dabhadre, N.; Yacoub, M.; Barton, P.J.R.
 Biochem. Biophys. Res. Commun. 179, 1255-1258, 1991
 A:Title: Determination of the 5' exon structure of the human cardiac alpha-myosin heavy
 A:Reference number: S18830; MUID:92028859
 A:Accession: S18830
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-32 <BRA>
 A:Cross-references: EMBL:X56181; NID:g28318; PIDN:CAA39642.1; PID:g28319
 R:Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989
 A:Title: Characterization of human cardiac myosin heavy chain genes.
 A:Reference number: A94224; MUID:89264452
 A:Accession: B32562
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1848 <YAL>
 R:Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
 A:Reference number: A94226
 A:Accession: B33835
 A:Contents: erratum
 A:Molecule type: DNA
 A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1939 <YAZ>
 R:Soez, L.J.; Glanville, K.M.; McNally, E.M.; Feighall, R.; Eddy, R.; Shows, T.B.; Leinwand
 Nucleic Acids Res. 15, 5443-5459, 1987
 A:Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
 A:Reference number: A93669; MUID:87260010
 A:Accession: B27858
 A:Molecule type: DNA
 A:Residues: 1-3, 'S', 5-10, 'T', 12, 14-67 <SAE>
 R:Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
 J. Clin. Invest. 82, 524-531, 1988
 A:Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
 human atrium.
 A:Reference number: A92770; MUID:80229163
 A:Accession: A28908
 A:Molecule type: mRNA
 A:Residues: 1407-1532, 'N', 1534-1539, 'W', 1541-1576, 'NW', 1579-1704, 'EQ', 1707-1762, 'D', 1764
 A:Cross-references: GB:M21664; NID:9189006; PIDN:AAA36344.1; PID:g386972
 A:Experimental source: fetal heart
 C:Genetics:
 A:Gene: GDB:MYH6
 A:Cross-references: GDB:120214; OMIM:160710
 A:Map position: 14q11.2-14q13
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate
 F:88-768/Domain: myosin motor domain homology <MMOT>
 F:178-185/Region: nucleotide-binding motif A (P-loop)
 F:549-586/Region: actin binding #status predicted
 F:657-679/Region: actin binding #status predicted
 F:841-1939/Domain: coiled coil #status predicted <COI>
 F:841-1281/Region: S2
 F:1282-1939/Region: light meromyosin
 F:129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

F:184/Binding site: ATP (Lys) #status predicted
 F:697,707/Active site: Cys #status predicted

Query Match 75.0%; Score 36; DB 1; Length 1939;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WKIYTAG 8
 | | | | |
 DB 112 WMITYSG 119

RESULT 24
 I48175
 myosin heavy chain alpha, cardiac muscle [similarity] - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
 C:Accession: I48175; A23938
 R:Wang, R.; Sole, M.J.; Cukerman, E.; Llew, C.C.
 J. Mol. Cell. Cardiol. 26, 1155-1165, 1994
 A:Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy c
 A:Reference number: I48153; MUID:95115033
 A:Accession: I48175
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1939 <RES>
 A:Cross-references: GB:I15351; NID:g402373; PIDN:AAB59701.1; PID:g402374
 R:Llew, C.C.; Jandreski, M.A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 3175-3179, 1986
 A:Title: Construction and characterization of the alpha-form of a cardiac myosin heav
 A:Reference number: A23938; MUID:86205859
 A:Accession: A23938
 A:Molecule type: mRNA
 A:Residues: 1630-1843, 'R', 1845-1878, 'T', 1880-1927, 'N', 1929-1932, 1934-1939 <IE>
 C:Genetics: 67/3; 115/3; 168/1; 177/2; 214/3; 245/3; 267/1; 300/1; 334/3; 381/1; 470/3
 352/2; 1453/3; 1509/1; 1550/3; 1633/3; 1721/3; 1763/3; 1855/3; 1867/3; 1932/3
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop
 F:88-768/Domain: myosin motor domain homology <MMOT>
 F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 36; DB 2; Length 1939;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WKIYTAG 8
 | | | | |
 DB 112 WMITYSG 119

RESULT 25
 S04090
 myosin heavy chain 3, skeletal muscle, embryonic - human
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C:Accession: S04090; S06146; S05442; S12460; S09333; A35082
 R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Ferteis, S.H.; Rubinstein, N.A.; Kelly,
 Nucleic Acids Res. 17, 3591-3592, 1989
 A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.
 A:Reference number: S04090; MUID:89263803
 A:Accession: S04090
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1940 <ELD>
 A:Cross-references: EMBL:X13988; NID:g34843; PIDN:CAA32167.1; PID:g34844
 R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Ferteis, S.H.; Wu, Q.L.; Raychowdhury, M
 FEBS Lett. 256, 21-26, 1989
 A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation
 A:Reference number: S06146; MUID:90033298

A:Accession: S06146
 A:Molecule type: mRNA
 A:Residues: 774-1662; 'GT', 1665-1940 <EU2>
 A:Cross-references: EMBL:X13100; NID:931143; PIDN:CAA31492.1; PID:931144
 R:Karsch-Wizlisch, T.; Travls, M.; Biau, H.; Leinwand, L.A.
 Nucleic Acids Res. 17, 6167-6179, 1989
 A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin
 A:Reference number: S05442; MUID:89366648
 A:Accession: S05442
 A:Molecule type: DNA
 A:Residues: 856-1390, 'KK', 1393-1940 <KAR>
 A:Cross-references: EMBL:X15696; NID:936504; PIDN:CAA3731.1; PID:91335313
 R:Stedman, H.H.; Eller, M.; Julian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.; K
 J. Biol. Chem. 265, 3568-3576, 1990
 A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals evol
 A:Reference number: A35082; MUID:90154023
 A:Contents: annotation; chromosomal assignment
 R:Bober, E.
 submitted to the EMBL Data Library, January 1989
 A:Reference number: S12458
 A:Accession: S12460
 A:Molecule type: mRNA
 A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>
 A:Cross-references: EMBL:X51593; NID:929463; PIDN:CAA35942.1; PID:929464
 A:Experimental source: clone gEMHC-E
 R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
 Eur. J. Biochem. 189, 55-65, 1990
 A:Title: Identification of three developmentally controlled isoforms of human myosin hea
 A:Reference number: S09331; MUID:90235862
 A:Accession: S09333
 A:Molecule type: mRNA
 A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-1251, '
 1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOB>
 A:Cross-references: EMBL:X51593
 C:Genetics:
 A:Gene: GDB:MYH3
 A:Cross-references: GDB:119443; OMIM:160720
 A:Map position: 17p13.1-17p13.1
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co
 F:89-767/Domain: myosin motor domain homology <MMOT>
 F:179-186/Region: nucleotide-binding motif A (P-loop)
 F:549-586/Region: actin binding #status predicted
 F:656-678/Region: actin binding #status predicted
 F:840-1940/Domain: coiled coil #status predicted <COI>
 F:840-1280/Region: S2
 F:1281-1940/Region: light meromyosin
 F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F:185/Binding site: ATP (Lys) #status predicted
 F:696,706/Active site: Cys #status predicted

Query Match 75.0%; Score 36; DB 1; Length 1940;
 Best Local Similarity 62.5%; Pred. NO. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKITYSYAG 8
 | ||:|:|
 DB 113 WKITYSYG 120

Search completed: January 14, 2002, 06:21:38
 Job time: 96 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 06:39:54 ; Search time 128.48 Seconds
(without alignments)
9.108 Million cell updates/sec

Title: US-09-185-908-34
Perfect score: 48
Sequence: 1 WKIYSYAC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP_RenML_17:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Protoct:*
12: SP_Virus:*
13: SP_Unclassified:*
14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	77.1	288	2	Q9RS05
2	37	77.1	423	5	Q9VGG8
3	36	75.0	110	4	Q9BQM6
4	36	75.0	151	6	Q29623
5	36	75.0	168	13	Q90914
6	36	75.0	169	13	Q90908
7	36	75.0	169	13	Q90909
8	36	75.0	169	13	Q90910
9	36	75.0	169	13	Q90913
10	36	75.0	175	6	Q29107
11	36	75.0	175	6	Q29107
12	36	75.0	307	4	Q93765
13	36	75.0	372	4	Q93558
14	36	75.0	411	13	Q91495
15	36	75.0	576	6	Q28701
16	36	75.0	576	13	Q13143
17	36	75.0	840	13	Q918N4
18	36	75.0	840	13	Q918N3
19	36	75.0	841	13	Q918N5

20	36	75.0	847	13	Q918N2	Q918N2 rana pipien
21	36	75.0	1287	13	Q93498	Q93498 Chetragra ch
22	36	75.0	1610	4	Q9NNX0	Q9NNX0 homo sapien
23	36	75.0	1889	4	Q9H430	Q9H430 homo sapien
24	36	75.0	1929	13	Q98T06	Q98T06 notothenia
25	36	75.0	1930	13	Q9NGD5	Q9NGD5 penneha ar
26	36	75.0	1931	13	Q91973	Q91973 coturnix co
27	36	75.0	1931	13	Q42352	Q42352 cyprinus ca
28	36	75.0	1932	13	Q98TQ4	Q98TQ4 notothenia
29	36	75.0	1933	13	Q90337	Q90337 cyprinus ca
30	36	75.0	1935	4	Q9H1D5	Q9H1D5 homo sapien
31	36	75.0	1935	6	Q9CKR1	Q9CKR1 sus scrofa
32	36	75.0	1935	6	Q9BE39	Q9BE39 bos taurus
33	36	75.0	1937	6	Q9TV62	Q9TV62 sus scrofa
34	36	75.0	1937	13	Q91BD4	Q91BD4 gallus gall
35	36	75.0	1938	6	Q9GJ99	Q9GJ99 oryctolagus
36	36	75.0	1938	6	Q9BE40	Q9BE40 bos taurus
37	36	75.0	1938	13	Q9TBD7	Q9TBD7 seriola dum
38	36	75.0	1939	6	Q9TV63	Q9TV63 sus scrofa
39	36	75.0	1939	6	Q9TV61	Q9TV61 sus scrofa
40	36	75.0	1939	13	Q9PTV2	Q9PTV2 gallus gall
41	36	75.0	1940	6	Q9BE41	Q9BE41 bos taurus
42	36	75.0	1941	13	Q9DGM4	Q9DGM4 gallus gall
43	36	75.0	1944	13	Q9DGM5	Q9DGM5 gallus gall
44	35	72.9	240	5	Q9V402	Q9V402 dtrosophila
45	35	72.9	317	2	Q9RCY0	Q9RCY0 streptomyc
46	35	72.9	345	11	Q9D790	Q9D790 mus musculu
47	35	72.9	664	10	Q9LDQ3	Q9LDQ3 arabidopsis
48	35	72.9	817	5	Q93560	Q93560 caenorhabd
49	35	72.9	947	5	Q15696	Q15696 plasmodium
50	35	72.9	948	5	Q9U4U6	Q9U4U6 plasmodium

ALIGNMENTS

RESULT 1
ID Q9RS05 PRELIMINARY: PRT: 288 AA.
AC Q9RS05;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SERINE PROTEASE, SUBTILASE FAMILY, C-TERMINAL FRAGMENT.
GN DR2322.
OS Delnoccocus radiodurans.
OC Bacteria; Thermus/Delnoccocus group; Delnoccocales; Delnoccoccus.
OX NCBI_TaxID=1299;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Motilal K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarov K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Delnoccoccus
RT radiodurans RI.";
RL Science 286:1571-1577(1999).
DR EMBL; AF002064; AAF1870.1; -;
DR HSSP; P06873; 2PRK.
DR TIGR; DR2322; -;
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease; Complete proteome.
SQ SEQUENCE 288 AA; 28640 MW; 0B1DC42C2C915B0C CRC64;

Query Match 77.1%; Score 37; DB 2; Length 288;

[illegible]

Query Match	77.1%	Score 37	DB 5	Length 423
Best Local Similarity	75.0%	Pred. No. 53		
Matches 6	Conservative	0	Mismatches 2	Indels 0
				Gaps 0
Oy	1 WKIYSYAG 8			
Db	45 WPYHYAG 52			
RESULT 3				
Q9BQM6				
1D	Q9BQM6	PRELIMINARY	PRT	110 AA.
AC	Q9BQM6			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	DJ756N5.1.2 (CONTINUES IN EM:AL133324 AS DJ1161H23.3) (FRAGMENT).			
GN	DJ756N5.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_TaxID	9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Moore M.			
RL	Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AL132825; CAC34277.1; -.			
FT	NON TER			
SD	SEQUENCE . 110 AA; 12872 MM; E9693F2F32AD23B8 CAC64;			

	Query Match	75.0%;	Score 36;	DB 4;	Length 110;
	Best Local Similarity	62.5%;	Pred. No. 19;		
Matches	5;	Conservative	2;	Mismatches	1; Indels 0; Gaps 0;
OY	1 WKISYAG 8 :				
Db	45 WMIYYSG 52				
RESULT	4				
Q29623		PRELIMINARY;	PRT;	151 AA.	
ID Q29623;					
AC Q29623;					
DT 01-NOV-1996 (TREMBLrel. 01, Created)					
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)					
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)					
DE MYOSIN HEAVY CHAIN (FRAGMENT).					
OS Sus scrofa (Pig).					
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
OX NCBI_TaxID=9823;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=LARGE WHITE/LANDRACE CROSS; TISSUE=SKELETAL MUSCLE;					
RX MEDLINE=95340706; PubMed=7615692;					
RA Chang K., Fernandes K.;					
RT "Molecular characterization of a developmentally regulated porcine					
skeletal myosin heavy chain gene and its 5' regulatory region.";					
RL J. Cell Sci. 108:1779-1789(1995).					
DR EMBL; U11772; AAC48466.2; -					
DR EMBL; U11771; AAC48465.1; -					
DR HSSP; P08799; ILVK.					
DR InterPro; IPR001609; myosin_head.					
DR Pfam; PF00065; myosin_head.1.					
DR ProDom; PD000355; myosin_head.1.					
FT CONFLICT 68			A -> G (IN AAC48465).		
FT NON_TER 151					
SQ SEQUENCE 151 AA; 17252 MW; 8BD8F796BC7371799 CRC64;					
Query Match	75.0%;	Score 36;	DB 6;	Length 151;	
Best Local Similarity	62.5%;	Pred. No. 26;			

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Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 WKIYSYAG 8
    |||:|
Db 113 WMITYSG 120

RESULT 5
Q09014 PRELIMINARY; PRT; 168 AA.
AC Q09014;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88059036; PubMed=2824498;
RA Kropp K.E., Gulick J., Robbins J.;
RT "Structural and transcriptional analysis of a chicken myosin heavy
chain gene subset."
RL J. Biol. Chem. 262:16536-16545(1987).
DR EMBL: M18139; AAA48973.1; -.
DR HSSP: P08799; ILVK.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Prodom: PD000355; myosin_head; 1.
KW Myosin.
FT NON_TER
SQ SEQUENCE 168 AA; 19260 MW; 07DA98E943653E5A CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 168;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 WKIYSYAG 8
    |||:|
Db 113 WMITYSG 120

RESULT 6
Q09008 PRELIMINARY; PRT; 169 AA.
AC Q09008;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FAST-WHITE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196090; PubMed=3009464;
RA Robbins J., Horan T., Gulick J., Kropp K.;
RT "The chicken myosin heavy chain family."
RL J. Biol. Chem. 261:6606-6612(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196091; PubMed=3009465;
RA Kropp K., Gulick J., Robbins J.;
RT "A canonical sequence organization at the 5'-end of the myosin heavy
chain genes."
RL J. Biol. Chem. 261:6613-6618(1986).
DR EMBL: M13513; AAA48965.1; -.
DR HSSP: P08799; ILVK.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Prodom: PD000355; myosin_head; 1.
KW Myosin.
FT NON_TER
SQ SEQUENCE 169 AA; 19239 MW; 126AD6896F4DC87 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 169;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 WKIYSYAG 8
    |||:|
Db 114 WMITYSG 121

RESULT 8
Q09010 PRELIMINARY; PRT; 169 AA.
```

```
DR HSSP: P08799; ILVK.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Prodom: PD000355; myosin_head; 1.
KW Myosin.
FT NON_TER
SQ SEQUENCE 169 AA; 19301 MW; 70A70A9465252573 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 169;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 WKIYSYAG 8
    |||:|
Db 114 WMITYSG 121

RESULT 7
Q09009 PRELIMINARY; PRT; 169 AA.
AC Q09009;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE FAST-WHITE MYOSIN HEAVY CHAIN (ADULT ISOFORM) (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196090; PubMed=3009464;
RA Robbins J., Horan T., Gulick J., Kropp K.;
RT "The chicken myosin heavy chain family."
RL J. Biol. Chem. 261:6606-6612(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196091; PubMed=3009465;
RA Kropp K., Gulick J., Robbins J.;
RT "A canonical sequence organization at the 5'-end of the myosin heavy
chain genes."
RL J. Biol. Chem. 261:6613-6618(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86033956; PubMed=2997212;
RA Gulick J., Kropp K., Robbins J.;
RT "The structure of two fast-white myosin heavy chain promoters. A
comparative study."
RL J. Biol. Chem. 260:14513-14520(1985).
DR EMBL: M13512; AAA48966.1; -.
DR HSSP: P08799; ILVK.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR Prodom: PD000355; myosin_head; 1.
KW Myosin.
FT NON_TER
SQ SEQUENCE 169 AA; 19239 MW; 126AD6896F4DC87 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 169;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 WKIYSYAG 8
    |||:|
Db 114 WMITYSG 121

RESULT 8
Q09010 PRELIMINARY; PRT; 169 AA.
```

```

AC Q90910;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE FAST-WHITE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196090; PubMed=3009464;
RA Robbins J., Horan T., Gulick J., Kropp K.;
RT "The chicken myosin heavy chain family.";
RL J. Biol. Chem. 261:6606-6612(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196091; PubMed=3009465;
RA Kropp K., Gulick J., Robbins J.;
RT "A canonical sequence organization at the 5'-end of the myosin heavy
chain genes.";
RL J. Biol. Chem. 261:6613-6618(1986).
DR HSSP; M13516; AAA48967.1; -.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00063; myosin_head; 1.
DR Prodom; PD000355; myosin_head; 1.
KM MYOSIN.
FT NON_TER.
SQ SEQUENCE 169 AA; 19365 MW; 617B6ADE860E6C0 CRC64;

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```

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 169;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 WKIYSYAG 8
   | | | | |
DB 113 WMITYTSG 120

```

```

RESULT 9
Q90913 PRELIMINARY; PRT; 169 AA.
AC Q90913;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE FAST WHITE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196090; PubMed=3009464;
RA Robbins J., Horan T., Gulick J., Kropp K.;
RT "The chicken myosin heavy chain family.";
RL J. Biol. Chem. 261:6606-6612(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196091; PubMed=3009465;
RA Kropp K., Gulick J., Robbins J.;
RT "A canonical sequence organization at the 5'-end of the myosin heavy
chain genes.";
RL J. Biol. Chem. 261:6613-6618(1986).
DR HSSP; P08799; ILVK.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00063; myosin_head; 1.
DR Prodom; PD000355; myosin_head; 1.

```

```

KM MYOSIN.
FT NON_TER.
SQ SEQUENCE 169 AA; 19297 MW; 993CF04C0442CCEE CRC64;

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```

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 169;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 WKIYSYAG 8
   | | | | |
DB 114 WMITYTSG 121

```

```

RESULT 10
Q29107 PRELIMINARY; PRT; 175 AA.
AC Q29107;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE SLOW MYOSIN HEAVY CHAIN-BETA (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE X LANDRACE; TISSUE=SKLETAL MUSCLE;
RX MEDLINE=94095666; PubMed=8270635;
RA Chang K.C., Fernandes K., Goldslink G.;
RT "In vivo expression and molecular characterization of the porcine
slow-myosin heavy chain.";
RL J. Cell Sci. 106:331-341(1993).
DR EMBL; L10129; AAC37313.1; -.
DR HSSP; P08799; ILVK.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00063; myosin_head; 1.
DR Prodom; PD000355; myosin_head; 1.
FT NON_TER.
SQ SEQUENCE 175 AA; 20226 MW; 1E46A6D5E7C31395 CRC64;

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```

Query Match
Best Local Similarity 75.0%; Score 36; DB 6; Length 175;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 WKIYSYAG 8
   | | | | |
DB 112 WMITYTSG 119

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```

RESULT 11
Q9NWE2 PRELIMINARY; PRT; 176 AA.
AC Q9NWE2;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE HYPOTHETICAL 20.4 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Iisogi T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human CDNA sequencing project.";

```


RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK000947; BAA91440.1; -
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF000063; myosin_head.1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head.1.
SQ SEQUENCE 176 AA; 20442 MW; 91A61F7A24A55CA2 CRC64;

Query Match 75.0%; Score 36; DB 4; Length 176;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| | | | |
DB 111 WMITYSG 118

RESULT 12
O93765 PRELIMINARY; PRT; 307 AA.

AC Q93765;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE F53C11.1 PROTEIN.
GN F53C11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Poloderinae; Caenorhabditis.
NCBI_TaxID=6239;
RX SEQUENCE FROM N.A.
RA Baynes C.;
RP Submitted (SRP-1996) to the EMBL/Genbank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE:94150718; PubMed:7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierley-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z79756; CAB02120.1; -
SQ SEQUENCE 307 AA; 34281 MW; 8D285E7600C97B08 CRC64;

Query Match 75.0%; Score 36; DB 5; Length 307;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| | | | |
DB 175 WKIYYDG 182

RESULT 13
O95558 PRELIMINARY; PRT; 372 AA.

AC O95558;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHEICAL 43.9 KDA PROTEIN.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL035122; CAA22684.1; -
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 43900 MW; E645DCFBEBE8E415A6 CRC64;

Query Match 75.0%; Score 36; DB 4; Length 372;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYA 7
| | | | |
DB 117 WKIYSYS 123

RESULT 14
O91495 PRELIMINARY; PRT; 411 AA.

AC O91495;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MYOSIN HEAD (FRAGMENT).
OS Theragra chalcogramma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae;
OC Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA Nishita K.;
RT "Primary structure of Walleye Pollack Myosin Head.";
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: D85857; BAA12887.1; -
DR HSSP: P08799; ILVK.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head.1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head.1.
KW Myosin.
FT NON-TER 411 411
SQ SEQUENCE 411 AA; 46449 MW; 32120B96D228CA81 CRC64;

Query Match 75.0%; Score 36; DB 13; Length 411;
Best Local Similarity 62.5%; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| | | | |
DB 34 WMITYSG 41

RESULT 15
O28701 PRELIMINARY; PRT; 571 AA.

AC O28701;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EMBRYONIC/NEONATAL MYOSIN HEAVY CHAIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

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RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=MUSCLE, SKELETAL:
RA Jaenicke T., Goldspink G.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; 234849; CAA84358.1; -.
DR HSSP; P08799; 1MMD.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR Prodom; PD000355; myosin_head; 1.
KW Myosin.
FT NON_TER 571
SQ SEQUENCE 571 AA; 65105 MW; 96881797CF2AE584 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 6; Length 571;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 113 WMITYSG 120

RESULT 16
O13143 PRELIMINARY; PRT; 576 AA.
AC O13143;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SLOW MYOSIN HEAVY CHAIN 2 (FRAGMENT).
GN OMVHC2.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RA Dimario J.X., Stockdale F.E.;
RL Dev. Biol. 0:0-0(0).
DR EMBL; AF006829; AAB61475.1; -.
DR HSSP; P08799; 1MMD.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR000169; Thiolprot_act_site.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR Prodom; PD000355; myosin_head; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
FT NON_TER 576
SQ SEQUENCE 576 AA; 65675 MW; 8B1779BB094006C2 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 576;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 112 WMITYSG 119

RESULT 17
O918M4 PRELIMINARY; PRT; 840 AA.
AC O918M4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE 2 MYOSIN HEAVY CHAIN (FRAGMENT).
OS Rana pipiens (Northern leopard frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTERIOR TIBIALIS SKELETAL MUSCLE;
RX MEDLINE=20314481; PubMed=10854783;
RA Lutz G.J., Razzaghi S., Lieber R.L.;
RT "Cloning and characterization of the S1 domain of four myosin isoforms
from functionally divergent fiber types in adult Rana pipiens skeletal
muscle.";
RT Gene 250:97-107(2000).
DR EMBL; AF240689; AAF82091.1; -.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR Pfam; PF00612; IO; 1.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR Prodom; PD000355; myosin_head; 1.
DR SMART; SM00015; IO; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IO; 1.
FT NON_TER 840
SQ SEQUENCE 840 AA; 95677 MW; 414C917967FC432B CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 840;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 112 WMITYSG 119

RESULT 18
O918N3 PRELIMINARY; PRT; 840 AA.
AC O918N3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TYPE 3 MYOSIN HEAVY CHAIN (FRAGMENT).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTERIOR TIBIALIS SKELETAL MUSCLE;
RX MEDLINE=20314481; PubMed=10854783;
RA Lutz G.J., Razzaghi S., Lieber R.L.;
RT "Cloning and characterization of the S1 domain of four myosin isoforms
from functionally divergent fiber types in adult Rana pipiens skeletal
muscle.";
RT Gene 250:97-107(2000).
DR EMBL; AF240690; AAF82092.1; -.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR Pfam; PF00612; IO; 1.
DR Pfam; PF00063; myosin_head; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR Prodom; PD000355; myosin_head; 1.
DR SMART; SM00015; IO; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IO; 1.
FT NON_TER 840
SQ SEQUENCE 840 AA; 95677 MW; 414C917967FC432B CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 840;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 WKIYSYAG 8
1111111
Db 113 WMIYTYSG 120

RESULT 19
Q918N5 PRELIMINARY; PRT: 841 AA.
ID Q918N5
AC Q918N5;
DT 01-OCT-2000 (TREMBLREL. 15, Created)
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE TYPE 1 MYOSIN HEAVY CHAIN (FRAGMENT).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;

RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=ANTERIOR TIBIALIS SKELETAL MUSCLE;
RX MEDLINE=20314481; PubMed=10854783;
RA Lutz G.J., Razzaghi S., Lieber R.L.;
RT Cloning and characterization of the S1 domain of four myosin isoforms from functionally divergent fiber types in adult Rana pipiens skeletal muscle."
RT Gene 250:97-107(2000).
RL EMBL: AF240691; AAF82093.1; -
RL Interpro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ: 1.
DR Pfam: PF00063; myosin_head.1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head.1.
DR SMART: SM00015; IQ: 1.
DR SMART: SM00242; MYSC: 1.
DR PROSITE: PSS0096; IQ: 1.
FT NON_TER 841 841
SQ SEQUENCE 841 AA; 96115 MW; 5F502546BDECDAA4 CRC64;

Query Match 75.0%; Score 36; DB 13; Length 841;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
1111111
Db 112 WMIYTYSG 119

RESULT 20
Q918N2 PRELIMINARY; PRT: 847 AA.
ID Q918N2
AC Q918N2;
DT 01-OCT-2000 (TREMBLREL. 15, Created)
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE TYPE TONIC MYOSIN HEAVY CHAIN (FRAGMENT).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;

RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=ANTERIOR TIBIALIS SKELETAL MUSCLE;
RX MEDLINE=20314481; PubMed=10854783;
RA Lutz G.J., Razzaghi S., Lieber R.L.;
RT Cloning and characterization of the S1 domain of four myosin isoforms from functionally divergent fiber types in adult Rana pipiens skeletal muscle."
RT Gene 250:97-107(2000).
RL EMBL: AF240691; AAF82093.1; -
RL Interpro: IPR000634; dehydrtse_ser_thr.
FT Interpro: IPR000634; dehydrtse_ser_thr.

DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR000169; Thiolprol_act_site.
DR Pfam: PF00063; myosin_head.1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head.1.
DR SMART: SM00015; IQ: 1.
DR SMART: SM00242; MYSC: 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
FT NON_TER 847 847
SQ SEQUENCE 847 AA; 97012 MW; 7003975DA01EC138 CRC64;

Query Match 75.0%; Score 36; DB 13; Length 847;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
1111111
Db 113 WMIYTYSG 120

RESULT 21
Q93498 PRELIMINARY; PRT: 1287 AA.
ID Q93498
AC Q93498;
DT 01-NOV-1998 (TREMBLREL. 08, Created)
DT 01-NOV-1998 (TREMBLREL. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Theragra chalcogramma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae;
OC Theragra.
OX NCBI_TaxID=48550;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=SKELETAL MUSCLE;
RA Ojima T., Kawashima N., Inoue A., Amauchi A., Togashi M., Watabe S.,
RA Nishida K.;
RT "Determination of Primary Structure of Heavy Meromyosin Region of Walleye Pollack Myosin Heavy Chain by cDNA Cloning."
RL Fisheries Sci. 0:0-0(1998).
DR EMBL: AB017819; BAA33452.1; -
DR HSSP: P08799; 1MND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ: 1.
DR Pfam: PF00063; myosin_head.1.
DR Pfam: PF01576; Myosin_tail.1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head.1.
DR SMART: SM00015; IQ: 1.
DR SMART: SM00242; MYSC: 1.
KW Myosin.
FT NON_TER 1287 1287
SQ SEQUENCE 1287 AA; 146467 MW; BAD93CB005D6A7CD CRC64;

Query Match 75.0%; Score 36; DB 13; Length 1287;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
1111111
Db 114 WMIYTYSG 121

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RESULT 22
Q9NNX0 PRELIMINARY; PRT; 1610 AA.
AC Q9NNX0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OS SOLUBLE ADENYLYL CYCLASE (EC 4.6.1.1).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jaiswal B.S., Contl M.;
RT "Human soluble adenylyl cyclase.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99093493; Pubmed=9874775;
RX Buck J., Sinclair M.L., Schapal L., Cann M.J., Levin L.R.;
RT "Cytosolic adenylyl cyclase defines a unique signaling molecule in
mammals.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:79-84(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Matlia M., Buck J., Levin L.R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271058; AAF74296.1; -.
DR EMBL; AF176813; AAF65931.1; -.
DR InterPro; IPR001054; Guanylt_cyclase.
DR Pfam; PF00211; guanylate_cyc; 2.
DR SMART; SM00044; CYCC; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 2.
KM Lyase.
SQ SEQUENCE 1610 AA; 187134 MW; B131F4BF1B03E304 CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 4; Length 1610;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYA 7
DB 1216 WRITYSYS 1222

RESULT 23
Q9H430 PRELIMINARY; PRT; 1889 AA.
AC Q9H430;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DJ756N5.1 (MYOSIN HEAVY CHAIN PROTEIN IIB (K1A151212) ) (FRAGMENT).
GN DJ756N5.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132825; CAC14945.1; -.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF01576; myosin_tail; 2.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.

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DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
FT NON_TER 1
SQ SEQUENCE 1889 AA; 215226 MW; 692E664AE17E132A CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 4; Length 1889;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
DB 45 WMITYSYG 52

RESULT 24
Q98T06 PRELIMINARY; PRT; 1929 AA.
AC Q98T06;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN HEAVY CHAIN.
GN MYOHC-A1.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
OC Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaury L., Enion S., Ettelaie C., Goldsplek G.;
RT "Characterisation of red and white muscle myosin heavy chain gene
coding sequences from Antarctic and tropical fish.";
RL Comp. Biochem. Physiol. 127:575-588(2000).
DR EMBL; AJ243767; CAC27776.1; -.
SQ SEQUENCE 1929 AA; 221167 MW; 20A78CBA19DE851B CRC64;

Query Match
Best Local Similarity 75.0%; Score 36; DB 13; Length 1929;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
DB 114 WMITYSYG 121

RESULT 25
Q9DGD5 PRELIMINARY; PRT; 1930 AA.
AC Q9DGD5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Pennahia argentata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sciaenidae; Pennahia.
OX NCBI_TaxID=118565;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=FAST SKELETAL MUSCLE;
RC Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
RT "cDNA cloning and characterization of the complete primary structure of
myosin heavy chain from white croaker fast skeletal muscle.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039672; BAB12571.1; -.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001609; myosin_head.

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DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1930 AA; 221208 MW; C6219EB07CB4C5A1 CRC64;

Query Match 75.0%; Score 36; DB 13; Length 1930;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
DB 114 WMTYVSG 121

Search completed: January 14, 2002, 06:39:56
Job time: 1094 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:43:19 ; Search time 23.97 Seconds
(without alignments)
25.423 Million cell updates/sec

Title: US-09-185-908-34

Perfect score: 48
Sequence: 1 WKIVSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	39.6	5	2	S68326 blood cell protein
2	18	37.5	7	2	A60139 fatty-acid synthas
3	16	33.3	7	2	S33244 neuromodulatory pe
4	16	33.3	7	2	S33246 neuromodulatory pe
5	16	33.3	8	2	S68325 blood cell protein
6	14	29.2	6	2	I49421 lamelin B1 - weste
7	14	29.2	7	2	S71870 glutathione transf
8	14	29.2	7	2	PT0269 Ig heavy chain CRD
9	14	29.2	7	2	A38081 amine oxidase (cop
10	14	29.2	8	2	S66646 cardioacceleratory
11	14	29.2	8	2	D47393 neuropeptide calia
12	13	27.1	5	2	B61445 leu-enkephalin - b
13	13	27.1	5	2	A61445 Met-enkephalin - b
14	13	27.1	7	1	NYPG7 hypothalamic hepta
15	13	27.1	7	2	A60224 Met-enkephalin-Arg
16	13	27.1	7	2	S33245 neuromodulatory pe
17	13	27.1	7	4	I56695 hypothetical L2 pr
18	13	27.1	8	2	S19288 acylase - Kluyvera
19	13	27.1	8	2	S63493 dissimilatory sulf
20	13	27.1	8	2	J50318 leucokinin VIII -
21	12	25.0	4	2	PT0240 Ig heavy chain CRD
22	12	25.0	5	2	PT0308 Ig heavy chain CRD
23	12	25.0	6	2	S66195 alcohol dehydrogen
24	12	25.0	6	2	A31263 dihydrofolate redu
25	12	25.0	6	2	B31263 dihydrofolate redu
26	12	25.0	6	2	B35640 cerebellar degener
27	12	25.0	6	2	PT0531 T-cell receptor be
28	12	25.0	6	2	A41946 T-cell receptor be
29	12	25.0	7	2	PT0623 T-cell receptor be

30	12	25.0	8	2	PQ0012 cholecystokinin -
31	12	25.0	8	2	A43001 cholecystokinin -
32	12	25.0	8	2	ACHUEU urine glycopeptide
33	12	25.0	8	2	C61512 variant surface gl
34	12	25.0	8	2	D61512 variant surface gl
35	12	25.0	8	2	A61467 penalbumin - Adell
36	12	25.0	8	2	A42057 fibroblast growth
37	11	22.9	3	2	F37196 bradykinin-potentl
38	11	22.9	4	2	A37832 phenol 2-monooxyge
39	11	22.9	4	2	A34626 RPNH-related neuro
40	11	22.9	4	2	B53284 T-cell receptor be
41	11	22.9	4	2	PT0661 T-cell receptor be
42	11	22.9	5	2	A32516 cholecystokinin-5
43	11	22.9	5	2	A14046 dnazx-like protein
44	11	22.9	5	2	A60803 neuropeptide - sea
45	11	22.9	5	2	JH0253 gut pentapeptide -
46	11	22.9	5	2	G37196 bradykinin-potentl
47	11	22.9	5	2	PT0278 Ig heavy chain CRD
48	11	22.9	5	2	PT0281 Ig heavy chain CRD
49	11	22.9	5	2	PT0729 T-cell receptor be
50	11	22.9	5	2	PT0580 T-cell receptor be

ALIGNMENTS

RESULT 1
S68326
blood cell protein B - Ascidia ceratodes (fragment)
N:Alternate names: Abcp-B
C:Species: Ascidia ceratodes
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch Biochem Biophys. 324, 228-240, 1995
A:Title: Novel 3',4'-di- and 3',4',5'-trihydroxyphenylalanine-containing polypeptides from
A:Reference number: S68325; MUID:96132650
A:Accession: S68326
A:Molecule type: protein
A:Residues: 1-5 <TAY>
F:2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
F:4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 39.6%; Score 19; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSTA 7
1:11
DB 2 YAYA 5

RESULT 2
A60139
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
R:Harder, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase d
A:Reference number: A60139; MUID:85175165
A:Accession: A60139
A:Molecule type: protein
A:Residues: 1-7 <HAR>
C:Superfamily: rat fatty-acid synthase: 3-oxoacyl-[acyl-carrier-protein] synthase I h
hydrolyase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein]
C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolyase) #status experimental

Query Match 37.5%; Score 18; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
111
DB 4 YSY 6

RESULT 3

S33244

neuromodulatory peptide Wwamide-1 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33244

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of

A:Reference number: S33244; MUID:93265912

A:Accession: S33244

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
111
DB 1 WK 2

RESULT 4

S33246

neuromodulatory peptide Wwamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of

A:Reference number: S33244; MUID:93265912

A:Accession: S33246

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
111
DB 1 WK 2

RESULT 5

S68325

blood cell protein A8 - Ascidia ceratodes (fragment)

N:Alternate names: Abcp-A

C:Species: Ascidia ceratodes

C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999

C:Accession: S68325

R:Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A:Reference number: S68325; MUID:96132650

A:Accession: S68325

A:Molecule type: protein

A:Residues: 1-8 <TAY>

F:2,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 33.3%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSYA 7
111
DB 2 YSYA 5

RESULT 6

I49421

laminin B1 - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49421

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau,

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082

A:Accession: I49421

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 29.2%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YYS 5
111
DB 1 YYS 3

RESULT 7

S71870

glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)

N:Alternate names: glutathione S-transferase class mu 9

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 07-May-1999

C:Accession: S71870

R:Rouml, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electros

A:Reference number: S71864; MUID:96332484

A:Accession: S71870

A:Molecule type: protein

A:Residues: 1-7 <ROU>

C:Comment: At least five species-independent classes of cytosolic glutathion transfer

s mitochondrial form are known.

C:Function: dimer

A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to

A:Pathway: detoxification; xenobiotics metabolism

A:Note: increased hydrophilicity of GSH-conjugates facilitates their further metaboli

es of damage

C:Superfamily: glutathione transferase

C:Keywords: acetylated amino end; blocked amino end; dimer; transferase

F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 YYSVA 7
111
DB 3 YYSVA 7


```
RESULT 8
PRO269
Ig heavy chain CRD3 region (clone 3-97) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PR0269
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PR0222; MUID:91108337
A:Accession: PR0269
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match          29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.2e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KITYAG 8
  1 1
  1 1
Db 1 EIIAVAG 7

RESULT 9
A38081
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (Pichia angusta) (fragment)
C:Species: Pichia angusta
C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C:Accession: A38081
R:Wu, D.; James, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klimman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A:Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine C
A:Reference number: A38081; MUID:92235001
A:Accession: A38081
A:Molecule type: protein
A:Residues: 1-7 <MUA>
C:Keywords: copper; oxidoreductase; quinoprotein; topaquinone
F:4/Modified site: topaquinone (Tyr) #status experimental

Query Match          29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSY 6
  1 1
  1 1
Db 4 YEY 6

RESULT 10
S66646
cardioacceleratory protein 2b - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66646
R:Huesmann, G.R.; Cheung, C.C.; Lol, P.K.; Lee, T.D.; Swiderrek, K.M.; Tüblitz, N.J.
FEBS Lett. 371, 311-314, 1995
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the t
A:Reference number: S66646; MUID:96013159
A:Accession: S66646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HUE>

Query Match          29.2%; Score 14; DB 2; Length 8;
Best Local Similarity 20.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 KITYV 6
```

```
Db 1 ELYAF 5

RESULT 11
D47393
neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C:Accession: D47393
R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagl, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A:Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with seq
A:Reference number: A47393; MUID:93211980
A:Accession: D47393
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Experimental source: thoracic ganglia
A:Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match          29.2%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSY 6
  1 1
  1 1
Db 4 YSF 6

RESULT 12
B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A:Reference number: A61445; MUID:84144823
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match          27.1%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YAG 8
  1 1
  1 1
Db 1 YGG 3

RESULT 13
A61445
Met-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A:Reference number: A61445; MUID:84144823
A:Accession: A61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide
```

Query Match 27.1%; Score 13; DB 2; Length 5;
A:Species: Sus scrofa domestica (domestic pig)
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
| |
| |
Db 1 YGG 3

RESULT 14

NYPG7
hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
C:Accession: A01417
R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981
A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release
A:Reference number: A01417; MUID:81213980
A:Accession: A01417
A:Molecule type: protein
A:Residues: 1-7 <CH>
A:Superfamily: hypothalamic heptapeptide
C:Keywords: hypothalamus

Query Match 27.1%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
| |
| |
Db 4 HSY 6

RESULT 15

A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E. J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680
A:Accession: A60224
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAD>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Query Match 27.1%; Score 13; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
| |
| |
Db 1 YGG 3

RESULT 16

S33245
neuromodulatory peptide Wamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Munekata, Y.; Kobayashi, M.; Nomoto, K. FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A:Reference number: S33244; MUID:93265912

A:Accession: S33245
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 27.1%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
| |
Db 1 WR 2

RESULT 17

I56695
hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)
C:Species: human papillomavirus type 16
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: I56695
R:Schneider-Maunoury, S.; Croissant, O.; Orth, G. J. Virol. 61, 3295-3298, 1987
A:Title: Integration of human papillomavirus type 16 DNA sequences: a possible early
A:Reference number: I56695; MUID:87311896
A:Accession: I56695
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <SCH>
A:Cross-references: GB:M30709; NID:9190253; PIDN:AAA65995.1; PID:9553616
C:Comment: This is the hypothetical translation of a viral sequence integrated into t
C:Comment: It is translated in an incorrect, -1, reading frame of the L2 protein.

Query Match 27.1%; Score 13; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
| |
| |
Db 1 HSY 3

RESULT 18

S19288
acylase - Kluyvera cryocrescens
C:Species: Kluyvera cryocrescens
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S19288
R:Martin, J.; Slade, A.; Altken, A.; Arche, R.; Virden, R. Biochem. J. 280, 659-662, 1991
A:Title: Chemical modification of serine at the active site of penicillin acylase fro
A:Reference number: S19288; MUID:92109664
A:Accession: S19288
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 27.1%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKI 3
| |
| |
Db 4 WVI 6

RESULT 19

S63493
disulfide reductase gamma chain, membrane-bound and soluble - Desulfovibr
C:Species: Desulfovibrio desulfuricans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S63493; S63494
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152
A:Accession: S63493
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STE>
A:Accession: S63494
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <ST2>

Query Match 27.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 SYAC 8
1 1
4 TYKC 7

Db

RESULT 20
JS0318
Leucokinin VIII - Madelira cockroach
C:Species: Leucophaea maderea (Madelira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0318
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the first
A:Reference number: JS0317
A:Accession: JS0318
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.1%; Score 13; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSX 6
1 1
5 YSW 7

Db

RESULT 21
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; Immunoglobulin

Query Match 25.0%; Score 12; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8

Db 1 WK 3
1 YPG 3

RESULT 22
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; Immunoglobulin

Query Match 25.0%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
1 1
2 WE 3

Db

RESULT 23
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fra
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltny, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases
nzyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HJE>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 25.0%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
1 1
5 WE 6

Db

RESULT 24
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:99057886
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 25.0%; Score 12; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
 1;
 Db 3 WE 4

RESULT 25

B31263
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
 C:Species: Plasmodium falciparum
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
 C:Accession: B31263
 R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
 Proc. Natl. Acad. Sci. U.S.A. 85, 914-918, 1988
 A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
 A:Reference number: A94217; MUID:89057886
 A:Accession: B31263
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-6 <PEP>
 C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 25.0%; Score 12; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
 1;
 Db 3 WE 4

Search completed: January 14, 2002, 06:43:20
 Job time: 348 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:48:45 ; Search time 16.62 Seconds
(without alignments)
17.649 Million cell updates/sec

Title: US-09-185-908-34

Perfect score: 48

Sequence: 1 WKIVSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	37.5	8	1	AL16_CARMA
2	16	33.3	7	1	ALL7_CYPDPO
3	16	33.3	7	1	WMA2_ACHFU
4	16	33.3	7	1	WMA3_ACHFU
5	15	31.2	8	1	AL18_CARMA
6	14	29.2	5	1	AL14_CARMA
7	14	29.2	8	1	AL15_CARMA
8	14	29.2	8	1	AL17_CARMA
9	14	29.2	8	1	ALL3_CYPDPO
10	14	29.2	8	1	ALL4_CALVO
11	14	29.2	7	1	ALL4_CALVO
12	13	27.1	7	1	HY7_PIG
13	13	27.1	7	1	WMA1_ACHFU
14	13	27.1	8	1	ALL6_CYPDPO
15	13	27.1	8	1	LCK8_LEUMA
16	12	25.0	5	1	PSK_DAUCA
17	12	25.0	7	1	ALL2_CARMA
18	12	25.0	7	1	MNP1_LEPDE
19	12	25.0	8	1	AL12_CARMA
20	12	25.0	8	1	ANG2_BOTJA
21	12	25.0	8	1	CCKN_MACEU
22	12	25.0	8	1	GLUR_HUMAN
23	12	25.0	8	1	UPPA_HUMAN
24	11	22.9	5	1	BPP7_BOTIN
25	11	22.9	5	1	UF01_MOUSE
26	11	22.9	6	1	LOK1_LOCMT
27	11	22.9	7	1	ALL3_CARMA
28	11	22.9	7	1	ALL4_CARMA
29	11	22.9	7	1	ALL5_CARMA
30	11	22.9	8	1	AC1_THUAL
31	11	22.9	8	1	AKHG_GRYBI
32	11	22.9	8	1	AKH1_LTBVU
33	11	22.9	8	1	AKH1_MELML

34	11	22.9	8	1	AKH1_TABAT	P14595 tabanus atr
35	11	22.9	8	1	ALL1_CYPDPO	P82152 cydia pomon
36	11	22.9	8	1	ALL7_CARMA	P81809 carcinus ma
37	11	22.9	8	1	ALL8_CARMA	P81811 carcinus ma
38	11	22.9	8	1	ALL9_CARMA	P81812 carcinus ma
39	11	22.9	8	1	HTF1_PERAM	P04548 periplaneta
40	11	22.9	8	1	HTF2_PERAM	P04549 periplaneta
41	11	22.9	8	1	HTF_TENMO	P25419 tenebrio mo
42	11	22.9	8	1	LCK1_LEUMA	P21140 leucophaea
43	11	22.9	8	1	LCK2_LEUMA	P21141 leucophaea
44	11	22.9	8	1	LCK3_LEUMA	P21142 leucophaea
45	11	22.9	8	1	LCK4_LEUMA	P21143 leucophaea
46	11	22.9	8	1	LCK5_LEUMA	P19987 leucophaea
47	11	22.9	8	1	LCK6_LEUMA	P19988 leucophaea
48	11	22.9	8	1	LCK7_LEUMA	P19989 leucophaea
49	11	22.9	8	1	PLP_BRANA	P81707 brassica na
50	11	22.9	8	1	RPCH_PANBO	P08939 pandanus bo

ALIGNMENTS

RESULT 1
AL16_CARMA
ID AL16_CARMA STANDARD: PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTATTIN 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
RA "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KN Neuropeptide; Amidation; Multigene family.
FT MOD.RES 8
FT AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 37.5%; Score 18; DB 1; Length 8;
Best local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YST 6
Db 4 YSY 6

RESULT 2
ALL7_CYPDPO
ID ALL7_CYPDPO STANDARD: PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATTIN 7.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;

RN [1]
 RP SEQUENCE.
 RC TISSUE-Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily."
 RL Peptides 18:1301-1309(1997).
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES
 SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 7;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 K1YSY 6
 Db 1 KMYDF 5

RESULT 3
 WMA2_ACHFV STANDARD; PRT; 7 AA.
 ID WMA2_ACHFV
 AC P35920;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WMAWIDE-2.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamwide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 KW Neuropeptide; Amidation.
 FT MOD_RES
 SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WK 2
 Db 1 WK 2

RESULT 4
 WMA3_ACHFV STANDARD; PRT; 7 AA.
 ID WMA3_ACHFV
 AC P35921;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WMAWIDE-3
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [4]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;

RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wamwide-1, -2 and -3: novel neuromodulatory peptides isolated from
 ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 DR PIR: S33244; S33244.
 KW Neuropeptide; Amidation.
 FT MOD_RES
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 33.3%; Score 16; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WK 2
 Db 1 WK 2

RESULT 5
 AL18_CARMA STANDARD; PRT; 8 AA.
 ID AL18_CARMA
 AC P81821;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSSTATIN 18.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OX Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -i- FUNCTION: MAY ACT AS A NEUROTANSMITTER OR NEUROMODULATOR.
 CC -i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES
 SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYSY 6
 Db 3 MYSY 6

RESULT 6
 AL14_CARMA STANDARD; PRT; 5 AA.
 ID AL14_CARMA
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSSTATIN 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OX Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE:98121193; PubMed:9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab *Carcinus maenas*.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 29.2%; Score 14; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
DB 1 YSF 3

RESULT 7
AL15_CARMA STANDARD; PRT; 8 AA.
ID AL15_CARMA
AC P81818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 15.
OS *Carcinus maenas* (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE:98121193; PubMed:9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab *Carcinus maenas*.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
DB 4 YSF 6

RESULT 8
AL17_CARMA STANDARD; PRT; 8 AA.
ID AL17_CARMA
AC P81820;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 17.
OS *Carcinus maenas* (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;

RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE:98121193; PubMed:9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab *Carcinus maenas*.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
DB 4 YSF 6

RESULT 9
AL13_CYPDO STANDARD; PRT; 8 AA.
ID AL13_CYPDO
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASSTATIN 3.
OS *Cydia pomonella* (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP TISSUE=Larva;
RC TISSUE=Larva;
RX MEDLINE:98054539; PubMed:9392829;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 926 MW; C82879D5AB477415 CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
DB 4 YSF 6

RESULT 10
AL14_CALVO STANDARD; PRT; 8 AA.
ID AL14_CALVO
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).
OS *Calliphora vomitoria* (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.

OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duvé H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
Thorppe A.;
"Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatins.";
Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duvé H., Thorpe A.;
"Distribution and functional significance of Leu-callatostatins in
the blowfly Calliphora vomitoria.";
Cell Tissue Res. 276:367-379(1994).
RL
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -I- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL
COMPLEX, THORACIC-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
SYSTEM AND INTESTINE.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR: D47393; D47393.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT UNSTRE 1
FT OR N.
FT SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
I I
Db 4 YSF 6

RESULT 11
ALL4_CYPDPO STANDARD; PRT; 8 AA.
AC P82155;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASPTATIN 4.
OS Cydia pomonella (Codling moth).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylsia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX MEDLINE=98054539; PubMed=9392829;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davy M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
RL
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 910 MW; 922879D5AB47740D CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
I I
Db 4 YSF 6

RESULT 12
HY7_PIG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE HYPOTHALAMIC HEPTAPEPTIDE.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
"Isolation, structure and synthesis of a heptapeptide with in vitro
ACTH-releasing activity from porcine hypothalamus.";
Horm. Metab. Res. 13:228-232(1981).
DR PIR: A01417; NYPG7.
FT MOD_RES 7
FT SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6
I I
Db 4 HSY 6

RESULT 13
WMA1_ACHFV STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA1DE-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
RL
CC -I- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
CC PIR: S33245; S33245.
DR Neuropeptide; Amidation.
FT MOD_RES 7
FT SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
I I
Db 1 WR 2

RESULT 14
ALL6_CVDP0
ID ALL6_CVDP0 STANDARD: PRT: 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATIN 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptera;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
[1]
RN SEQUENCE.
RP TISSUE=larva;
RX MEDLINE=98054539; PubMed=9392829;
RA DAVEY H., JOHNSON A.H., MAESTRO J.-L., SCOTT A.G., WINSTANLEY D.,
RA DAVEY M., EAST P.D., THORPE A.;
RT "Lepidopteran peptides of the allatostatin superfamily";
RL Peptides 18:1301-1309(1997).
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 936 MW: 0B2879C45B573767 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 YSY 6
: : :
DB 3 LYNF 6

RESULT 15
LCK8_LEUMA
ID LCK8_LEUMA STANDARD: PRT: 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidae; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
[1]
RN SEQUENCE.
RP TISSUE=Head;
RA HOLMAN G.M., COOK B.J., NACHMAN R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHODIUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
CC PIR: JS0318; JS0318.
KM Neuropeptide; Amidation.
RN MOD_RES 8
SQ SEQUENCE 8 AA: 902 MW: 736365AB59CAAD8 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YSY 6

DB 5 YSW 7

RESULT 16
PSK_DAUCA
ID PSK_DAUCA STANDARD: PRT: 5 AA.
AC P58261;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHYTOSULFOKINE-ALPHA (PSK-ALPHA) [CONTAINS: PHYTOSULFOKINE-BETA (PSK-BETA)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids II; Apiales; Apiaceae; Daucus.
NCBI_TaxID=4039;
[1]
RN SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RP STRAIN=cv. US-Harumakigosun;
RX PubMed=10750705;
RA HANAI H., MATSUNO T., YAMAMOTO M., MATSUBAYASHI Y., KOBAYASHI T.,
RA KAMADA H., SAKAGAMI Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -I- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -I- SUBCELLULAR LOCATION: SECRETED.
CC -I- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA: 687 MW: 76C1BB504B300000 CRC64;

Query Match 25.0%; Score 12; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSY 6
: : :
DB 1 YIT 3

RESULT 17
ALL2_CARMA
ID ALL2_CARMA STANDARD: PRT: 7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
NCBI_TaxID=6759;
[1]
RN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA DUVE H., JOHNSON A.H., MAESTRO J.-L., SCOTT A.G., JAROS P.P.,
RA THORPE A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA: 770 MW: 672879CDB5DBD70 CRC64;

Query Match 25.0%; Score 12; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SYA 7
 : :
 Db 2 AYA 4

RESULT 18
 MNPL_LEPDE STANDARD; PRT; 7 AA.

AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
 OS Lepidoptarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiforma; Phycophaga; Chrysomeloidea; Chrysomelidae;
 OC Chrysomellinae; Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN (1)
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;

RA Spittaels K., Van Leuven F., de Loof A.,
 Grauwels L., Torrekens S.,
 "Identification, characterization, and immunological localization of
 a novel myotropic neuropeptide in the Colorado potato beetle,
 Leptinotarsa decemlineata.";
 RT Peptides 16:365-374(1995).
 RL
 CC -I- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 CC Neuropeptide; Amidation.

KW Neuropeptide; Amidation.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA: 705 MW: 6DD73768745B5D80 CRC64;

Query Match 25.0%; Score 12; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 SYA 8
 : :
 Db 1 AYG 4

RESULT 19
 ALI2_CARMA STANDARD; PRT; 8 AA.

AC P81815;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINOSTATIN 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN (1)
 RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestero J.-L., Scott A.G., Jaros P.P.,

RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -I- FUNCTION: MAY ACT AS A NEUROTANSITTER OR NEUROMODULATOR.
 CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 8 AA: 913 MW: 672879CDB569AB7 CRC64;

Query Match 25.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1e+05;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYSY 6
 : :
 Db 3 MYAF 6

RESULT 20
 ANG2_BOTJA STANDARD; PRT; 8 AA.

AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ANGIOTENSIN-LIKE PEPTIDE II (FRAGMENT).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN (1)
 RP SEQUENCE.

RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucra J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC Interpro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasconstrictor; Plasma; Serpin.
 FT NON TER 8
 SQ SEQUENCE 8 AA: 1046 MW: DDD761E04B42D40A CRC64;

Query Match 25.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KIY 4
 : :
 Db 2 RYV 4

RESULT 21
 CCKN_MACEU STANDARD; PRT; 8 AA.

AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CHOLECYSTOKININ (CCK).
 GN CCK.

OS Macropus eugenii (Trammar wallaby), and
 OS Dasyurus viverrinus (Southeastern quoll).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315; 9279;
 RN (1)
 RP SEQUENCE.

RC TISSUE-Brain;
 RX MEDLINE=88234141; PubMed:3375140;
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
 RT "Cholecystokinin octapeptide purified from brains of Australian
 mammals";
 RL Peptides 9:429-431(1988).
 CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
 AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
 IN THE BRAIN IS NOT CLEAR.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 CC PIR: A43001; A43001.
 DR PIR: P00012; P00012.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Amidation; Sulfation; Hormone.
 FT MOD_RES 2 2 SULFATION.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA: 1064 MW; DDCAA68378768B5A CRC64;

Query Match 25.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
 1 1
 DB 2 YMG 4

RESULT 22
 ID GLUR_HUMAN STANDARD; PRT; 8 AA.
 AC P02729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE URINE GLYCOPROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_Taxid:9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72062338; PubMed=5126885;
 RA Lote C.J., Weiss J.B.;
 RT "Identification in urine of a low-molecular-weight highly polar
 glycopeptide containing cysteinyl-galactose";
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
 IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
 CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
 DR PIR: A03188; XGHUEU.
 KW Glycoprotein.
 FT CARBOHYD 1 1 S-LINKED (GAL. . .);
 SO SEQUENCE 8 AA: 855 MW; C2D87A1F5B1B1E CRC64;

Query Match 25.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YSYAG 8
 1 1
 DB 3 HSHDG 7

RESULT 23
 ID UPAA_HUMAN STANDARD; PRT; 8 AA.
 AC P30096;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 36) (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Fruiter S., Paquet N., Ravier F., Pasquall C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7. ITS MW IS: 12 KDA.
 DR SWISS-2DPAGE; P30096; HUMAN.
 FT NON_TER 1 5 F -> P.
 FT NON_TER 5 5 /FTid=VAR_000004.
 FT NON_TER 8 8
 SO SEQUENCE 8 AA: 909 MW; 86677B59D1A72042 CRC64;

Query Match 25.0%; Score 12; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
 1 1
 DB 6 YPG 8

RESULT 24
 ID BPP7_BOTIN STANDARD; PRT; 5 AA.
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
 DE ENZYME INHIBITOR).
 OS Bothrops insularis (Island jararaca) (Quelamada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Viperidae; Crotalinae; Bothrops.
 NC NCB1_Taxid=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintrra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom";
 RL J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: G37196; G37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SO SEQUENCE 5 AA: 629 MW; 776DC37326B00000 CRC64;

Query Match 22.9%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 1 1
 DB 3 W 3

RESULT 25
 UF01_MOUSE STANDARD; PRT; 5 AA.
 ID UF01_MOUSE
 AC P38639;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994). THE DETERMINED PI OF THIS UNKNOWN
 CC -I- MISCELLANEOUS: ON THE 2D-GEL.
 CC PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
 FT NON_TER 5
 SO SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 22.9%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 |
 Db 1 W 1

Search completed: January 14, 2002, 06:48:45
 Job time: 358 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:47:41 ; Search time 37.85 Seconds
(without alignments)
30.916 Million cell updates/sec

Title: US-09-185-908-34
Perfect score: 48
Sequence: 1 WKIYSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: SPTRMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mmc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rhodent:*
13: sp_virus:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	18	37.5	7	8	Q95945
2	16	33.3	8	6	P82929
3	16	33.3	8	11	P82929
4	15	31.2	8	2	O85406
5	13	27.1	8	6	O9BFA7
6	12	25.0	8	5	O9TWH6
7	12	25.0	8	7	O95213
8	12	25.0	8	11	P70243
9	11	22.9	6	13	P82096
10	11	22.9	7	2	O50556
11	11	22.9	7	8	O99182
12	11	22.9	7	10	O49223
13	11	22.9	7	13	P82065
14	11	22.9	7	13	P82101
15	11	22.9	8	2	O9R057
16	11	22.9	8	2	O9R049
17	11	22.9	8	4	O15888
18	11	22.9	8	4	O15890
19	11	22.9	8	4	O15890

20	11	22.9	8	4	O15898	O15898 homo sapien
21	11	22.9	8	5	O9VRD2	O9VRD2 dirosophila
22	11	22.9	8	5	P82685	P82685 periplaneta
23	11	22.9	8	5	P82686	P82686 periplaneta
24	11	22.9	8	5	P82687	P82687 periplaneta
25	11	22.9	8	5	P82688	P82688 periplaneta
26	11	22.9	8	5	P82689	P82689 periplaneta
27	11	22.9	8	6	O02831	O02831 oryctolagus
28	11	22.9	8	6	O9TRX3	O9TRX3 sus sp. ins
29	11	22.9	8	8	O34909	O34909 locusta mlg
30	11	22.9	8	8	O9TD02	O9TD02 terranatos
31	11	22.9	8	8	O9TY42	O9TY42 asterina pe
32	11	22.9	8	8	O9GD47	O9GD47 hyariscalcie
33	11	22.9	8	8	O9GD00	O9GD00 masocala mad
34	11	22.9	8	8	O9GCZ4	O9GCZ4 nenga pumil
35	11	22.9	8	10	O9S824	O9S824 splinacia ol
36	11	22.9	8	11	O35835	O35835 rattus norv
37	11	22.9	8	11	P82598	P82598 rattus norv
38	11	22.9	8	11	O9ET21	O9ET21 mus musculu
39	11	22.9	8	11	O9ET18	O9ET18 mus spretus
40	11	22.9	8	11	O9ET17	O9ET17 mus caroll
41	11	22.9	8	11	O9ET16	O9ET16 mesocricetu
42	11	22.9	8	11	O99MNO	O99MNO mus musculu
43	11	22.9	8	13	P79940	P79940 xenopus lae
44	11	22.9	8	13	O98TR5	O98TR5 xenopus lae
45	10	20.8	7	11	O63668	O63668 rattus norv
46	10	20.8	7	12	O07624	O07624 rous sarcom
47	10	20.8	8	2	O44463	O44463 agrobacteri
48	10	20.8	8	3	P82858	P82858 puccinia re
49	10	20.8	8	3	O9HDS4	O9HDS4 aspergillus
50	10	20.8	8	6	O9BF82	O9BF82 ursus arcto

ALIGNMENTS

RESULT 1
ID O95945 PRELIMINARY; PRT: 7 AA.
AC O95945;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSIDE INTRON 5 (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81069885; PubMed=6254985;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit I of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL: V00694; CAA24066.1; -
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 7 AA: 859 MW: 7587232362CDC460 CRC64;

Query Match 37.5%; Score 18; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKI 3
DB 4 WKL 6
RESULT 2

P82929 PRELIMINARY; PRT; 8 AA.
 AC P82929;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LIVER;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "Small subunit of the mammalian mitochondrial ribosome. Identification
 of the full complement ribosomal proteins present.";
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 8
 FT NON_TER 1 8
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 33.3%; Score 16; DB 6; Length 8;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIYSY 6
 | | | | |
 DB 2 WGLTFF 7

RESULT 3
 ID Q62721 PRELIMINARY; PRT; 8 AA.
 AC Q62721;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE PROHIBITIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FISHER;
 RX MEDLINE=95331633; PubMed=7607556;
 RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
 Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
 McClung J.K.;
 RT "Regions of evolutionary conservation between the rat and human
 RT Prohibitin-encoding genes.";
 RL Gene 158:291-294(1995).
 DR EMBL: U17178; AAA86692.1; -.
 FT NON_TER 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 33.3%; Score 16; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
 | |
 DB 6 WK 7

RESULT 4
 085406

ID 085406 PRELIMINARY; PRT; 8 AA.
 AC 085406;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
 OS CoxIELla burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC CoxIELla group; CoxIELla.
 NCBI_TaxID=777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE I;
 RA Williams H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 RT CoxIELla burnetii.";
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF064963; AAD09947.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 31.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIY 4
 | |
 DB 4 WNDY 7

RESULT 5
 ID Q9BFA7 PRELIMINARY; PRT; 8 AA.
 AC Q9BFA7;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT MODERATOR (FRAGMENT).
 GN CREM.
 OS Macroselides proboscideus (Short-eared elephant shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Macroscelidae; Macroscelididae; Macroscelides.
 NCBI_TaxID=29082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21082082; PubMed=11214319;
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals.";
 RL Nature 409:614-618(2001).
 DR EMBL: AY011636; AAG47551.1; -.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 940 MW; DF1DD33AB5AB572A CRC64;

Query Match 27.1%; Score 13; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 IYS 5
 | | |
 DB 2 LYS 4

RESULT 6
 O9TWH6
 ID O9TWH6 PRELIMINARY; PRT; 8 AA.
 AC O9TWH6;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)

```
DE BIOACTIVE PEPTIDE P4-PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OC Perinereis vancouverica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllodoidea; Nereididae; Perinereis.
OX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95333338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancouverica.";
RL Comp. Biochem. Physiol. C,
RL Pharmacol. Toxicol. Endocrinol. 110:297-304(1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 25.0%; Score 12; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
   1
   1
Db 2 YEG 4

RESULT 7
ID 095213 PRELIMINARY; PRT; 8 AA.
AC 095213;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 02, Last annotation update)
DE GERMLINE DH (DF) GENE (FRAGMENT).
CN DE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F-1/RGM;
RA Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
RL Mol. Immunol. 0:0-0(0).
DR EMBL; U62585; AAB18735.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 845 MW; 5CA861B5AB58677B CRC64;

Query Match 25.0%; Score 12; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YAG 8
   1
   1
Db 1 YPG 3

RESULT 8
ID P70243 PRELIMINARY; PRT; 8 AA.
AC P70243;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Ophiof. R.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98325; CAA66969.1; -.
KW Calcium channel.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 25.0%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
   1
Db 7 WQ 8

RESULT 9
ID 090VD3 PRELIMINARY; PRT; 8 AA.
AC 090VD3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA; 1047 MW; D72415BB06C37041 CRC64;

Query Match 25.0%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
   1
Db 3 WQ 4

RESULT 10
ID P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
```

KW Amphibian skin; Amidation.
 FT MOD_RES 6 6 AMIDATION.
 SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 22.9%; Score 11; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 W 1
 Db 5 W 5

RESULT 11
 050556 PRELIMINARY; PRT; 7 AA.
 AC 050556;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE GLYA (FRAGMENT).
 GN GLYA.
 OS Actinobacillus actinomycetecomitans (Haemophilus
 actinomycetecomitans).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Actinobacillus.
 CX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 33384;
 RX MEDLINE=96355846; PubMed=8751884;
 RA Kolodrubetz D., Spitnagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
 Kraig E.;
 RT "cis Elements and trans factors are both important in strain-specific
 regulation of the leukotoxin gene in Actinobacillus
 actinomycetecomitans.";
 RT Infect. Immun. 64:3451-3460(1996).
 RL EMBL: U51862; AAB88721.1; -.
 DR EMBL: U51862; AAB88721.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 22.9%; Score 11; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 IYS 5
 :1:
 Db 5 VYA 7
 RESULT 12
 099182 PRELIMINARY; PRT; 7 AA.
 ID 099182;
 AC 099182;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 GN COI.
 OS Gnatholebias zonatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
 CX NCBI_TaxID=135316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy W.J., Thomerson J.E., Collier G.E.;
 RT "A molecular phylogeny of Neotropical aplocheiloid killifishes
 (Cyprinodontiformes, Rivulidae).";

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF002591; AAD01074.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 22.9%; Score 11; DB 8; Length 7;
 Best Local Similarity 25.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 IYSY 6
 :1:
 Db 2 LYQH 5

RESULT 13
 049223 PRELIMINARY; PRT; 7 AA.
 ID 049223;
 AC 049223;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE HMG-1-LIKE PROTEIN (FRAGMENT).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
 CX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
 RX MEDLINE=91367679; PubMed=1891369;
 RA Iaux T., Goldberg R.B.;
 RT "A plant DNA binding protein shares highly conserved sequence motifs
 with HMG-box proteins.";
 RT Nucleic Acids Res. 19:4769-4769(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
 RA Mahalingam R., Knapp H.T.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF047050; AAC03556.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 850 MW; 6AAAAB378637810 CRC64;

Query Match 22.9%; Score 11; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
 :1:
 Db 2 W 2
 RESULT 14
 P82065 PRELIMINARY; PRT; 7 AA.
 ID P82065;
 AC P82065;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE TRYPROPHYLIN 5.1.
 OS Ilfordia rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Ilfordia.
 CX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,

RA Tyler M.J., Wallace J.C.:
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW:965; METHOD:FMAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 983 MW: 7401E9D3676046B0 CRC64:

Query Match 22.9%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 4 W 4

RESULT 15
ID P82101 PRELIMINARY; PRT; 7 AA.
AC P82101;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxId=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION.
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.:
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 834 MW: 6DD05B076B0B5030 CRC64:

Query Match 22.9%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IV 4
DB 1 IV 2

RESULT 16
ID Q9RO57 PRELIMINARY; PRT; 8 AA.
AC Q9RO57;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NIFS PROTEIN HOMOLOG (FRAGMENT).
GN NIFS.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxId=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;

RA Clark M.A., Moran N.A., Baumann P.:
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL: AF130812; AAF13797.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 980 MW: F3A73B504771A336 CRC64:

Query Match 22.9%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IV 4
DB 5 IV 6

RESULT 17
ID Q9RO49 PRELIMINARY; PRT; 8 AA.
AC Q9RO49;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NIFS PROTEIN HOMOLOG (FRAGMENT).
GN NIFS.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxId=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.:
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL: AF130814; AAF13805.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 992 MW: F3A73B504771A336 CRC64:

Query Match 22.9%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 IV 4
DB 5 IV 6

RESULT 18
ID Q15888 PRELIMINARY; PRT; 8 AA.
AC Q15888;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE (CLONE XP158A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Cooibaugn M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32069; AAA73878.1; -.
FT NON_TER 1 1
FT NON_TER 8 8

SO SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match
Best Local Similarity 22.9%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 6 W 6

RESULT 19
ID Q15890 PRELIMINARY; PRT: 8 AA.
AC Q15890;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP19612A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.T., Chinnault C.A., Baldwin A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32083; AAA73880.1; -;
FT NON_TER 1
FT SEQUENCE 8 AA; 975 MW; 605EAC5BEA5A2D3 CRC64;

Query Match
Best Local Similarity 22.9%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 1 W 1

RESULT 20
ID Q15898 PRELIMINARY; PRT: 8 AA.
AC Q15898;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XPC611B) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.T., Chinnault C.A., Baldwin A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32078; AAA73888.1; -;
FT NON_TER 1
FT SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match
Best Local Similarity 22.9%; Score 11; DB 4; Length 8;
Matches 1; Conservative 100.0%; Pred. No. 4.7e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SY 6
DB 2 SY 3

RESULT 21
ID Q09VRD2 PRELIMINARY; PRT: 8 AA.
AC Q09VRD2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Asparyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., Meleod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003569; AAF50870.1; -;
DR FlyBase: FBgn0040648; CG11666.
SO SEQUENCE 8 AA; 1062 MW; ED11B5B044004376 CRC64;

Query Match
Best Local Similarity 22.9%; Score 11; DB 5; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1

Db 2 W 2

RESULT 22

P82685 PRELIMINARY; PRT: 8 AA.
AC P82685; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 22.9%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 7 W 7

RESULT 23

P82686 PRELIMINARY; PRT: 8 AA.
AC P82686; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

Query Match 22.9%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 7 W 7

RESULT 24

P82687 PRELIMINARY; PRT: 8 AA.
AC P82687; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 22.9%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 7 W 7

RESULT 25

P82688 PRELIMINARY; PRT: 8 AA.
AC P82688; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9DDDD8 CRC64;

Query Match 22.9%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
 |
 Db 7 W 7

Search completed: January 14, 2002, 06:47:42
 Job time: 385 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 06:42:42 ; Search time 23.1 Seconds
(without alignments)
7.793 Million cell updates/sec

Title: US-09-185-908-34
Perfect score: 48
Sequence: 1 MKIVSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/laa/6A.COMB.pep:*
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6: /cgn2_6/ptodata/2/laa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	56.2	8	2	US-08-031-538-32
2	26	54.2	8	2	US-08-350-260A-464
3	24	50.0	6	1	US-08-338-890B-2
4	24	50.0	6	1	US-08-338-890B-3
5	24	50.0	6	2	US-08-340-208B-2
6	24	50.0	6	2	US-08-340-208B-3
7	24	50.0	6	3	US-08-997-263-2
8	24	50.0	6	3	US-08-997-263-3
9	22	45.8	4	3	US-09-222-373-49
10	22	45.8	6	1	US-08-338-890B-4
11	22	45.8	6	1	US-08-338-890B-5
12	22	45.8	6	2	US-08-340-208B-4
13	22	45.8	6	2	US-08-340-208B-5
14	22	45.8	6	3	US-08-997-263-4
15	22	45.8	6	3	US-08-997-263-5
16	22	45.8	8	4	US-08-444-818-282
17	21	43.8	4	4	US-08-435-568A-19
18	21	43.8	5	1	US-08-170-360-10
19	21	43.8	6	2	US-09-127-574-9
20	21	43.8	6	2	US-09-127-574-17
21	21	43.8	7	2	US-09-131-995-13
22	21	43.8	7	2	US-09-131-995-14
23	21	43.8	7	2	US-08-832-087B-13
24	21	43.8	7	2	US-08-832-087B-14
25	21	43.8	7	3	US-08-851-350-6
26	21	43.8	7	3	US-08-851-350-18
27	21	43.8	7	4	US-09-132-154-13

28	21	43.8	7	4	US-09-132-154-14	Sequence 14, Appl
29	21	43.8	8	3	US-08-828-712-19	Sequence 19, Appl
30	21	43.8	8	4	US-09-063-276-19	Sequence 8, Appl
31	20	41.7	6	3	US-08-907-403A-8	Sequence 36, Appl
32	20	41.7	6	3	US-09-222-373-36	Sequence 45, Appl
33	20	41.7	6	3	US-09-222-373-45	Sequence 36, Appl
34	20	41.7	6	4	US-08-893-654B-16	Sequence 45, Appl
35	20	41.7	6	4	US-09-001-511-36	Sequence 36, Appl
36	20	41.7	6	4	US-09-001-511-45	Sequence 45, Appl
37	20	41.7	7	1	US-08-253-854-75	Sequence 75, Appl
38	20	41.7	7	2	US-08-637-759B-146	Sequence 146, App
39	20	41.7	7	3	US-08-871-355A-146	Sequence 146, App
40	20	41.7	7	4	US-09-461-697-254	Sequence 254, App
41	20	41.7	7	4	US-09-326-718-6	Sequence 6, Appl
42	20	41.7	8	3	US-08-836-325-4	Sequence 4, Appl
43	20	41.7	8	4	US-08-444-818-326	Sequence 326, App
44	20	41.7	8	4	US-08-444-818-327	Sequence 327, App
45	20	41.7	8	4	US-09-171-878-15	Sequence 15, Appl
46	20	41.7	8	4	US-09-082-379B-146B	Sequence 146B, Ap
47	19	39.6	4	2	US-08-671-487A-8	Sequence 8, Appl
48	19	39.6	4	2	US-08-651-179B-2	Sequence 2, Appl
49	19	39.6	5	1	US-08-332-071B-1	Sequence 1, Appl
50	19	39.6	5	5	PCT-US94-01321-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-031-538-32
; Sequence 32, Application US/08031538
; Patent No. 5968817
; GENERAL INFORMATION:
; APPLICANT: Sutcliffe, J Gregor
; APPLICANT: Erlanger, Mark G
; APPLICANT: Lowenberg, Timothy W
; TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,538
; FILING DATE: 19930315
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-031-538-32

Query Match 56.2%; Score 27; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIX 4
1111
Db 4 WKIX 7

RESULT 2

US-08-350-260A-464
; Sequence 464, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Missim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 464:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-350-260A-464

Query Match 54.2%; Score 26; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIXY 6
1111
Db 3 WKIFDY 8

RESULT 3

US-08-338-890B-2
; Sequence 2, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spaneavello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2-3, Xaa at line 72
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /notes="an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
US-08-338-890B-2

Query Match 50.0%; Score 24; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WKIXY 6
1111
Db 1 WKXPPY 6

RESULT 4
US-08-338-890B-3
; Sequence 3, Application US/08338890B

```
Patent No. 5700905
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6, Xaa at line 100
OTHER INFORMATION: /label=protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-338-890B-3

Query Match      50.0%; Score 24; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIYSY 6
      11 : 1
DB      1 WKXFPY 6

RESULT      5
US-08-340-208B-2
Sequence 2, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-340-208B-2
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STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-340-208B-2

Query Match      50.0%; Score 24; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIYSY 6
      11 : 1
DB      1 WKXFPY 6

RESULT      6
US-08-340-208B-3
Sequence 3, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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```
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3, Xaa at line 100
OTHER INFORMATION: /label=protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
present or absent on the hydroxyl group", Xaa=Orn
US-08-340-208B-3
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Query Match 50.0%; Score 24; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 WKIY 6
11:1
DB 1 WKXPY 6
```

```
RESULT 7
US-08-997-263-2
Sequence 2, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanewello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
```

```
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /notes="an amine protecting group or a solid
support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-997-263-2
```

```
Query Match 50.0%; Score 24; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 WKIY 6
11:1
DB 1 WKXPY 6
```

```
RESULT 8
US-08-997-263-3
Sequence 3, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanewello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
support can be present or absent on the primary
OTHER INFORMATION: support can be present or absent on the primary
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```

: OTHER INFORMATION: amino group", Xaa: -Orn
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6, Xaa at Line 100
: OTHER INFORMATION: /label="protecting2
: OTHER INFORMATION: /note="a carboxyl protecting group can be
: OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-997-263-3

Query Match      50.0%; Score 24; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIYSY 6
      1 1 1
      1 WKXEPY 6

Db

RESULT 9
US-09-222-373-49
: Sequence 49, Application US/09222373
: Patent No. 6110747
: GENERAL INFORMATION:
: APPLICANT: Blaschuk, Orest W.
: APPLICANT: Gour, Barbara J.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING TISSUE
: FILE REFERENCE: 100086.405C1
: CURRENT APPLICATION NUMBER: US/09/222,373
: CURRENT FILING DATE: 1998-12-29
: EARLIER APPLICATION NUMBER: US 09/001,511
: EARLIER FILING DATE: 1997-12-31
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 49
: LENGTH: 4
: TYPE: PR1
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:
: OTHER INFORMATION: Representative claudin cell adhesion recognition
US-09-222-373-49

Query Match      45.8%; Score 22; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 IYSY 6
      1 1 1
      1 IYSY 4

Db

RESULT 10
US-08-338-890B-4
: Sequence 4, Application US/08338890B
: Patent No. 5700905
: GENERAL INFORMATION:
: APPLICANT: Hirschmann, Ralph
: APPLICANT: Spangello, Rolando
: APPLICANT: Nutt, Ruth
: TITLE OF INVENTION: Synthetic Somatostatin Mimics
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
: STREET: One Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/WINDOWS
: SOFTWARE: WORDPERECT SAVED AS ASCII (DOS) TEXT(*.*)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/338,890B
: FILING DATE: NOV. 14, 1994
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Malinoski, Lynn
: REGISTRATION NUMBER: 38,788
: REFERENCE/DOCKET NUMBER: UPN-2040
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215)568-3100
: TELEFAX: (215)568-3439
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1,2,4
: OTHER INFORMATION: /label="protecting1
: OTHER INFORMATION: /note="an amine protecting group or a solid
: OTHER INFORMATION: support can be present or absent on the primary
: OTHER INFORMATION: amino group"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /label="methyl
: OTHER INFORMATION: /note="a methyl group is present on the amino
: OTHER INFORMATION: group"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: /label="protecting3
: OTHER INFORMATION: /notes="a hydroxyl protecting group can be
: OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-338-890B-4

Query Match      45.8%; Score 22; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIYSY 6
      1 1 1
      1 WKXKEY 6

Db

RESULT 11
US-08-338-890B-5
: Sequence 5, Application US/08338890B
: Patent No. 5700905
: GENERAL INFORMATION:
: APPLICANT: Hirschmann, Ralph
: APPLICANT: Spangello, Rolando
: APPLICANT: Nutt, Ruth
: TITLE OF INVENTION: Synthetic Somatostatin Mimics
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
: STREET: One Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/WINDOWS

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SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2,4
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=methyl
OTHER INFORMATION: /note="a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label=protecting3
OTHER INFORMATION: /note="a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-338-890B-5

Query Match      45.8%; Score 22; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIVSY 6
      11: |
Db      1 WKVKFY 6

RESULT 12
US-08-340-208B-4
Sequence 4, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
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FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1,2,4
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=methyl
OTHER INFORMATION: /note="a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label=protecting3
OTHER INFORMATION: /note="a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-340-208B-4

Query Match      45.8%; Score 22; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WKIVSY 6
      11: |
Db      1 WKVKFY 6

RESULT 13
US-08-340-208B-5
Sequence 5, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
```

NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2, 4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-340-208B-5

Query Match 45.8%; Score 22; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WKVSY 6
1 1 1
DB 1 WKVSY 6

RESULT 14
US-08-997-263-4
Sequence 4, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nult, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960rls
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1,2,4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-263-4

Query Match 45.8%; Score 22; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WKVSY 6
1 1 1
DB 1 WKVSY 6

RESULT 15
US-08-997-263-5
Sequence 5, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nult, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960rls
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Malnoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2, 4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-263-5

Query Match 45.8%; Score 22; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WKIVSY 6
||:|
Db 1 WKVKFY 6

RESULT 16
US-08-444-818-282
Sequence 282, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Ruteer, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hardin, Alisha A.

REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-282

Query Match 45.8%; Score 22; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WKIVSYAG 8
|:|:|
Db 1 WPLYGNMG 8

RESULT 17
US-08-435-568A-19
Sequence 19, Application US/08435568A
Patent No. 6143298
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
APPLICANT: Davis, Gary
TITLE OF INVENTION: Soluble Truncated Forms of ICAM-1
FILE REFERENCE: MCI 208.4C2D2
CURRENT APPLICATION NUMBER: US/08/435,568A
CURRENT FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-08-435-568A-19

Query Match 43.8%; Score 21; DB 4; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIV 4
||:|
Db 1 WKIVF 4

RESULT 18
US-08-170-360-10
Sequence 10, Application US/08170360
Patent No. 5656602
GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Ingilis, Adam
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-MAR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-104A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-170-360-10

Query Match 43.8%; Score 21; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIY 4
1 11
DB 1 WDIY 4

RESULT 19
US-09-127-574-9
Sequence 9, Application US/09127574
Patent No. 5985836
GENERAL INFORMATION:
APPLICANT: Bastek, Patrick
APPLICANT: Lang, John M.
APPLICANT: Baumbach, George A.
APPLICANT: Cardonelli, Ruben G.
TITLE OF INVENTION: Alpha-1 Protecnase Inhibitor Binding Peptides
FILE REFERENCE: MSB-7248
CURRENT APPLICATION NUMBER: US/09/127,574
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-127-574-9

Query Match 43.8%; Score 21; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYSY 6
1 11::
DB 1 WKLMRW 6

RESULT 20
US-09-127-574-17
Sequence 17, Application US/09127574
Patent No. 5985836
GENERAL INFORMATION:
APPLICANT: Bastek, Patrick
APPLICANT: Lang, John M.
APPLICANT: Baumbach, George A.
APPLICANT: Cardonelli, Ruben G.
TITLE OF INVENTION: Alpha-1 Protecnase Inhibitor Binding Peptides
FILE REFERENCE: MSB-7248
CURRENT APPLICATION NUMBER: US/09/127,574
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-127-574-17

Query Match 43.8%; Score 21; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WKIYS 5
1 11
DB 2 WKIYS 6

RESULT 21
US-09-131-995-13
Sequence 13, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
OTHER INFORMATION: Tyr number 7 is 3-I-Tyr.
US-09-131-995-13

Query Match 43.8%; Score 21; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KIYSY 6
1:11
DB 3 KLYDY 7

RESULT 22
US-09-131-995-14
Sequence 14, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
OTHER INFORMATION: Tyr number 5 is 3-I-Tyr.
US-09-131-995-14

Query Match 43.8%; Score 21; DB 2; Length 7;

Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KIYSY 6
1:11
DB 3 KLYDY 7

RESULT 23
US-08-832-087B-13
Sequence 13, Application US/08832087B
Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
OTHER INFORMATION: Tyr number 7 is 3-I-Tyr.
US-08-832-087B-13

Query Match 43.8%; Score 21; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KIYSY 6
1:11
DB 3 KLYDY 7

RESULT 24
US-08-832-087B-14
Sequence 14, Application US/08832087B
Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES

TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: Internal fragment
FEATURE:
OTHER INFORMATION: Tyr number 5 is 3-I-Tyr.
US-08-832-087B-14

Query Match 43.8%; Score 21; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KIYSY 6
|:| |
DB 3 KLYDY 7

RESULT 25
US-08-851-350-6
Sequence 6, Application US/08851350
Patent No. 6057122
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
NUMBER OF INVENTION: FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-851-350-6

Query Match 43.8%; Score 21; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 KIYSY 6
|:| |
DB 3 KLYDY 7

Search completed: January 14, 2002, 06:42:43
Job time: 701 sec



GenCore version 4.5
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Om protein - protein search, using sw model

Run on: January 14, 2002, 07:37:34 ; Search time 43.28 seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1A
Perfect score: 36
Sequence: 1 wkxsyxsy 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq Length: 0
Maximum DB seq Length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	50.0	7	2 S33244	neuromodulatory pe
2	18	50.0	7	2 S33246	neuromodulatory pe
3	15	41.7	7	2 S33245	neuromodulatory pe
4	13	36.1	8	2 S63493	dissimulatory sulf
5	13	36.1	8	2 A38887	T-cell receptor ga
6	12	33.3	5	2 B61445	Leu-enkephalin - b
7	12	33.3	5	2 A61445	Met-enkephalin - b
8	12	33.3	5	2 PT0278	Ig heavy chain CRD
9	12	33.3	5	2 PT0308	Ig heavy chain CRD
10	12	33.3	6	2 S66195	alcohol dehydrogen
11	12	33.3	6	2 A31263	dihydrofolate redu
12	12	33.3	6	2 B31263	dihydrofolate redu
13	12	33.3	6	2 B35640	cerebellar degener
14	12	33.3	6	2 A41946	T-cell receptor ga
15	12	33.3	7	2 A60224	Met-enkephalin-Arg
16	12	33.3	8	2 P00012	cholecystokinin -
17	12	33.3	8	2 A43001	cholecystokinin -
18	12	33.3	8	2 C61512	variant surface gl
19	12	33.3	8	2 D61512	variant surface gl
20	12	33.3	8	2 A42057	fibroblast growth
21	11	30.6	3	2 F37196	bradykinin-potenti
22	11	30.6	4	2 A37832	phenol 2-monooxyge
23	11	30.6	4	2 A34626	KPCH-related neuro
24	11	30.6	4	2 PT0240	Ig heavy chain CRD
25	11	30.6	4	2 B53284	T-cell receptor be
26	11	30.6	4	2 PT0661	T-cell receptor be
27	11	30.6	5	2 A32516	cholecystokinin-5
28	11	30.6	5	2 A40469	dnaaz-like protein
29	11	30.6	5	2 A60803	neuropeptide - sea

30	11	30.6	5	2 JH0253	gut pentapeptide -
31	11	30.6	5	2 G37196	bradykinin-potenti
32	11	30.6	5	2 PT0281	Ig heavy chain CRD
33	11	30.6	5	2 PT0729	T-cell receptor be
34	11	30.6	5	2 PT0580	T-cell receptor be
35	11	30.6	6	2 B34835	dnaa protein - pse
36	11	30.6	6	2 A61068	locustakinin - mig
37	11	30.6	6	2 PT0629	T-cell receptor be
38	11	30.6	6	2 PT0532	T-cell receptor be
39	11	30.6	6	2 PT0519	T-cell receptor be
40	11	30.6	6	2 PT0637	T-cell receptor be
41	11	30.6	6	2 PT0641	T-cell receptor be
42	11	30.6	6	2 PT0726	T-cell receptor be
43	11	30.6	6	2 F41946	T-cell receptor ga
44	11	30.6	6	2 PD0028	rev-kinin 2 - pena
45	11	30.6	6	2 I79564	hypothalamic hepta
46	11	30.6	7	1 NYPG7	hypothalamic hepta
47	11	30.6	7	2 A60139	fatty-acid synthas
48	11	30.6	7	2 S21230	dermorphin (Trp-4,
49	11	30.6	7	2 A58512	venom heptapeptide
50	11	30.6	7	2 A61081	tryptophyllin, bas

ALIGNMENTS

RESULT 1
S33244
neuromodulatory peptide Wamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 50.0%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxs 5
DB 1 WKEMS 5

RESULT 2
S33246
neuromodulatory peptide Wamide-3 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33246
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33246
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 50.0%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxs 5
DB 1 WKEMS 5

Db 1 WKOMS 5

RESULT 3
S33245
neuromodulatory peptide Wwamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A:Reference number: S33244; MUID:93265912
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 41.7%; Score 15; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxx 5
1: 1
Db 1 WREMS 5

RESULT 4
S63493
disulfidyl sulfito reductase gamma chain, membrane-bound and soluble - Desulfovibrio
C:Species: Desulfovibrio desulfuricans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63493; S63494
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the disulfidyl sulfito reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152
A:Accession: S63493
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STE>
A:Accession: S63494
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STR>

Query Match 36.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 syxx 8
1: 1
Db 4 TYKG 7

RESULT 5
A38887
T-cell receptor gamma chain (5L.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHE>
C:Keywords: T-cell receptor

Query Match 36.1%; Score 13; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 wkxxx 6
1: 1
Db 3 WDSGF 8

RESULT 6
B61445
Leu-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: B61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A:Reference number: A61445; MUID:84144823
A:Accession: B61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxx 8
1: 1
Db 1 YGG 3

RESULT 7
A61445
Met-enkephalin - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A61445
R:Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A:Reference number: A61445; MUID:84144823
A:Accession: A61445
A:Molecule type: protein
A:Residues: 1-5 <LEU>
A:Experimental source: pedal ganglia
C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxx 8
1: 1
Db 1 YGG 3

RESULT 8
PT0278
Ig heavy chain CND3 region (clone 4-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0278
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0278

A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 YXG 8
| |
DB 1 YFG 3

RESULT 9
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
DB 2 WE 3

RESULT 10
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragme
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltnes, L.; Hackett, M.; Shafgat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FRBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
nzyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HUE>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
DB 5 WE 6

RESULT 11
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996

C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
DB 3 WE 4

RESULT 12
B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886
A:Accession: B31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
DB 3 WE 4

RESULT 13
B35640
cerebellar degeneration-related protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C:Accession: B35640
R:Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner,
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal
A:Reference number: A35640; MUID:90222173
A:Accession: B35640
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6 <CHE>

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
| |
DB 2 WE 3

RESULT 14

A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316
A:Accession: A41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WH>
C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
Db 1 yrg 3

RESULT 15
A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680
A:Accession: A60224
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAD>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
Db 1 yrg 3

RESULT 16
PQ0012
cholecystokinin - southeastern quoll
N:Alternate names: CCK
C:Species: Dasyurus viverrinus (southeastern quoll)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C:Accession: PQ0012
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: PQ0012
A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
Db 2 ymg 4

RESULT 17
A43001
cholecystokinin - tammar wallaby
N:Alternate names: CCK
C:Species: Macropus eugenii (tammar wallaby)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C:Accession: A43001; PQ0012
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: A43001
A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
Db 2 ymg 4

RESULT 18
C61512
variant surface glycoprotein M1rat 1.4 - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C:Accession: C61512
R:Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te
A:Reference number: A61512; MUID:81172836
A:Accession: C61512
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Keywords: glycoprotein

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
| |
Db 1 WE 2

RESULT 19
D61512
variant surface glycoprotein M1rat 1.6 - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C:Accession: D61512
R:Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te
A:Reference number: A61512; MUID:81172836

A:Accession: D61512
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Keywords: glycoprotein

Query Match
Best Local Similarity 33.3%; Score 12; DB 2; Length 8;
50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 1 WE 2

RESULT 20
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor
A:Reference number: A42057; MUID:92107200
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-References: GB:M80363
C:Keywords: growth factor receptor

Query Match
Best Local Similarity 33.3%; Score 12; DB 2; Length 8;
50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 syxg 8
1:
DB 5 SFG 8

RESULT 21
F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196
R:Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557
A:Accession: F37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity 30.6%; Score 11; DB 2; Length 3;
100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1:
DB 3 W 3

RESULT 22
A37832
phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment

C:Species: Pseudomonas sp.
C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
C:Accession: A37832
R:Powlowski, J.; Shindler, V.
J. Bacteriol. 172, 6834-6840, 1990
A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydro
A:Reference number: A37832; MUID:91072231
A:Accession: A37832
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <POW>
C:Keywords: oxidoreductase

Query Match
Best Local Similarity 30.6%; Score 11; DB 2; Length 4;
100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sy 6
1:
DB 1 SY 2

RESULT 23
A34626
RPCH-related neuropeptide - ferruginous spindle
C:Species: Fusinus ferrugineus (ferruginous spindle)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake,
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:90179762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match
Best Local Similarity 30.6%; Score 11; DB 2; Length 4;
100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1:
DB 4 W 4

RESULT 24
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 30.6%; Score 11; DB 2; Length 4;
66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1:
DB 1 YPG 3

RESULT 25

B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and
A:Reference number: A53284; MUID:91342695
A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:q233916; PID:AB19518.1; PID:q233918
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60738)
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. NO. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
1
DB 2 W 2

Search completed: January 14, 2002, 07:44:21
Job time: 407 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:40:45 ; Search time 29.66 seconds
(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1A
Perfect score: 36
Sequence: 1 wkxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	50.0	7	1	WMA2_ACHFU
2	18	50.0	7	1	WMA3_ACHFU
3	15	41.7	7	1	WMA1_ACHFU
4	13	36.1	7	1	WNP1_LEPDE
5	12	33.3	8	1	CCKN_MACEU
6	11	30.6	5	1	BPP7_BORTN
7	11	30.6	5	1	UF01_MOUSE
8	11	30.6	6	1	LOK1_LOCOMI
9	11	30.6	7	1	HY7_PIG
10	11	30.6	8	1	ACI_THUAI
11	11	30.6	8	1	AKHG_GRYBI
12	11	30.6	8	1	AKH_LIBAU
13	11	30.6	8	1	AKH_MELML
14	11	30.6	8	1	AKH_TYBAT
15	11	30.6	8	1	AL16_CARMA
16	11	30.6	8	1	GLUR_HUMAN
17	11	30.6	8	1	HTF1_PERAM
18	11	30.6	8	1	HTF2_PERAM
19	11	30.6	8	1	HTF_TENMO
20	11	30.6	8	1	LCK1_LEUMA
21	11	30.6	8	1	LCK2_LEUMA
22	11	30.6	8	1	LCK3_LEUMA
23	11	30.6	8	1	LCK4_LEUMA
24	11	30.6	8	1	LCK5_LEUMA
25	11	30.6	8	1	LCK6_LEUMA
26	11	30.6	8	1	LCK7_LEUMA
27	11	30.6	8	1	LCK8_LEUMA
28	11	30.6	8	1	PLP_BRANA
29	11	30.6	8	1	RPH_PANBO
30	11	30.6	8	1	UPAA_HUMAN
31	8	22.2	5	1	TPIS_CANPA
32	8	22.2	6	1	OMI_LEPDE
33	8	22.2	7	1	ALL2_CARMA

ALIGNMENTS

RESULT	ID	WMA2_ACHFU	STANDARD:	PRT:	7 AA.
AC	P35920:				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-OCT-1994 (Rel. 30, Last annotation update)				
DE	WMA2IDE-2.				
OS	Achatina fulica (Giant African snail).				
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;				
OC	Achatinacea; Achatinidae; Achatina.				
OX	NCBI_Taxid=6530;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-Ganglion;				
RX	MEDLINE-93265912; Pubmed-8495720;				
RA	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;				
RT	"Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from				
RT	ganglia of the African giant snail, Achatina fulica.";				
RU	FEBS Lett. 323:104-108(1993).				
KW	Neuropeptide; Amidation.				
FT	MOD_RSS				
SQ	SEQUENCE 7 AA; 964 MW; 7362D5B68D32310 CRC64;				
Query Match	50.0%;	Score 18;	DB 1;	Length 7;	
Best Local Similarity	60.0%;	Pred. No. 1e+05;			
Matches	3;	Conservative	0;	Mismatches	2;
				Indels	0;
				Gaps	0;
OY	1 wkxxs 5				
DB	1 WKOMS 5				
RESULT	2				
WMA3_ACHFU					
ID	WMA3_ACHFU	STANDARD:	PRT:	7 AA.	
AC	P35921:				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-OCT-1994 (Rel. 30, Last annotation update)				
DE	WMA3IDE-3.				
OS	Achatina fulica (Giant African snail).				
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;				
OC	Achatinacea; Achatinidae; Achatina.				
OX	NCBI_Taxid=6530;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-Ganglion;				
RX	MEDLINE-93265912; Pubmed-8495720;				
RA	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;				

RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 DR PIR: S33244; S33244.
 KW Neuropptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 50.0%; Score 18; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1e+05; Mismatches 2; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
 I I
 DB 1 WKEMS 5

RESULT 3

WMAL_ACHFV STANDARD; PRT; 7 AA.
 ID WMAL_ACHFV
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WMAMIDE-1.
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxId=6530;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720;
 RA Minakata H., Ikeda T., Munekata Y., Kobayashi M., Nomoto K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
 CC PIR: S33245; S33245.
 KW Neuropptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 41.7%; Score 15; DB 1; Length 7;
 Best Local Similarity 40.0%; Pred. No. 1e+05; Mismatches 2; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
 I I
 DB 1 WKEMS 5

RESULT 4

MNPL_LEPDE STANDARD; PRT; 7 AA.
 ID MNPL_LEPDE
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phycophaga; Chrysomeloidae; Chrysomelidae;
 CC Chrysomelinae; Leptinotarsa.
 OX NCBI_TaxId=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;

RA Splitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Leptinotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KW Neuropptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 36.1%; Score 13; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05; Mismatches 1; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 syxx 8
 I I
 DB 1 AYNG 4

RESULT 5

CCKN_MACEU STANDARD; PRT; 8 AA.
 ID CCKN_MACEU
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CHOLECYSTOKININ (CCK).
 CC CCK.
 OS Macropus eugenii (Tamar wallaby), and
 OS Dasyurus viverrinus (Southeastern quoll).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxId=9315, 9279;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=88234141; PubMed=3375140;
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
 RT "Cholecystokinin octapeptide purified from brains of Australian
 RT marsupials.";
 RL Peptides 9:429-431(1988).
 CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
 CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GIT. ITS FUNCTION
 CC IN THE BRAIN IS NOT CLEAR.

CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 CC PIR: A43001; A43001.
 DR PIR: PQ0012; PQ0012.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Amidation; Sulfation; Hormone.
 FT MOD_RES 2
 FT MOD_RES 2
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 1064 MW; DDCAAA68378768B5A CRC64;

Query Match 33.3%; Score 12; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1e+05; Mismatches 1; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxxg 8
 I I
 DB 2 YMG 4

RESULT 6

BPP7_BOTIN STANDARD; PRT; 5 AA.
 ID BPP7_BOTIN
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
 ENZYME INHIBITOR).
 OS Bothrops insularis (Island jararaca) (Quelamda jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Chordata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE:Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintrá A.C.O., Vieira C.A., Gliglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IF ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 CC PIR: G37196; G37196.
 DR Hypotensive agent; Venom.
 KW Hypotensive agent; Venom.
 FT MOD.RES 1
 SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 DB 3 W 3

RESULT 7
 ID UF01_MOUSE STANDARD; PRT; 5 AA.
 AC P38639;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE:Fibroblast;
 RX MEDLINE=9500907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:735-745(1994).
 -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
 CC NON TER 5
 SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 DB 1 W 1

RESULT 8
 ID LOK1_LOCM1 STANDARD; PRT; 6 AA.
 ID LOK1_LOCM1

AC P41491;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE LOCUSTAKININ I.
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE:Corpora cardiaca;
 RX MEDLINE=92262851; PubMed=1585017;
 RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
 RA de Loof A.;
 RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
 isolation, primary structure and synthesis.";
 RL Regul. Pept. 37:49-57(1992).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
 OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
 TUBULES.
 CC PIR: A61068; A61068.
 DR Neuropeptide; Amidation.
 FT MOD.RES 6
 SQ SEQUENCE 6 AA: 654 MW: 686365A5B9CDB000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 DB 5 W 5

RESULT 9
 ID HY7_PIG STANDARD; PRT; 7 AA.
 AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE HYPOTHALAMIC HEPTAPEPTIDE.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=81213980; PubMed=6263778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 RA Safitan M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro
 ACTH-releasing activity from porcine hypothalamus";
 RL Horm. Metab. Res. 13:228-232(1981).
 DR PIR: A01417; NYPG7.
 SQ SEQUENCE 7 AA: 957 MW: 632B45B1FB5059A0 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SY 6
 DB 5 SY 6

RESULT 10
 ID ACL_THUAL STANDARD; PRT; 8 AA.
 ID ACL_THUAL

AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE ANGIOGENESIS-CONVERTING ENZYME INHIBITOR.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OC NCBI_TaxID=8236;
 RX MEDLINE=88326322; PubMed=3415688;
 RP SEQUENCE.
 RA TISSUE=Muscle;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
 muscle.";
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR: A31570; A31570.
 SO SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 Db 6 w 6

RESULT 11

AKHG_GRYBI STANDARD; PRT; 8 AA.
 ID AKHG_GRYBI
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ADIPOKINETIC HORMONE G (AKH-G) (RO. II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthoptera; Orthopteroidea; Ensifera; Gryllidae;
 CC Gryllinae; Gryllus.
 OC NCBI_TaxID=6999, 7007;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RA MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 of a peptide with adipekinetic activity from the corpora cardiaca of
 the cricket Gryllus bimaculatus.";
 RT Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hildlich C., Beyreuther K., Rinehart K.L. Jr.;
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: A28004; A28004.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH, 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1
 PYROLIDONE CARBOXYLIC ACID.

FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 Db 8 w 8

RESULT 12

AKH_LIBAU STANDARD; PRT; 8 AA.
 ID AKH_LIBAU
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ADIPOKINETIC HORMONE (AKH).
 OS Libellula auripennis (Skimmer dragonfly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
 OC NCBI_TaxID=6966;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90359055; PubMed=2390213;
 RA Gaede G.;
 RT "The putative ancestral peptide of the adipokinetin/red-pigment-
 concentrating hormone family isolated and sequenced from a
 dragonfly.";
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
 -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR PIR: S10596; S10596.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH, 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1
 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 Db 8 w 8

RESULT 13

AKH_MEI ML STANDARD; PRT; 8 AA.
 ID AKH_MEI ML
 AC P25423;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ADIPOKINETIC HORMONE (AKH).
 OS Melolontha melolontha (Cockchafer),
 OS Geotrupes stercorosus (Dor beetle), and
 OS Pachoda marginata (Flower beetle).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
 OC NCBI_TaxID=7061, 7087, 7058;
 RN [1]

RP SEQUENCE.
RC SPECIES=M. melolontha, and G. stercorarius; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."
RL Biochem. J. 275:671-677(1991).
[2]
RP SEQUENCE.
RC SPECIES=P. marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
-I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S15422; S15422.
PIR: S21663; S21663.
DR InterPro; IP002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
|
Db 8 w 8

RESULT 14
AKH_TABAT
ID AKH_TABAT STANDARD: PRT: 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I) (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae; Tabanus.
OX NCBI_TaxID=7207;
[1]
RN SEQUENCE.
RP TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raine A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuroepitide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
-I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro; IP002047; AKH.

DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
|
Db 8 w 8

RESULT 15
ALL6_CARMA
ID ALL6_CARMA STANDARD: PRT: 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTATIN 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
[1]
RN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sy 6
||
||
Db 5 sy 6

RESULT 16
GLUR_HUMAN
ID GLUR_HUMAN STANDARD: PRT: 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE.
RP MEDLINE=72062338; PubMed=5126885;
RX Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).

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CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03188; XGHU0U.
DR GLYCOPROTEIN.
FT CARBOHYD
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1E1B1E CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 syxg 8
   1: 1
   4 SHDG 7

RESULT 17
HTF1_PERAM STANDARD; PRT; 8 AA.
ID HTF1_PERAM
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-1)
DE (PEA-CAH-1) (UED-CC-1) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach),
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadocnina portentosa, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).

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CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HTH / RPCH FAMILY.
DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A4960; A4960.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1: 1
   8 w 8

RESULT 18
HTF2_PERAM STANDARD; PRT; 8 AA.
ID HTF2_PERAM
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
DE (PEA-CAH-II) (UED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
OS Periplaneta americana (American cockroach),
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;

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RT "Primary structures of hypertrichalosemic neuropetides isolated from
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphodromia portentosa*, *Blattella germanica* and *Blattella orientalis*
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERTRICHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05170; A05170.
DR PIR: S08996; S08996.
DR PIR: B44960; B44960.
DR PIR: B49823; B49823.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropetide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1 1
DB 8 W 8

RESULT 19
HTF_TEMNO STANDARD; PRT; 8 AA.
AC P25419;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTRICHALOSEMIC FACTOR (HOTH) (HYPERTRICHALOSEMIC NEUROPEPTIDE).
CC Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067, 7075;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RC MEDLINE=90341081; PubMed=2381871;
RX Gaele G., Rosinski G.;
RA "The primary structure of the hypertrichalosemic neuropetide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:455-459(1990).
CC -1- FUNCTION: HYPERTRICHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A43976; A43976.
DR PIR: B43976; B43976.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropetide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1 1
DB 8 W 8

RESULT 20
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RC Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropetides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotrotopins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropetide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CD76A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1 1
DB 7 W 7

RESULT 21
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RC Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropetides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotrotopins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropetide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 7 w 7

RESULT 22

LCK3_LEUMA STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN (1)
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
from Leucophaea maderae: members of a new family of
Cephalomyotroptins.";
RT Comp. Biochem. Physiol. 84C:271-276(1986).
RL -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

QY 1 w 1
|
Db 7 w 7

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 23

LCK4_LEUMA STANDARD; PRT; 8 AA.
ID LCK4_LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN (1)
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
from Leucophaea maderae: members of a new family of
Cephalomyotroptins.";
RT Comp. Biochem. Physiol. 84C:271-276(1986).
RL -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD8A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 7 w 7

RESULT 24

LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN (1)
RN SEQUENCE.
RC TISSUE=Head;
RA MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
myotropic peptides of Leucophaea maderae.";
RT Comp. Biochem. Physiol. 88C:27-30(1987).
RL -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

QY 1 w 1
|
Db 7 w 7

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25

LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN (1)
RN SEQUENCE.
RC TISSUE=Head;
RA MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
myotropic peptides of Leucophaea maderae.";
RT Comp. Biochem. Physiol. 88C:27-30(1987).
RL -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOWHIS ZEA ADIPOKINETIC HORMONE.
DR PIR: JS0316; JS0316.

KW Neuropeptide; Amidation. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA: 935 MW: 9D6365B1E9D5A5A6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

OY 1 W 1
 DB 7 W 7

Search completed: January 14, 2002, 07:52:04
 Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:40 ; Search time 80.15 Seconds
(without alignments)
14.600 Million cell updates/sec

Title: 09-185908-1A
Perfect score: 36
Sequence: 1 wxxxxxyx 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

- Database :
- 1: SP_ARCHAEA:*
 - 2: SP_BACTERIA:*
 - 3: SP_FUNGI:*
 - 4: SP_HUMAN:*
 - 5: SP_INVERTEBRATE:*
 - 6: SP_MAMMAL:*
 - 7: SP_MHC:*
 - 8: SP_ORGANELLE:*
 - 9: SP_PHAGE:*
 - 10: SP_PLANT:*
 - 11: SP RODENT:*
 - 12: SP_VIRUS:*
 - 13: SP_VERTEBRATE:*
 - 14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	16	44.4	7	8	Q95945
2	16	44.4	8	11	Q62721
3	12	33.3	8	5	Q9TWH6
4	12	33.3	8	11	P70243
5	12	33.3	8	11	O9QVDS
6	11	30.6	6	13	P82096
7	11	30.6	7	10	O49223
8	11	30.6	7	13	P82065
9	11	30.6	8	2	O85406
10	11	30.6	8	4	O15888
11	11	30.6	8	4	O15890
12	11	30.6	8	4	O15898
13	11	30.6	8	5	O9VRD2
14	11	30.6	8	5	P82685
15	11	30.6	8	5	P82686
16	11	30.6	8	5	P82687
17	11	30.6	8	5	P82688
18	11	30.6	8	5	P82689
19	11	30.6	8	6	O02831

20	11	30.6	8	6	O9TRY3	O9TRY3 sus sp. ins
21	11	30.6	8	6	P82929	P82929 bos taurus
22	11	30.6	8	7	O95213	O95213 oryctolagus
23	11	30.6	8	8	O34909	O34909 locusta mig
24	11	30.6	8	8	O9TD02	O9TD02 terranacos
25	11	30.6	8	8	O9TAY2	O9TAY2 asterina pe
26	11	30.6	8	10	O9S874	O9S874 spinacia ol
27	11	30.6	8	11	O35835	O35835 rattus norv
28	11	30.6	8	11	P82598	P82598 rattus norv
29	11	30.6	8	11	O9ETI8	O9ETI8 mus spreus
30	11	30.6	8	11	O9ETI7	O9ETI7 mus caroli
31	11	30.6	8	11	O9ETI6	O9ETI6 mesocricetu
32	11	30.6	8	11	O99MND	O99MND mus musculu
33	11	30.6	8	13	P79940	P79940 xenopus lae
34	11	30.6	8	13	O98T05	O98T05 xenopus lae
35	9	25.0	8	2	O09258	O09258 synechococc
36	8	22.2	8	2	O52062	O52062 bacillus me
37	8	22.2	8	2	O9S443	O9S443 pseudomonas
38	8	22.2	8	2	O9R057	O9R057 bucherna ap
39	8	22.2	8	2	O9R9E0	O9R9E0 bacillus su
40	8	22.2	8	2	O9R9C2	O9R9C2 borrelia bu
41	8	22.2	8	8	O9GD00	O9GD00 mascola mad
42	8	22.2	8	10	P82324	P82324 pisum sativ
43	8	22.2	8	11	O9QVFA	O9QVFA rattus sp.
44	7	19.4	7	2	O07354	O07354 synechococc
45	7	19.4	7	2	O50556	O50556 actinobacil
46	7	19.4	7	8	O99182	O99182 gnatholablia
47	7	19.4	7	12	O9YVE3	O9YVE3 human adeno
48	7	19.4	7	12	O9YQ10	O9YQ10 porcine tra
49	7	19.4	7	12	O9YIR0	O9YIR0 human adeno
50	7	19.4	7	12	O9YIQ9	O9YIQ9 human adeno

ALIGNMENTS

RESULT 1

Q95945 ID AC Q95945 PRELIMINARY: PRT: 7 AA.

DT 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE INSIDE INTRON 5 (FRAGMENT).

OS Saccharomyces cerevisiae (Baker's yeast).

OG Mitochondrion.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81069885; PubMed=6254986;

RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;

RT "Assembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase."

RL J. Biol. Chem. 255:11927-11941(1980).

DR EMBL: V00694; CAA24066.1; -.

KW Mitochondrion.

FT NON_TER

SO SEQUENCE 7 AA; 859 MW; 75B7232362CDCA60 CRC64;

Query Match 44.4%; Score 16; DB 8; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.7e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2

Db 4 wk 5

RESULT 2

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062721
ID 062721 PRELIMINARY; PRT; 8 AA.
AC
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
NCBI_TaxID=10116;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RL Gene 158:291-294(1995).
DR EMBL, U17178; AAA86692.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 44.4%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   11
DB 6 WK 7

RESULT 3
Q9TWH6 PRELIMINARY; PRT; 8 AA.
ID Q9TWH6
AC Q9TWH6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE BIOACTIVE PEPTIDE P4=PUTATIVE ESCOPHAGEAL NEUROREGULATOR.
OS Perinereis vancouverica.
NC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Acoluata;
OC Phyllozoa; Nereididae; Perinereis.
RX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95323338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RL a polychaete annelid, Perinereis vancouverica."
RL Comp. Biochem. Physiol. C,
RL Pharmacol. Toxicol. Endocrinol. 110:297-304(1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 33.3%; Score 12; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
   11
DB 2 YEG 4

RESULT 4
P70243 PRELIMINARY; PRT; 8 AA.
ID P70243
AC P70243;
DT 01-FEB-1997 (TReMBLrel. 02, Created)

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DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Ophoff R.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98325; CAA66969.1; -.
KW Calcium channel.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 865 MW; D9C37DB1861ADDE CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   11
DB 7 WQ 8

RESULT 5
Q9QVD3 PRELIMINARY; PRT; 8 AA.
ID Q9QVD3
AC Q9QVD3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RL cytosol."
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA; 1047 MW; D72415BB06C37041 CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   11
DB 3 WQ 4

RESULT 6
P82096 PRELIMINARY; PRT; 6 AA.
ID P82096
AC P82096;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
NCBI_TaxID=104895;

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RN [1] /
RP SEQUENCE.
RC TISSUE:SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
  Litoria electrica. Comparison with the skin peptides from Litoria
  rubella.";
RL Aust. J. Chem. 52:0-0(1999).
RW Amphibian skin; Amidation.
FT MOD.RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 13; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 7
ID 049223 PRELIMINARY; PRT; 7 AA.
AC 049223:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
  eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
CX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:CV. ESSEX; TISSUE:ROOTS;
RX MEDLINE:91367679; PubMed:1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
  with HMG-box proteins.";
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN:CV. ESSEX; TISSUE:ROOTS;
RA Mahalingam R., Knap H.T.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047050; AAC03556.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 10; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 8
ID P82065 PRELIMINARY; PRT; 7 AA.
AC P82065:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE TRYPTOPHYLLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
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OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE:SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
  Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
  'Litoria rubella'. The skin peptide profile as a probe for the study
  of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD.RES 1
FT MOD.RES 7
FT MOD.RES 1
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 13; Length 7;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 4 W 4

RESULT 9
ID 083406 PRELIMINARY; PRT; 8 AA.
AC 083406:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE HYPOTHEICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
  Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:NINE MILE PHASE I;
RA Williams H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
  Coxiella burnetii.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 4 W 4

RESULT 10
ID 015888 PRELIMINARY; PRT; 8 AA.
AC 015888:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32069; AAA73878.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 11
ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32083; AAA73880.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 1 w 1

RESULT 12
ID Q15898 PRELIMINARY; PRT; 8 AA.
AC Q15898:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP6A11B) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
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RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32078; AAA73888.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 4; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sy 6
DB 2 sy 3

RESULT 13
ID Q9VRD2 PRELIMINARY; PRT; 8 AA.
AC Q9VRD2:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajaeli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson R., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RT "the genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003569; AAF50870.1; -.
DR Flybase: FBgn0040648; CG11666.
SQ SEQUENCE 8 AA: 1062 MW: ED1B5B044004376 CRC64:

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 14
P82685 PRELIMINARY: PRT; 8 AA.

AC P82685:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RM [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 950 MW: 326365B449D5A774 CRC64:

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 15
P82686 PRELIMINARY: PRT; 8 AA.

AC P82686:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RM [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 856 MW: DC6365A5B9D5BDDA CRC64:

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 16
P82687 PRELIMINARY: PRT; 8 AA.

AC P82687:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RM [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 909 MW: DC6365B449D5A76A CRC64:

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 17
P82688 PRELIMINARY: PRT; 8 AA.

AC P82688:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KM Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 18
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KM Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 865 MW; C76365B449C0C775 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 19
002831 PRELIMINARY; PRT; 8 AA.
AC 002831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PRO ALPBA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Mersaranta M., Kujala U.M., Pellinlemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; .
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 2 w 2

RESULT 20
Q9TRY3 PRELIMINARY; PRT; 8 AA.
AC Q9TRY3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RX Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 5 w 5

RESULT 21
P82929 PRELIMINARY; PRT; 8 AA.
AC P82929;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;

RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremull L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
of the full complement ribosomal proteins present."
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 935 MW: 9639D1A72058637D CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 2 w 2

RESULT 22

ID 095213 PRELIMINARY; PRT; 8 AA.
AC 095213;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE GERMLINE DH (DF) GENE (FRAGMENT).
CN DF.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P-1/RGM;
RA Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
RL Mol. Immunol. 0:0-0(0).
DR EMBL: U62585; AAB18735.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 845 MW: 5CA861B5A58677B CRC64;

Query Match 30.6%; Score 11; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
DB 1 ypg 3

RESULT 23

ID 034909 PRELIMINARY; PRT; 8 AA.
AC 034909;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
OS Locusta migratoria (Migratory locust).
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:88223478; PubMed-2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:

RT restriction mapping and sequence of its ND-1 (UNF-1) gene."
RL Curr. Genet. 11:623-630(1987).
DR EMBL: X05286; CAA28905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 1019 MW: F8E33723304BA5B6 CRC64;

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sy 6
DB 2 sy 3

RESULT 24

ID 09TD02 PRELIMINARY; PRT; 8 AA.
AC 09TD02;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Terranotus dolichopterus.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranotos.
OX NCBI_TaxID=61836;
RN [1]
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
(Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective."
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AAF03041.1; -.
KW Mitochondrion.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 1084 MW: F0C9D3640DD44056 CRC64;

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 6 w 6

RESULT 25

ID 09T4Y2 PRELIMINARY; PRT; 8 AA.
AC 09T4Y2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Asterina pectinifera (Starfish).
OS Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89354669; PubMed=2766382;
RA Jacobs H.T., Asakawa S., Arai T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA."
RL Curr. Genet. 15:193-206(1989).

DR EMBL: X16886: CAA34767.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA: 1114 MW; F0C9D36415B736D6 CRC64;

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
1
Db 6 W 6

Search completed: January 14, 2002, 07:53:45
Job time: 725 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:36:09 ; Search time 80.55 seconds
(Without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1A
Perfect score: 36
Sequence: 1 wksxyxg 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: A.Gencseq_1101:*
2: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp/AA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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18: /SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	86.1	8	21	AAB06419	Claudin-1 cell adh
2	31	86.1	8	21	AAB06479	Claudin-1 cyclic c
3	29	80.6	8	21	AAB06521	Claudin-2 cell adh
4	29	80.6	8	21	AAB06574	Claudin-2 cyclic c
5	28	77.8	8	21	AAB06426	Claudin-1 cell adh
6	28	77.8	8	21	AAB06512	Claudin-1 cyclic c
7	28	77.8	8	21	AAB06823	Claudin-7 cell adh
8	28	77.8	8	21	AAB06876	Claudin-7 cyclic c
9	28	77.8	8	21	AAB06917	Claudin-7 cell adh
10	25	69.4	6	21	AAB06417	Claudin-1 cell adh
11	25	69.4	6	21	AAB06477	Claudin-1 cyclic c

12	25	69.4	7	21	AAB06418	Claudin-1 cell adh
13	25	69.4	7	21	AAB06478	Claudin-1 cyclic c
14	25	69.4	8	21	AAB06434	Claudin-1 cyclic c
15	25	69.4	8	21	AAB06443	Claudin-1 cyclic c
16	25	69.4	8	21	AAB06452	Claudin-1 cyclic c
17	25	69.4	8	21	AAB06461	Claudin-1 cyclic c
18	25	69.4	8	21	AAB06470	Claudin-1 cyclic c
19	24	66.7	6	21	AAB06519	Claudin-2 cell adh
20	24	66.7	7	21	AAB06572	Claudin-2 cyclic c
21	24	66.7	7	21	AAB06520	Claudin-2 cell adh
22	24	66.7	7	21	AAB06573	Claudin-2 cyclic c
23	24	66.7	8	21	AAB06528	Claudin-2 cyclic c
24	24	66.7	8	21	AAB06537	Claudin-2 cyclic c
25	24	66.7	8	21	AAB06546	Claudin-2 cyclic c
26	24	66.7	8	21	AAB06555	Claudin-2 cyclic c
27	24	66.7	8	21	AAB06564	Claudin-2 cyclic c
28	24	66.7	8	21	AAB06764	Claudin-6/9 cell a
29	24	66.7	8	21	AAB06814	Claudin-6/9 cyclic
30	24	66.7	8	21	AAB06916	Claudin cell adhes
31	22	61.1	6	4	AAP30170	Sequence of a cycl
32	22	61.1	6	21	AAB06424	Claudin-1 cell adh
33	22	61.1	6	21	AAB06510	Claudin-1 cyclic c
34	22	61.1	6	21	AAB06821	Claudin-7 cell adh
35	22	61.1	6	21	AAB06874	Claudin-7 cyclic c
36	22	61.1	7	21	AAB06425	Claudin-1 cell adh
37	22	61.1	7	21	AAB06511	Claudin-1 cyclic c
38	22	61.1	7	21	AAB06822	Claudin-7 cell adh
39	22	61.1	7	21	AAB06875	Claudin-7 cyclic c
40	22	61.1	8	21	AAB06483	Claudin-1 cyclic c
41	22	61.1	8	21	AAB06489	Claudin-1 cyclic c
42	22	61.1	8	21	AAB06495	Claudin-1 cyclic c
43	22	61.1	8	21	AAB06501	Claudin-1 cyclic c
44	22	61.1	8	21	AAB06507	Claudin-1 cyclic c
45	22	61.1	8	21	AAB06830	Claudin-7 cyclic c
46	22	61.1	8	21	AAB06839	Claudin-7 cyclic c
47	22	61.1	8	21	AAB06848	Claudin-7 cyclic c
48	22	61.1	8	21	AAB06857	Claudin-7 cyclic c
49	22	61.1	8	21	AAB06866	Claudin-7 cyclic c
50	21	58.3	6	7	AAP61337	Sequence of novel

ALIGNMENTS

RESULT 1
ID AAB06419 standard; peptide: 8 AA.
XX
AC AAB06419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX
OS Mammalia.
PN W0200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PK 03-NOV-1998; 98US-0185908.
XX
PK 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 86.1%; Score 31; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsxyxg 8
| | | | |
Db 1 wklysyag 8

RESULT 2
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
DE
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 86.1%; Score 31; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsxyxg 8
| | | | |
Db 1 wklysyag 8

RESULT 3
AAB06521
ID AAB06521 standard; peptide; 8 AA.
XX
AC AAB06521;
XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
DE
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 46; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 80.6%; Score 29; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsxyxg 8
| | | | |
Db 1 wrtsyvg 8

Query Match	Best Local Similarity	Score 29;	DB 21;	Length 8;
Matches 4;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
oy	1 wxxsyvg 8			
Db	1 wtsysvg 8			
RESULT 5				
AAB06426				
ID AAB06426	standard; peptide; 8 AA.			
XX AAB06426;				
XX 28-SEP-2000	(first entry)			
XX Claudin-2	cyclic cell adhesion recognition sequence SFG ID NO: 163.			
XX Claudin-2	modulating agent; cell adhesion recognition sequence;			
XX CAR sequence;	autoimmune disease; inflammatory disease; cancer;			
XX graft rejection;	cyclic.			
XX Mammalia.				
XX WO200026360-A1.				
XX 11-MAY-2000.				
XX 03-NOV-1999;	99WO-CA01029.			
XX 03-NOV-1998;	98US-0185908.			
XX 30-MAR-1999;	99US-0282029.			
XX (ADHE-) ADHEREX TECHNOLOGIES INC.				
XX Blaschuck OW, Symonds JM, Gour BJ:				
XX WPI: 2000-365610/31.				
XX Antibody modulation of claudin-mediated cell adhesion for increasing				
XX vasopermeability, for delivering drugs to tumors and the nervous system				
XX and across the skin -				
XX Claim 49; Page 98; 121pp; English.				
XX The present invention relates to the use of peptides as claudin-mediated				
XX cell adhesion modulators. The claudin-2 group of proteins are cadherins,				
XX which are membrane glycoproteins involved in cell adhesion. In some				
XX situations, cell adhesion occurs at abnormal levels, and these peptides				
XX can be used to modulate these levels, and thus treat autoimmune diseases,				
XX inflammatory diseases and cancer, and aid wound healing and implant				
XX adhesion. In addition, they can also be used to facilitate drug delivery				
XX to the desired target site. The present sequence has a cyclic				
XX conformation.				
XX Sequence 8 AA:				

OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PE	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI: 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PP	vasopermeability, for delivering drugs to tumors and the nervous system
XX	and across the skin -
PS	Claim 39; Page 96; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	Inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site.
XX	
SQ	Sequence 8 AA:
OY	1 wkxxyxg 8 : Db 1 wriysyag 8
RESULT 6	
AAB06512	
ID AAB06512	standard: peptide; 8 AA.
XX AC AAB06512;	
XX DT 28-SEP-2000	(first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.	
XX CW Claudin-1 modulating agent; cell adhesion recognition sequence; KW CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.	
XX OS Mammalia.	
XX PN WO200026360-A1.	
XX PD 11-MAY-2000.	
XX PE 03-NOV-1999; 99WO-CA01029.	
XX PR 03-NOV-1998; 98US-0185908.	
XX PA 30-MAR-1999; 99US-0282029.	
XX (ADHE-) ADHEREX TECHNOLOGIES INC.	
PI Blaschuck OW, Symonds JM, Gour BJ;	

DR WPI; 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxsyxg 8
I: | | |
Db 1 wriysyag 8

RESULT 7
AAB06823
ID AAB06823 standard; peptide; 8 AA.
XX AAB06823;
XX 28-SEP-2000 (first entry)
DE Claudin-7 cell adhesion recognition sequence SEQ ID NO: 394.
XX Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PE
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 76; Page 104; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxsyxg 8
I: | | |
Db 1 wgmssyag 8

RESULT 8
AAB06876
ID AAB06876 standard; peptide; 8 AA.
XX AAB06876;
XX 28-SEP-2000 (first entry)
DE Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.
XX Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PE
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 79; Page 105; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxsyxg 8
I: | | |
Db 1 wgmssyag 8

RESULT	9	
AAB06917		
ID	AAB06917	standard; Protein; 8 AA.
AC		
AA06917;		
xx		
DT	05-OCT-2000	(first entry)
DE		
CD	Claudin-7	cell adhesion recognition modulating sequence SEQ ID NO: 50.
xx		
DE	Claudin-7	modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW	graft rejection.	
xx		
OS	Synthetic.	
xx		
FI	Key	Location/Qualifiers
FI	Modified-site	1
FI	Modified-site	/note= "N-terminal acetyl"
FI	Modified-site	8
FI	Modified-site	/note= "C-terminal amide"
xx		
PN	WO200026360-A1.	
xx		
PD	11-MAY-2000.	
xx		
PE	03-NOV-1999;	99WO-CA01029.
xx		
PR	03-NOV-1998;	98US-0185908.
PR	30-MAR-1999;	99US-0282029.
xx		
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
xx		
PI	Blaschuck OW, Symonds JM, Gour BJ;	
xx		
DR	WPI: 2000-365610/31.	
xx		
PT	Antibody modulation of claudin-mediated cell adhesion for increasing	
PT	vasopermeability, for delivering drugs to tumors and the nervous system	
PT	and across the skin -	
xx		
PS	Claim 77; Page 104; 121pp; English.	
xx		
CC	The present sequence is a peptide which can be used in a claudin-mediated	
CC	cell adhesion modulator. The claudin group of proteins are cadherins,	
CC	which are membrane glycoproteins involved in cell adhesion. In some	
CC	situations, cell adhesion occurs at abnormal levels, and this peptide	
CC	can be used to modulate these levels, and thus treat autoimmune diseases,	
CC	inflammatory diseases and cancer, and aid wound healing and implant	
CC	adhesion. In addition, it can also be used to facilitate drug delivery	
CC	to the desired target site.	
xx		
SO	Sequence	8 AA:
xx		
Query Match	77.8%;	Score 28; DB 21; Length 8;
Best Local Similarity	50.0%;	Pred. No. 4.3e+05;
Matches	4; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
Oy	1 wkxxyxg 8	
	1: 111	
Db	1 wqmsayag 8	
xx		
RESULT	10	
AAB06417		
ID	AAB06417	standard; peptide; 6 AA.
xx		
AC	AAB06417;	
xx		
DT	28-SEP-2000	(first entry)
xx		

DE	Claudin-1 cell adhesion recognition sequence SEQ ID NO: 32.
XX	
KW	Claudin-1 modulating agent; cell adhesion recognition sequence;
KM	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection.
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PA	30-MAR-1999; 99US-0282029.
XX	
PP	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Biaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI: 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 39; Page 95; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site.
XX	
SQ	Sequence 6 AA;
OY	1 wxksxy 6 69.4%; Score 25; DB 21; Length 6; Best Local Similarity 66.7%; Pred. No. 4.3e+05; Db 1 wkysy 6 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 11	
AAB06477	
ID AAB06477	standard; peptide; 6 AA.
AC AAB06477;	
XX	
DT 28-SEP-2000	(first entry)
XX	
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 108.	
XX	
XX	Claudin-1 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM	graft rejection; cyclic.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 6 AA;

Query Match 69.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxy 6
| | | |
Db 1 wklysy 6

RESULT 12
AAB06418
ID AAB06418 standard; peptide; 7 AA.
XX
AC AAB06418;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 33.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
FN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 7 AA;

Query Match 69.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxy 6
| | | |
Db 1 wklysy 6

RESULT 13
AAB06478
ID AAB06478 standard; peptide; 7 AA.
XX
AC AAB06478;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 109.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
FN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 7 AA;

Query Match 69.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;

Matches	4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
OY	1	wkxxy 6							
		1111							
DB	1	wklysy 6							
RESULT 14									
ID	AAB06434	standard; peptide; 8 AA.							
XX									
AC	AAB06434;								
DT	28-SEP-2000	(first entry)							
XX									
DE	Claudin-1	cyclic cell adhesion recognition sequence SEQ ID NO: 65.							
XX									
KW	Claudin-1	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							
XX									
PR	03-NOV-1998;	98US-0185908.							
PR	30-MAR-1999;	99US-0282029.							
XX									
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.								
XX									
PI	Blaschuck OW, Symonds JM, Gour BJ;								
XX									
DR	WPI: 2000-365610/31.								
XX									
PT	Antibody modulation of claudin-mediated cell adhesion for increasing								
PT	vasopermeability, for delivering drugs to tumors and the nervous system								
PT	and across the skin -								
XX									
PS	Claim 43; Page 96; 121pp; English.								
XX									
CC	The present invention relates to the use of peptides as claudin-mediated								
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,								
CC	which are membrane glycoproteins involved in cell adhesion. In some								
CC	situations, cell adhesion occurs at abnormal levels, and these peptides								
CC	can be used to modulate these levels, and thus treat autoimmune diseases,								
CC	inflammatory diseases and cancer, and aid wound healing and implant								
CC	adhesion. In addition, they can also be used to facilitate drug delivery								
CC	to the desired target site. The present sequence has a cyclic								
CC	conformation.								
XX									
SQ	Sequence 8 AA;								
Query Match		69.4%;	Score 25;	DB 21;	Length 8;				
Best Local Similarity	66.7%;	Pred. No. 4.3e+05;							
Matches	4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
OY	1	wkxxy 6							
		1111							
DB	2	wklysy 7							
RESULT 15									
ID	AAB06443	standard; peptide; 8 AA.							
XX									
AC	AAB06443;								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							

XX									
DE	Claudin-1	cyclic cell adhesion recognition sequence SEQ ID NO: 74.							
XX									
KW	Claudin-1	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							
XX									
PS	Claim 43; Page 96; 121pp; English.								
XX									
CC	The present invention relates to the use of peptides as claudin-mediated								
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,								
CC	which are membrane glycoproteins involved in cell adhesion. In some								
CC	situations, cell adhesion occurs at abnormal levels, and these peptides								
CC	can be used to modulate these levels, and thus treat autoimmune diseases,								
CC	inflammatory diseases and cancer, and aid wound healing and implant								
CC	adhesion. In addition, they can also be used to facilitate drug delivery								
CC	to the desired target site. The present sequence has a cyclic								
CC	conformation.								
XX									
SQ	Sequence 8 AA;								
Query Match		69.4%;	Score 25;	DB 21;	Length 8;				
Best Local Similarity	66.7%;	Pred. No. 4.3e+05;							
Matches	4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
OY	1	wkxxy 6							
		1111							
DB	2	wklysy 7							
RESULT 16									
ID	AAB06452	standard; peptide; 8 AA.							
XX									
AC	AAB06452;								
XX									
DT	28-SEP-2000	(first entry)							
XX									
DE	Claudin-1	cyclic cell adhesion recognition sequence SEQ ID NO: 83.							
XX									
KW	Claudin-1	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxy 6
| | |
Db 2 wklysy 7

RESULT 17
AAB06461
ID AAB06461 standard; peptide: 8 AA.
XX
AC AAB06461;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 92.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PE
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
XX antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 43; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxy 6
| | |
Db 2 wklysy 7

RESULT 18
AAB06470
ID AAB06470 standard; peptide: 8 AA.
XX
AC AAB06470;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 101.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PE
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxxy 6
DB 2 wklysy 7

RESULT 19
AAB06519
ID AAB06519 standard; peptide: 6 AA.
AC AAB06519;
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 40.
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection.
XX
XX Mammalia.
OS
PN WO200026360-A1.
XX
XX 11-MAY-2000.
PD
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI: 2000-365610/31.
XX
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 46; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
SQ Sequence 6 AA;

Query Match 66.7%; Score 24; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxxy 6
DB 1 wrtsy 6

RESULT 20
AAB06572
ID AAB06572 standard; peptide: 6 AA.
XX
AC AAB06572;

XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 161.
DE
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection; cyclic.
XX
XX Mammalia.
OS
PN WO200026360-A1.
XX
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
SQ Sequence 6 AA;

Query Match 66.7%; Score 24; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxxy 6
DB 1 wrtsy 6

RESULT 21
AAB06520
ID AAB06520 standard; peptide: 7 AA.
XX
XX
AC AAB06520;
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 41.
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection.
XX
XX Mammalia.
OS
PN WO200026360-A1.
XX
XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 46; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 7 AA:

Query Match 66.7%; Score 24; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxy 6
I: |
Db 1 wrtsy 6

RESULT 22
AAB06573
ID AAB06573 standard; peptide; 7 AA.
XX
XX AAB06573;
AC
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 162.
DE
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Sequence 7 AA:

XX Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 7 AA:

Query Match 66.7%; Score 24; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxy 6
I: |
Db 1 wrtsy 6

RESULT 23
AAB06528
ID AAB06528 standard; peptide; 8 AA.
XX
XX AAB06528;
AC
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 117.
DE
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 8 AA:

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxy 6
1: 11
Db 2 wrtsyy 7

RESULT 24

ID AAB06537 standard; peptide: 8 AA.

AC AAB06537;

DT 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 126.

KW Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

PS Claim 49; Page 98; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,

CC which are membrane glycoproteins involved in cell adhesion. In some

CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic

CC conformation.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxy 6
1: 11
Db 2 wrtsyy 7

RESULT 25

ID AAB06546 standard; peptide: 8 AA.

XX AAB06546;

AC 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 135.

KW Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

PS Claim 49; Page 98; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,

CC which are membrane glycoproteins involved in cell adhesion. In some

CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic

CC conformation.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxy 6
1: 11
Db 2 wrtsyy 7

Search completed: January 14, 2002, 07:43:16
Job time: 427 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:33:59 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1A
Perfect score: 36
Sequence: 1 wxxxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.3	8	2	US-08-687-219B-36	Sequence 36, Appl
2	55.6	6	1	US-08-338-890B-2	Sequence 3, Appl
3	55.6	6	1	US-08-338-890B-3	Sequence 2, Appl
4	55.6	6	2	US-08-340-208B-2	Sequence 2, Appl
5	55.6	6	2	US-08-340-208B-3	Sequence 3, Appl
6	55.6	6	3	US-08-997-263-2	Sequence 2, Appl
7	55.6	6	3	US-08-997-263-3	Sequence 3, Appl
8	55.6	8	2	US-08-687-219B-34	Sequence 34, Appl
9	55.6	8	2	US-08-687-219B-37	Sequence 37, Appl
10	55.6	6	1	US-08-338-890B-4	Sequence 4, Appl
11	55.6	6	2	US-08-338-890B-5	Sequence 5, Appl
12	55.6	6	2	US-08-340-208B-4	Sequence 4, Appl
13	55.6	6	2	US-08-340-208B-5	Sequence 5, Appl
14	55.6	6	3	US-08-997-263-4	Sequence 4, Appl
15	55.6	6	3	US-08-997-263-5	Sequence 5, Appl
16	55.6	7	4	US-09-326-718-6	Sequence 6, Appl
17	55.6	7	4	US-09-258-754-268	Sequence 268, App
18	55.0	7	4	US-09-042-107-268	Sequence 268, App
19	50.0	8	2	US-08-350-260A-464	Sequence 464, App
20	47.2	6	4	US-09-196-934-16	Sequence 16, Appl
21	47.2	7	1	US-07-980-520-2	Sequence 2, Appl
22	47.2	7	1	US-08-680-634-2	Sequence 2, Appl
23	47.2	7	4	US-08-977-680-2	Sequence 2, Appl
24	47.2	8	3	US-08-467-472C-2	Sequence 2, Appl
25	47.2	8	3	US-08-467-472C-3	Sequence 3, Appl
26	47.2	8	3	US-08-467-472C-4	Sequence 4, Appl
27	47.2	8	3	US-08-335-733D-23	Sequence 23, Appl

28	17	47.2	8	3	US-08-335-733D-24	Sequence 24, Appl
29	17	47.2	8	3	US-08-335-733D-25	Sequence 25, Appl
30	17	47.2	8	4	US-08-444-818-325	Sequence 325, App
31	17	47.2	8	4	US-08-444-818-326	Sequence 326, App
32	17	47.2	8	4	US-08-444-818-327	Sequence 327, App
33	17	47.2	8	4	US-09-384-061-2	Sequence 2, Appl
34	17	47.2	8	4	US-09-384-061-3	Sequence 3, Appl
35	17	47.2	8	4	US-09-384-061-4	Sequence 4, Appl
36	16	44.4	3	1	US-09-461-697-405	Sequence 405, App
37	16	44.4	4	1	US-08-079-445-3	Sequence 3, Appl
38	16	44.4	4	1	US-07-840-077A-7	Sequence 7, Appl
39	16	44.4	4	1	US-08-454-950-7	Sequence 7, Appl
40	16	44.4	4	1	US-08-434-761-3	Sequence 3, Appl
41	16	44.4	4	1	US-08-338-890B-1	Sequence 1, Appl
42	16	44.4	4	1	US-08-454-949-7	Sequence 7, Appl
43	16	44.4	4	2	US-08-671-487A-8	Sequence 8, Appl
44	16	44.4	4	2	US-08-340-208B-1	Sequence 1, Appl
45	16	44.4	4	2	US-08-651-179B-2	Sequence 2, Appl
46	16	44.4	4	2	US-08-651-179B-3	Sequence 3, Appl
47	16	44.4	4	3	US-08-997-263-1	Sequence 1, Appl
48	16	44.4	4	3	US-09-315-861-5	Sequence 5, Appl
49	16	44.4	4	3	US-08-981-122-25	Sequence 25, Appl
50	16	44.4	4	4	US-08-435-568A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-687-219B-36
Sequence 36, Application US/08687219B
Patent No. 5985541
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVIER & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO.: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal or C-terminal or Internal
US-08-687-219B-36

Query Match 58.3% ; Score 21; DB 2; Length 8;

Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 kxxsxyg 8
1 1 1 1
Db 1 KASSYLG 7

RESULT 2

US-08-338-890B-2
; Sequence 2, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2-3, Xaa at Line 72
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /notes="an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
US-08-338-890B-2

Query Match 55.6%; Score 20; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxy 6
1 1 1 1
Db 1 WKXFPY 6

RESULT 3

US-08-338-890B-3
; Sequence 3, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando

; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 1-3
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /note="an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6, Xaa at Line 100
; OTHER INFORMATION: /label=protecting2
; OTHER INFORMATION: /note="a carboxyl protecting group can be
; OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-338-890B-3

Query Match 55.6%; Score 20; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxy 6
1 1 1 1
Db 1 WKXFPY 6

RESULT 4

US-08-340-208B-2
; Sequence 2, Application US/08340208B
; Patent No. 5965694
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA

```

;
; ZIP: 19103
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: MS-DOS/WINDOWS
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; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/340.208B
;
; FILING DATE: NOV. 16, 1994
;
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Malinoski, Lynn
;
; REGISTRATION NUMBER: 38,788
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (215)568-3100
;
; TELEFAX: (215)568-3439
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: circular
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;
; NAME/KEY: Modified-site
;
; LOCATION: 2-3, Xaa at Line 72
;
; OTHER INFORMATION: /label=protecting1
;
; OTHER INFORMATION: /note="an amine protecting group or a solid
;
; OTHER INFORMATION: support can be present or absent on the primary
;
; OTHER INFORMATION: amino group", Xaa=Orn
;
US-08-340-208B-2

Query Match      55.6%; Score 20; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
   |||
   1 WKXFPY 6

RESULT 5
US-08-340-208B-3
; Sequence 3, Application US/08340208B
; Patent No. 5965694
;
; GENERAL INFORMATION:
;
; APPLICANT: Hirschmann, Ralph
;
; APPLICANT: Spanevello, Rolando
;
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
;
; TITLE OF INVENTION: Methods Therefor
;
; NUMBER OF SEQUENCES: 5
;
; CORRESPONDENCE ADDRESSES:
;
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694rls
;
; STREET: One Liberty Place, 46th Floor
;
; CITY: Philadelphia
;
; STATE: PA
;
; COUNTRY: USA
;
; ZIP: 19103
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: MS-DOS/WINDOWS
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; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
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; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/340.208B
;
; FILING DATE: NOV. 16, 1994
;
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Malinoski, Lynn
;
; REGISTRATION NUMBER: 38,788
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (215)568-3100
;
; TELEFAX: (215)568-3439
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: circular
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;
; NAME/KEY: Modified-site
;
; LOCATION: 2-3, Xaa at Line 72
;
; OTHER INFORMATION: /label=protecting1
;
; OTHER INFORMATION: /note="an amine protecting group or a solid
;
; OTHER INFORMATION: support can be present or absent on the primary
;
; OTHER INFORMATION: amino group", Xaa=Orn
;
US-08-340-208B-2
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;
; TELEPHONE: (215)568-3100
;
; TELEFAX: (215)568-3439
;
; INFORMATION FOR SEQ ID NO: 3:
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; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6
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; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;
; NAME/KEY: Modified-site
;
; LOCATION: 1-3
;
; OTHER INFORMATION: /label=protecting1
;
; OTHER INFORMATION: /note="an amine protecting group or a solid
;
; OTHER INFORMATION: support can be present or absent on the primary
;
; OTHER INFORMATION: amino group", Xaa=Orn
;
;
; NAME/KEY: Modified-site
;
; LOCATION: 3, Xaa at Line 100
;
; OTHER INFORMATION: /label=protecting2
;
; OTHER INFORMATION: /note="a carboxyl protecting group can be
;
; OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
;
US-08-340-208B-3

Query Match      55.6%; Score 20; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
   |||
   1 WKXFPY 6

RESULT 6
US-08-997-263-2
; Sequence 2, Application US/08997263
; Patent No. 6001960
;
; GENERAL INFORMATION:
;
; APPLICANT: Hirschmann, Ralph
;
; APPLICANT: Spanevello, Rolando
;
; APPLICANT: Nutt, Ruth
;
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
;
; NUMBER OF SEQUENCES: 5
;
; CORRESPONDENCE ADDRESSES:
;
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960rls
;
; STREET: One Liberty Place, 46th Floor
;
; CITY: Philadelphia
;
; STATE: PA
;
; COUNTRY: USA
;
; ZIP: 19103
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: MS-DOS/WINDOWS
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; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
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; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/997,263
;
; FILING DATE:
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/338,890
;
; FILING DATE: NOV. 14, 1994
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Malinoski, Lynn
;
; REGISTRATION NUMBER: 38,788
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (215)568-3100
;
; TELEFAX: (215)568-3439
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: circular
;
; MOLECULE TYPE: peptide
;
; FEATURE:
;
; NAME/KEY: Modified-site
;
; LOCATION: 3, Xaa at Line 100
;
; OTHER INFORMATION: /label=protecting2
;
; OTHER INFORMATION: /note="a carboxyl protecting group can be
;
; OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
;
US-08-340-208B-3
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TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at Line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-997-263-2

Query Match 55.6%; Score 20; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
1111
Db 1 WKXFPY 6

RESULT 7

US-08-997-263-3
Sequence 3, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6, Xaa at Line 100

OTHER INFORMATION: /label=protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-997-263-3

Query Match 55.6%; Score 20; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
1111
Db 1 WKXFPY 6

RESULT 8

US-08-687-219B-34
Sequence 34, Application US/08687219B
Patent No. 5985541
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIF & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ. ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-34

Query Match 55.6%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 kxxyxg 8
1111
Db 1 KXSXYLG 7

RESULT 9
US-08-687-219B-37
Sequence 37, Application US/08687219B
Patent No. 5985541
GENERAL INFORMATION:


```
APPLICANT: JOLIVET-REYNAD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEF & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
SOFTWARE: Patcutin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
MOLECULE TYPE: unknown
FRAGMENT TYPE: N-terminal or C-terminal or Internal
US-08-687-219B-37

Query Match      55.6%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 kxxsyxg 8
      1 111
      1 KHSSYLG 7

RESULT 10
US-08-338-890B-4
; Sequence 4, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/MS-WINDOWS
; SOFTWARE: WORDPERECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1,2,4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-338-890B-4

Query Match      52.8%; Score 19; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 wkxxy 6
      1 111
      1 WKVKFY 6

RESULT 11
US-08-338-890B-5
; Sequence 5, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/MS-WINDOWS
; SOFTWARE: WORDPERECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
```

REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2, 4
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=methyl
OTHER INFORMATION: /note="a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label=protecting3
OTHER INFORMATION: /note="a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-338-890B-5

Query Match 52.8%; Score 19; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 wxxsy 6
| | |
Db 1 WKVKFY 6

RESULT 12
US-08-340-208B-4
Sequence 4, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340, 208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1,2,4
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=methyl
OTHER INFORMATION: /note="a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label=protecting3
OTHER INFORMATION: /notes="a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-340-208B-4

Query Match 52.8%; Score 19; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 wxxsy 6
| | |
Db 1 WKVKFY 6

RESULT 13
US-08-340-208B-5
Sequence 5, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340, 208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5:

```
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2, 4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-340-208B-5
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Query Match          52.8%: Score 19: DB 2: Length 6:
Best Local Similarity 50.0%: Pred. No. 1.6e+05:
Matches 3: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
Qy 1 wkxxy 6
  1 1 1
Db 1 WKVKFY 6
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1,2,4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-263-4
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Query Match          52.8%: Score 19: DB 3: Length 6:
Best Local Similarity 50.0%: Pred. No. 1.6e+05:
Matches 3: Conservative 0: Mismatches 3: Indels 0: Gaps 0:
Qy 1 wkxxy 6
  1 1 1
Db 1 WKVKFY 6
```

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RESULT 14
US-08-997-263-4
Sequence 4, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spavevillo, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997, 263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338, 890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 4:
```

```
RESULT 15
US-08-997-263-5
Sequence 5, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spavevillo, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997, 263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338, 890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 5:
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SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2, 4
OTHER INFORMATION: /label= protecting1
OTHER INFORMATION: /note= "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label= methyl
OTHER INFORMATION: /note= "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= protecting3
OTHER INFORMATION: /note= "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-263-5
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Query Match          52.8%; Score 19; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY      1 wkxxy 6
      ||  |
Db      1 WKVKFY 6
```

```
RESULT 16
US-09-326-718-6
Sequence 6, Application US/09326718
Patent No. 6303573
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Mackenna, Deidre A.
TITLE OF INVENTION: Heart Homing Peptides and Methods of
FILE REFERENCE: P-LJ 3512
CURRENT APPLICATION NUMBER: US/09/326,718
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-09-326-718-6
```

```
Query Match          52.8%; Score 19; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

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OY      1 wkxxy 6
      ||  |
Db      2 WGLASY 7
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```
RESULT 17
US-09-258-754-268
Sequence 268, Application US/09258754
Patent No. 6174687
GENERAL INFORMATION:
```

```
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
FILE REFERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
NUMBER OF SEQ ID NOS: 452
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 268
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-268
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```
Query Match          50.0%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY      1 wkxxy 5
      ||  |
Db      1 WKPAS 5
```

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RESULT 18
US-09-042-107-268
Sequence 268, Application US/09042107
Patent No. 6232287
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
FILE REFERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 268
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-268
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```
Query Match          50.0%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY      1 wkxxy 5
      ||  |
Db      1 WKPAS 5
```

```
RESULT 19
US-08-350-260A-464
Sequence 464, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
```

```

; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; FILE REFERENCE: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 2811/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 464:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-350-260A-464
;
Query Match          50.0%; Score 18; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 WKKXXY 6
      1:      1
      3 WRVEDY 8

RESULT 20
US-09-196-934-16
; Sequence 16, Application US/09196934
; Patent No. 6191256
; GENERAL INFORMATION:
; APPLICANT: Chon, Li Ang
; APPLICANT: Beutner, Joseph A.
```

```

; APPLICANT: Carbonell, Ruben G.
; TITLE OF INVENTION: Recombinant Factor VII Binding Peptides
; FILE REFERENCE: MSB-7251
; CURRENT APPLICATION NUMBER: US/09/196,934
; CURRENT FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; US-09-196-934-16
;
Query Match          47.2%; Score 17; DB 4; Length 6;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 WKKXXY 6
      1:      1
      1 WRRHRY 6

RESULT 21
US-07-980-520-2
; Sequence 2, Application US/07980520
; Patent No. 5582862
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Haber, Edgar
; APPLICANT: Matsueda, Gary R.
; TITLE OF INVENTION: Antibodies That Bind To '2-Antiplasmin
; TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 5582862 Inhibit Plasma
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/980,520
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,003
; FILING DATE: 27-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/177,222
; FILING DATE: 04-APR-1988
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 833-7533
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-07-980-520-2
;
Query Match          47.2%; Score 17; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 1 wxxxs 5
111
Db 2 WKPGS 6

RESULT 22
US-08-680-634-2
; Sequence 2, Application US/08680634
; Patent No. 5831031
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Haber, Edgar
; APPLICANT: Matsueda, Gary R.
; TITLE OF INVENTION: Antibodies That Bind To '2-Antiplasmin
; TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 5831031 Inhibit Plasma
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,634
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,520
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/943,372
; FILING DATE: 10-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,003
; FILING DATE: 27-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/177,222
; FILING DATE: 04-APR-1988
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-680-634-2

Query Match 47.2%; Score 17; DB 2; Length 7;
Best Local Similarity 60.08; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxs 5
111
Db 2 WKPGS 6

RESULT 23
US-08-977-680-2
; Sequence 2, Application US/08977680
; Patent No. 6280730
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Haber, Edgar

; APPLICANT: Matsueda, Gary R.
; TITLE OF INVENTION: Antibodies That Bind To '2-Antiplasmin
; TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 6280730 Inhibit Plasma
; TITLE OF INVENTION: '2-Antiplasmin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,680
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/680,634
; FILING DATE: 16-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,520
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/943,372
; FILING DATE: 10-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,003
; FILING DATE: 27-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/177,222
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0609.145006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-977-680-2

Query Match 47.2%; Score 17; DB 4; Length 7;
Best Local Similarity 60.08; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxs 5
111
Db 2 WKPGS 6

RESULT 24
US-08-467-472C-2
; Sequence 2, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDI HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY

COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
OTHER INFORMATION: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
US-08-467-472C-2
Query Match 47.2% Score 17; DB 3; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WXXXS 5
DB 4 WKST 8
RESULT 25
US-08-467-472C-3
; Sequence 3, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR

Db 4 WKTST 8

Search completed: January 14, 2002, 07:41:35
Job time: 456 sec

MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-3

Query Match 47.2%; Score 17; DB 3; Length 8;
Best local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxs 5
|||:

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:21 ; Search time 43.28 Seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1B
Perfect score: 36
Sequence: 1 wxxxxxxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	44.4	7	2 S33244	neuromodulatory pe
2	16	44.4	7	2 S33246	neuromodulatory pe
3	14	38.9	8	2 C61512	variant surface gl
4	13	36.1	7	2 S33245	neuromodulatory pe
5	13	36.1	8	2 A36887	T-cell receptor ga
6	12	33.3	5	2 B61445	Leu-enkephalin - b
7	12	33.3	5	2 A61445	Met-enkephalin - b
8	12	33.3	5	2 PT0278	Ig heavy chain CRD
9	12	33.3	5	2 PT0308	Ig heavy chain CRD
10	12	33.3	6	2 S66195	alcohol dehydrogen
11	12	33.3	6	2 A31263	dihydrofolate redu
12	12	33.3	6	2 B31263	dihydrofolate redu
13	12	33.3	6	2 B35640	cerebellar degener
14	12	33.3	6	2 A41946	T-cell receptor ga
15	12	33.3	7	2 A60224	Met-enkephalin-Arg
16	12	33.3	8	2 PQ0012	cholecystokinin -
17	12	33.3	8	2 A43001	cholecystokinin -
18	12	33.3	8	2 S63493	disinflammatory sulf
19	12	33.3	8	2 D61512	variant surface gl
20	11	30.6	3	2 F37196	bradykinin-potentl
21	11	30.6	4	2 A34626	RPCH-related neuro
22	11	30.6	4	2 PT0240	Ig heavy chain CRD
23	11	30.6	4	2 B53284	T-cell receptor be
24	11	30.6	4	2 PT0661	T-cell receptor be
25	11	30.6	5	2 A32516	cholecystokinin-5
26	11	30.6	5	2 E60274	major protein anti
27	11	30.6	5	2 A60803	neuropeptide - sea
28	11	30.6	5	2 JH0253	gut pentapeptide -
29	11	30.6	5	2 G37196	bradykinin-potentl

30	11	30.6	5	2 PT0281	Ig heavy chain CRD
31	11	30.6	5	2 PT0729	T-cell receptor be
32	11	30.6	5	2 PT0580	T-cell receptor be
33	11	30.6	5	2 S68326	blood cell protein
34	11	30.6	6	2 B34835	dna protein - pae
35	11	30.6	6	2 A61068	locustakinin - mig
36	11	30.6	6	2 PT0629	T-cell receptor be
37	11	30.6	6	2 PT0532	T-cell receptor be
38	11	30.6	6	2 PT0519	T-cell receptor be
39	11	30.6	6	2 PT0637	T-cell receptor be
40	11	30.6	6	2 PT0641	T-cell receptor be
41	11	30.6	6	2 PT0726	T-cell receptor be
42	11	30.6	6	2 F41946	T-cell receptor ga
43	11	30.6	6	2 PD0028	pev-kinin 2 - pana
44	11	30.6	6	4 I79564	hypothetical TGL3
45	11	30.6	7	2 S21230	dermorphin (TRP-4,
46	11	30.6	7	2 A58512	venom heptapeptide
47	11	30.6	7	2 A61081	tryptophyllin, bas
48	11	30.6	7	2 S57274	triacylglycerol 11
49	11	30.6	7	2 S09652	hypothetical prote
50	11	30.6	7	2 PN0649	alpha-dextrin endo

ALIGNMENTS

RESULT 1
S33244
neuromodulatory peptide Wwamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C>Date: 19-Mar-1997 #sequence-revision 19-Mar-1997 #text-change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A>Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Accession: S33244
A:Reference number: S33244; MUID:93265912
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 44.4% Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
DB 1 wk 2

RESULT 2
S33246
neuromodulatory peptide Wwamide-3 - giant African snail
C:Species: Achatina fulica (giant African snail)
C>Date: 19-Mar-1997 #sequence-revision 19-Mar-1997 #text-change 24-Jul-1997
C:Accession: S33246
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A>Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 44.4% Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wk 2
DB 1 wk 2

Db 1 WK 2

RESULT 3

C61512

variant surface glycoprotein M1rat 1.4 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: C61512

R:Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termi

A:Reference number: A61512; MUID:81172836

A:Accession: C61512

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Keywords: glycoprotein

Query Match

Best Local Similarity 38.9%; Score 14; DB 2; Length 8;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5

I: 1

Db 1 WENNA 5

RESULT 4

S33245

neuromodulatory peptide Wwamide-2 - giant African snail

C:Species: Achatina fullica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33245

R:Minakata, H.; Ikeda, T.; Nuneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33245

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match

Best Local Similarity 36.1%; Score 13; DB 2; Length 7;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2

I: 1

Db 1 WR 2

RESULT 5

A38887

T-cell receptor gamma chain (5t.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A38887

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge

A:Reference number: A41946; MUID:92049316

A:Accession: A38887

A:Status: Preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-8 <WHD>

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 36.1%; Score 13; DB 2; Length 8;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 wkxxay 6

I: 1

Db 3 WDSSGF 8

RESULT 6

B61445

Leu-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: B61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A:Reference number: A61445; MUID:84144823

A:Accession: B61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match

Best Local Similarity 33.3%; Score 12; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8

I: 1

Db 1 YGG 3

RESULT 7

A61445

Met-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: A61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A:Reference number: A61445; MUID:84144823

A:Accession: A61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match

Best Local Similarity 33.3%; Score 12; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8

I: 1

Db 1 YGG 3

RESULT 8

PT0278

Ig heavy chain CRD3 region (clone 4-88) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0278

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108537

A:Accession: PT0278

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1
1
Db 1 yfg 3

RESULT 9

PT0308 Ig heavy chain CRO3 region (clone 6-88) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1
1
Db 2 WE 3

RESULT 10

S66195 alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragme

C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltnes, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. A
nzyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195
A:Molecule type: Protein
A:Residues: 1-6 <HJE>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1
1
Db 5 WE 6

RESULT 11

A31263 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f

C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha

A:Reference number: A94217; MUID:89057886
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1
1
Db 3 WE 4

RESULT 12

B31263 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu

C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886
A:Accession: B31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1
1
Db 3 WE 4

RESULT 13

B35640 cerebellar degeneration-related protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C:Accession: B35640
R:Chen, Y.T.; Rettig, W.J.; Yennamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal
A:Reference number: A35640; MUID:90222173
A:Accession: B35640
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6 <CHE>

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1
1
Db 2 WE 3

RESULT 14

A41946 T-cell receptor gamma chain (1t.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: A41946
 R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol. 11, 5902-5909, 1991
 A>Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene
 A:Reference number: A41946; MUID:92049316
 A:Accession: A41946
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-6 <NHE>
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 yxg 8
 | |
 Db 1 yrg 3

RESULT 15
 A60224
 Met-enkephalin-Arg-Phe - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
 C:Accession: A60224
 R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
 J. Neurochem. 56, 1914-1920, 1991
 A>Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
 A:Reference number: A60224; MUID:91225680
 A:Accession: A60224
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 C:Superfamily: proenkephalin
 C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 yxg 8
 | |
 Db 1 yrg 3

RESULT 16
 PQ0012
 cholecystokinin - southeastern quoll
 N:Alternate names: CCK
 C:Species: Dasyurus viverrinus (southeastern quoll)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
 C:Accession: PQ0012
 R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
 Peptides 9, 429-431, 1988
 A>Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
 A:Reference number: PQ0012; MUID:88234141
 A:Accession: PQ0012
 A:Molecule type: protein
 A:Residues: 1-8 <FAN>
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
 F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
 F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
 | |
 Db 2 ymg 4

RESULT 17
 A43001
 cholecystokinin - tammar wallaby
 N:Alternate names: CCK
 C:Species: Macropus eugenii (tammar wallaby)
 C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
 C:Accession: A43001; PQ0012
 R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
 Peptides 9, 429-431, 1988
 A>Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
 A:Reference number: PQ0012; MUID:88234141
 A:Accession: A43001
 A:Molecule type: protein
 A:Residues: 1-8 <FAN>
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
 F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
 F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 yxg 8
 | |
 Db 2 ymg 4

RESULT 18
 S63493
 dissimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio
 C:Species: Desulfovibrio desulfuricans
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S63493; S63494
 R:Stender, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
 Eur. J. Biochem. 233, 873-879, 1995
 A>Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
 A:Reference number: S63489; MUID:96085152
 A:Accession: S63493
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <STB>
 A:Molecule type: protein
 A:Residues: 1-8 <STB>
 A:Accession: S63494
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <STB>

Query Match 33.3%; Score 12; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 yxg 8
 | |
 Db 5 ymg 7

RESULT 19
 D61512
 variant surface glycoprotein M1rat 1.6 - Trypanosoma brucei (fragment)
 C:Species: Trypanosoma brucei
 C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
 C:Accession: D61512
 R:Holder, A.A.; Cross, G.A.M.
 Mol. Biochem. Parasitol. 2, 135-150, 1981
 A>Title: Glycoproteins of variant surface glycoproteins of Trypanosoma brucei. C-
 A:Reference number: A61512; MUID:81172836

A:Accession: D61512
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <HOL>
C:Keywords: glycoprotein

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 2
1;
DB 1 w 2

RESULT 20
F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196
R:Clint, A.C.O.; Vieira, C.A.; Gagli, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557
A:Accession: F37196

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CLN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1;
DB 3 w 3

RESULT 21
A34626
RPCH-related neuropeptide - ferruginous spindie
C:Species: Fuschus ferrugineus (ferruginous spindie)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Blochm. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:9019762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1;
DB 4 w 4

RESULT 22
PT0240
Ig heavy chain CND3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1;
DB 1 ypg 3

RESULT 23
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity an
A:Reference number: A53284; MUID:91342695
A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:560737; NID:q233916; PIDN:AA819518.1; PID:q233918
A:Note: Sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60738)
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1;
DB 2 w 2

RESULT 24
PT0661
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0661
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEF>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1

Db 3 W 3

RESULT 25

A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestines
A:Reference number: A32516; MUID:87153871
A:Accession: A32516
A:Molecule type: Protein
A:Residues: 1-5 <SH1>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 2 W 2

Search completed: January 14, 2002, 07:44:21
Job time: 407 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds
(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1B
Perfect score: 36
Sequence: 1 WXXXXYXG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SWISSPROT_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	44.4	7	1 MNPI_LEPDE	P42984 lepliotars
2	44.4	7	1 WMA2_ACHFV	P35920 echatrina fu
3	44.4	7	1 WMA3_ACHFV	P35921 echatrina fu
4	36.1	7	1 WMA1_ACHFV	P35919 echatrina fu
5	33.3	8	1 CCKN_MACEU	P30369 bochrops eu
6	33.3	5	1 BPP7_BORIN	P30425 bochrops in
7	30.6	5	1 UF01_MOUSE	P38639 mus musculu
8	30.6	6	1 LOK1_LOCMT	P41491 locusta mig
9	30.6	6	1 OVM_LEPDE	P42985 lepliotars
10	30.6	7	1 ALI2_CARMA	P81805 carcinius ma
11	30.6	7	1 FAR3_HAECCO	P81298 haemochus
12	30.6	7	1 FAR3_PANRE	P41874 panagrellus
13	30.6	8	1 ACI_THUAL	P18691 thunnus alb
14	30.6	8	1 AKHG_GRTBI	P1086 gryllus bim
15	30.6	8	1 AKH_LIBAU	P23418 libellula a
16	30.6	8	1 AKH_MELAU	P23423 meioloncha
17	30.6	8	1 AKH_TABAT	P14595 tabanus atr
18	30.6	8	1 HTEF1_PERAM	P04548 periplaneta
19	30.6	8	1 HTEF2_PERAM	P04549 periplaneta
20	30.6	8	1 HTEF_TENMO	P23419 tenebrio mo
21	30.6	8	1 LCK1_LEUMA	P21140 leucophaea
22	30.6	8	1 LCK2_LEUMA	P21141 leucophaea
23	30.6	8	1 LCK3_LEUMA	P21142 leucophaea
24	30.6	8	1 LCK4_LEUMA	P21143 leucophaea
25	30.6	8	1 LCK5_LEUMA	P19987 leucophaea
26	30.6	8	1 LCK6_LEUMA	P19988 leucophaea
27	30.6	8	1 LCK7_LEUMA	P19989 leucophaea
28	30.6	8	1 LCK8_LEUMA	P19990 leucophaea
29	30.6	8	1 RPH_BBRANA	P81707 brassica na
30	30.6	8	1 RPH_PANBO	P08939 pandanus bo
31	30.6	8	1 UF06_MOUSE	P38644 mus musculu
32	30.6	8	1 UPAA_HUMAN	P30096 homo sapien
33	25.0	7	1 UC24_MAIZE	P80630 zea mays (m

34	8	22.2	5	1 TPIS_CANFA	P54714 canis fam11
35	8	22.2	7	1 HY7_PIG	P01153 sus scrofa
36	8	22.2	8	1 AL16_CARMA	P81819 carcinius ma
37	8	22.2	8	1 CLP_THICU	P80488 thibacillu
38	8	22.2	8	1 GLUR_HUMAN	P02729 homo sapien
39	7	19.4	4	1 FAR3_HIRME	P42562 hirudo med1
40	7	19.4	4	1 FAR4_HIRME	P42563 hirudo med1
41	7	19.4	5	1 AL14_CARMA	P81817 carcinius ma
42	7	19.4	5	1 FARP_ARTTR	P41853 artiposthl
43	7	19.4	5	1 PRCT_PERAM	P01373 periplaneta
44	7	19.4	5	1 PSK_DAUCA	P58261 daucus caro
45	7	19.4	6	1 ASP2_LACSN	P82655 lactobacill
46	7	19.4	7	1 ALL3_CARMA	P81806 carcinius ma
47	7	19.4	7	1 ALL4_CARMA	P81807 carcinius ma
48	7	19.4	7	1 ALL5_CARMA	P81808 carcinius ma
49	7	19.4	7	1 ALL7_CYPDO	P82158 cydia pomon
50	7	19.4	7	1 FAR2_ASCSU	P31890 ascaris suu

ALIGNMENTS

RESULT 1
ID MNPI_LEPDE STANDARD: PRT: 7 AA.

AC P42984;
AT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-I).
OS lepliotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RM
RS
RT SEQUENCE, AND SYNTHESIS.
RC
RP TISSUE-Head;
RA MEDLINE=95380343; PubMed=7651886;
RX Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA "identificatio, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC
CC -I- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT
FT MOD_RES 7
FT MOD_RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 44.4%; Score 16; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 3; Conservative 0;

OY 5 ayyxg 8
Db 1 alyng 4

RESULT 2
ID WMA2_ACHFV STANDARD: PRT: 7 AA.
AC P35920;
AT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.

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OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RX Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RU FEBS Lett. 323:104-108(1993).
RW Neuropetide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match          44.4%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   | |
Db 1 WK 2

RESULT 3
WMA3_ACHFV          STANDARD;      PRT;      7 AA.
ID WMA3_ACHFV
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RU FEBS Lett. 323:104-108(1993).
RW Neuropetide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match          44.4%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   | |
Db 1 WK 2

RESULT 4
WMA1_ACHFV          STANDARD;      PRT;      7 AA.
ID WMA1_ACHFV
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;

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RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RU FEBS Lett. 323:104-108(1993).
RW Neuropetide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match          36.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
   | |
Db 1 WK 2

RESULT 5
CCKN_MACEU          STANDARD;      PRT;      8 AA.
ID CCKN_MACEU
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLECYSTOKININ (CCK).
GN CCK.
OS Macropus eugenii ('marmar wallaby'), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RL marsupials.";
RU Peptides 9:429-431(1988).
CC - FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC - SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
CC PIR: AA3001; AA3001.
DR PIR: PQ0012; PQ0012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA6838768B5A CRC64;

Query Match          33.3%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
   | |
Db 2 YMG 4

RESULT 6
BPP7_BOTIN          STANDARD;      PRT;      5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Quilmeda jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_Taxid:8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RC MEDLINE=90351557; PubMed=2386615;
RA Chttra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
-1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
CC PIR: G37196; G37196.
DR Hypotensive agent; Venom.
KW MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;
SQ

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 7
ID UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE.
RP TISSUE=Fibroblast;
RC MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Michler L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON_TER 5
SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 1 W 1

RESULT 8
ID LOKI_LOCM1 STANDARD; PRT; 6 AA.
LOKI_LOCM1

AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_Taxid=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RC MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
-1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
CC OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
CC TUBULES.
CC PIR: A61068; A61068.
DR Neuropeptide; Amidation.
KW MOD_RES 6
FT SEQUENCE 6 AA: 654 MW: 686365A589CDB000 CRC64;
SQ

Query Match 30.6%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 9
ID OVM_LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).
OS Lepidoptera decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phyllophaga; Chrysomeloidea; Chrysomelidae;
OX NCBI_Taxid=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RC MEDLINE=91271080; PubMed=2052497;
RA Spitzels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Lepidoptera
RT decemlineata.";
RL Peptides 12:31-36(1991).
-1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC Neuropeptide; Amidation.
KW MOD_RES 6
FT SEQUENCE 6 AA: 720 MW: 6B07632B5DD03000 CRC64;
SQ

Query Match 30.6%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6

Db 2 AY 3

RESULT 10
ALL2_CARMA STANDARD; PRT; 7 AA.
ID ALI2_CARMA
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Euphrachyura; Portunoidae; Portunidae; Carcinus.
NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Duye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7 AA; 770 MW; 672879CDBC5DDB70 CRC64;
SQ SEQUENCE 7 AA; 770 MW; 672879CDBC5DDB70 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 ay 6
Db 2 AY 3

RESULT 11
FAR3_HAECO STANDARD; PRT; 7 AA.
ID FAR3_HAECO
AC P81298;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE).
OS Haemochus contortus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6289;
RN [1]
RP SEQUENCE.
RX TISSUE=Neuron;
RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Geary T.G.,
Thompson D.P., Shaw C.;
RL Submitted (MAY-1998) to the SWISS-PROT data bank.
CC -1- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 ay 6

Db 3 AY 4

RESULT 12
FAR3_PANRE STANDARD; PRT; 7 AA.
ID FAR3_PANRE
AC P41874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMRF-AMIDE).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94235053; PubMed=8179635;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
Geary T.G., Thim L.;
RT "KSAYMRFamide: a novel FMRFamide-related heptapeptide from the free-
living nematode, Panagrellus redivivus, which is myoactive in the
parasitic nematode, Ascaris suum";
RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
CC -1- FUNCTION: MYOACTIVE: INDUCES A RAPID CONCENTRATION-DEPENDENT
MUSCLE TENSION INCREASE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW PIR: PC2132; PC2132.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 5 ay 6
Db 3 AY 4

RESULT 13
ACT_THUAL STANDARD; PRT; 8 AA.
ID ACT_THUAL
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE ANGIOTENSIN-CONVERTING ENZYME INHIBITOR.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RX TISSUE=Muscle;
RC MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0;

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OY      1 W 1
DB      6 W 6

RESULT 14
AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE G (AKH-G) (RO II).
CC GRYLUS BIMACULATUS (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper), and
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus.
OX NCBI_Taxid=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; Pubmed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; Pubmed=326948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A28004, A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES. 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES. 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 W 1
DB      8 W 8

RESULT 15
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
CC Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_Taxid=6966;
RN [1]

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RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; Pubmed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
concentrating hormone family isolated and sequenced from a
dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES. 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES. 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 W 1
DB      8 W 8

RESULT 16
AKH_MEML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
CC Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_Taxid=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; Pubmed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
hormone/red-pigment-concentrating hormone peptide family isolated and
sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; Pubmed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
cardiaca of various cetonid beetle species determined by
pulsed-liquid phase sequencing and tandem fast atom bombardment mass
spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21663; S21663.
DR InterPro: IPR002047; AKH.

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DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB54736 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 17
AKH_TABAT
ID AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERA CORPORA CARDIACA FACTOR 1)
DE (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
OX NCBI_Taxid=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
Vogel V.W., Zhang Y.S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera).";
RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 18
HTF1_PERAM
ID HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOXAEMIC FACTOR I (NEUROPEPTIDE M-1) (PERIPLANETIN CC-1)
DE (PERA-CAH-1) (LED-CC-1) (HYPERTREHALOXAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach),

OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Wilten J.L., Schaffner M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry";
RT Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Rinehart K.L., Jr.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
RT Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Exaltosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RT Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOXAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match
Best Local Similarity 30.6%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 19
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;

DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
 DE (PEA-CAH-II) (LED-CC-II) (HYPERTREHALOSEMIC NEUROPEPTIDE II).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 NX NCBI_TaxId=6978, 7539, 6976;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kallish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-L.decemlineata; TISSUE-Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Rinehart R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical."
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES-B.orientalis; TISSUE-Corpora cardiaca;
 RX MEDLINE=90235659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Exaltosoma titatum assigned by tandem fast
 RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -I- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20
 ID HTF_TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tenebrio.
 NX NCBI_TaxId=7067, 7075;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH / HRTN / RPCH family."
 RL Peptides 11:455-459(1990).
 CC -I- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 8 w 8
 RESULT 21
 ID LCK1_LEUMA STANDARD; PRT; 8 AA.
 AC P21140;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE LEUCOKININ I (L-I).
 OS Leucophaea maderae (Madeira cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 NX NCBI_TaxId=6988;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotroptins."
 RL Comp. Biochem. Physiol. 84C:205-211(1986).
 CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8
 FT SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 |
 Db 7 w 7

RESULT 22

LCR2_LEUMA STANDARD; PRT; 8 AA.
 ID LCR2_LEUMA
 AC P21141;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE LEUCOKININ II (L-II).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 from Leucophaea maderae: members of a new family of
 Cephalomyotroptins.";
 RL Comp. Biochem. Physiol. 84C:205-211(1986).
 CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC Neuropeptide; Amidation.
 FT MOD_RES 8
 KW SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
 SQ

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 |
 Db 7 w 7

RESULT 23

LCR3_LEUMA STANDARD; PRT; 8 AA.
 ID LCR3_LEUMA
 AC P21142;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE LEUCOKININ III (L-III).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 from Leucophaea maderae: members of a new family of
 Cephalomyotroptins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 |
 Db 7 w 7

RESULT 24

LCR4_LEUMA STANDARD; PRT; 8 AA.
 ID LCR4_LEUMA
 AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE LEUCOKININ IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 from Leucophaea maderae: members of a new family of
 Cephalomyotroptins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC Neuropeptide; Amidation.
 FT MOD_RES 8
 KW SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDPA CRC64;
 SQ

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 |
 Db 7 w 7

RESULT 25

LCR5_LEUMA STANDARD; PRT; 8 AA.
 ID LCR5_LEUMA
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LEUCOKININ V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).

CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 784 MW; 736365A5B9C865B8 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
|
Db 7 W 7

Search completed: January 14, 2002, 07:52:04
Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:45 ; Search time 80.15 Seconds
(without alignments)
14.600 Million cell updates/sec

Title: 09-185908-1b
Perfect score: 36
Sequence: 1 wxxxxxxg 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

- Database :
- 1: SP-archaea:*
 - 2: SP-bacteria:*
 - 3: SP-fungi:*
 - 4: SP-human:*
 - 5: SP-invertebrate:*
 - 6: SP-mammal:*
 - 7: SP-mhc:*
 - 8: SP-organclle:*
 - 9: SP-phage:*
 - 10: SP-plant:*
 - 11: SP-rodent:*
 - 12: SP-virus:*
 - 13: SP-vertebrate:*
 - 14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	44.4	7	8 Q95945	Q95945 saccharomyc
2	16	44.4	8	11 Q62721	Q62721 ratius norv
3	12	33.3	8	2 O09258	O09258 synechococc
4	12	33.3	8	5 Q9TWH6	Q9TWH6 perlineireis
5	12	33.3	8	11 P70243	P70243 mus musculu
6	12	33.3	8	11 Q9QVD3	Q9QVD3 ratius sp.
7	11	30.6	6	13 P82096	P82096 litoria rub
8	11	30.6	7	10 O49223	O49223 glycine max
9	11	30.6	7	13 P82065	P82065 litoria rub
10	11	30.6	8	2 O85406	O85406 coxiella bu
11	11	30.6	8	2 O95443	O95443 pseudomonas
12	11	30.6	8	4 O15888	O15888 homo sapien
13	11	30.6	8	4 O15890	O15890 homo sapien
14	11	30.6	8	5 Q9VRD2	Q9VRD2 drosophila
15	11	30.6	8	5 P82685	P82685 periplaneta
16	11	30.6	8	5 P82686	P82686 periplaneta
17	11	30.6	8	5 P82687	P82687 periplaneta
18	11	30.6	8	5 P82688	P82688 periplaneta
19	11	30.6	8	5 P82689	P82689 periplaneta

20	11	30.6	8	6 O02831	O02831 oryctolagus
21	11	30.6	8	6 Q9TRJ3	Q9TRJ3 sus sp. ins
22	11	30.6	8	6 P82929	P82929 bos taurus
23	11	30.6	8	7 Q95213	Q95213 oryctolagus
24	11	30.6	8	8 Q9TD02	Q9TD02 terranatos
25	11	30.6	8	8 Q9TAY2	Q9TAY2 asterina pe
26	11	30.6	8	10 P82324	P82324 pisum saliv
27	11	30.6	8	11 O35835	O35835 ratius norv
28	11	30.6	8	11 P82598	P82598 ratius norv
29	11	30.6	8	11 Q9ET18	Q9ET18 mus spreus
30	11	30.6	8	11 Q9ET17	Q9ET17 mus caroli
31	11	30.6	8	11 Q9ET16	Q9ET16 mesocricetu
32	11	30.6	8	11 Q9PMN0	Q9PMN0 mus musculu
33	11	30.6	8	13 P79940	P79940 xenopus lae
34	11	30.6	8	13 Q98TU5	Q98TU5 xenopus lae
35	9	25.0	8	2 Q9RO57	Q9RO57 buchnera ap
36	8	22.2	8	2 Q9RO49	Q9RO49 buchnera ap
37	8	22.2	8	4 Q15898	Q15898 homo sapien
38	8	22.2	8	4 Q15900	Q15900 homo sapien
39	8	22.2	8	8 Q34909	Q34909 locusta mig
40	8	22.2	8	10 Q9S824	Q9S824 spinacia ol
41	7	19.4	7	2 O50556	O50556 actinobacil
42	7	19.4	7	4 O15903	O15903 homo sapien
43	7	19.4	7	8 Q99182	Q99182 gnatholebia
44	7	19.4	7	12 Q9YVE3	Q9YVE3 human adeno
45	7	19.4	7	12 Q9YQ10	Q9YQ10 porcine tra
46	7	19.4	7	12 Q9YIR0	Q9YIR0 human adeno
47	7	19.4	7	12 Q9YIO9	Q9YIO9 human adeno
48	7	19.4	7	13 P82101	P82101 litoria rub
49	7	19.4	8	2 O52062	O52062 bacillus me
50	7	19.4	8	2 Q56759	Q56759 xanthobacte

ALIGNMENTS

RESULT 1

Q95945 ID Q95945 PRELIMINARY: PRT: 7 AA.

AC Q95945;

DT 01-FEB-1997 (TREMBLrel. 02. Created)

DT 01-FEB-1997 (TREMBLrel. 02. Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08. Last annotation update)

DE INSIDE INTRON 5 (FRAGMENT).

OS Saccharomyces cerevisiae (Baker's yeast).

OG Mitochondrion.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81069885; PubMed=6254986;

RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;

RT "Assembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase.";

RT J. Biol. Chem. 255:11927-11941(1980).

DR EMBL; V00694; CAA24066.1; -.

KW Mitochondrion.

FT NON_TER

SO SEQUENCE 7 AA; 859 MW; 75B7232362C0C460 CRC64;

Query Match 44.4%; Score 16; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
11

Db 4 wk 5

RESULT 2

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062721
ID 062721 PRELIMINARY; PRT; 8 AA.
AC 062721:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jue E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL, U17178; AAA8692.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 4.4%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
| |
DB 6 WK 7

RESULT 3
ID 009258 PRELIMINARY; PRT; 8 AA.
AC 009258:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NIFH (FRAGMENT).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanobcece PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RA Chen H.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF001780; AAC33369.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 alyx 8
| |
DB 5 APLG 8

RESULT 4
ID 09TWH6 PRELIMINARY; PRT; 8 AA.
AC 09TWH6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

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DE BIOACTIVE PEPTIDE P4-PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculatea;
OC Phyllodoctida; Nereididae; Perinereis.
NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95323338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Kunoeka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancaurica.";
RL Comp. Biochem. Physiol. C.
RL Pharmacol. Toxicol. Endocrinol. 110:297-304(1995).
SQ SEQUENCE 8 AA; 989 MW; 95477ZCA87B0B59 CRC64;

Query Match 33.3%; Score 12; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
DB 2 YEG 4

RESULT 5
ID P70243 PRELIMINARY; PRT; 8 AA.
AC P70243:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Ophoff R.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98325; CAA66969.1; -.
KM Calcium channel.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
| |
DB 7 WQ 8

RESULT 6
ID 09QVD3 PRELIMINARY; PRT; 8 AA.
AC 09QVD3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=101118;
RN [1]
RP SEQUENCE.

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RX MEDLINE:92202192; PubMed:1313009;
RA Kanematsu T., Takaya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative Inositol 1,4,5-trisphosphate binding proteins in rat brain
cytosol."
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA: 1047 MW: D72415B806C37041 CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 2
DB 3 w 4

RESULT 7
P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRLN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
OX NCBI_TaxID:104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wadnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella."
RT Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA: 792 MW: 6683704772C9A000 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 5 w 5

RESULT 8
O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID:3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
RX MEDLINE:91367679; PubMed:1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
with HMG-box proteins.";

RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knapp H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF047050; AAC03556.1; .
FT NON_TER 1
SQ SEQUENCE 7 AA: 850 MW: 6AAAAB378637810 CRC64;

Query Match 30.6%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 9
P82065 PRELIMINARY; PRT; 7 AA.
AC P82065;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TRYPTOPHYLLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
OX NCBI_TaxID:104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steindorfer S.T., Wadnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella". The skin peptide profile as a probe for the study
of evolutionary trends of amphibians."
RT Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUOTRASMITTER.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM=965; METHOD=FAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1
FT PYROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 7 AA: 983 MW: 7401E9D3676046B0 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 4 w 4

RESULT 10
O85406 PRELIMINARY; PRT; 8 AA.
AC O85406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE 1;
 RA "Millems H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 RT *Coxiella burnetii*.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF064963; AAD09947.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA53772727 CRC64;

Query Match 30.6%; Score 11; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 4 w 4

RESULT 11
 ID 09S443 PRELIMINARY; PRT; 8 AA.
 AC 09S443;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE BETA-LACTAMASE (FRAGMENT).
 GN PSE2.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R545;
 RA Roy D., Coulombe M., Perron K., Roy P.H.;
 RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
 RT gene aac(6')-IIC from the integron of a Chinese *Pseudomonas aeruginosa*
 RT clinical isolate.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162771; AAD46628.1; -
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 930 MW; EBD85DDDD9D1A336 CRC64;

Query Match 30.6%; Score 11; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 DB 6 ay 7

RESULT 12
 ID 015888 PRELIMINARY; PRT; 8 AA.
 AC 015888;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE (CLONE XP15H8A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,

RA Caskey C.T.H.;
 RL Hum. Mol. Genet.. 0:0-0(0).
 DR EMBL; L32069; AAA73878.1; -
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5H0763 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 6 w 6

RESULT 13
 ID 015890 PRELIMINARY; PRT; 8 AA.
 AC 015890;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE (CLONE XP19G12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet.. 0:0-0(0).
 DR EMBL; L32083; AAA73880.1; -
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 1 w 1

RESULT 14
 ID 09VRD2 PRELIMINARY; PRT; 8 AA.
 AC 09VRD2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG11666 PROTEIN.
 GN CG11666.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
April J.F., Agbayan A., An H.-J., Andrews-Plankkoch C., Baldwin D.,
Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Modarity C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzo M., Platten G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
SC Science 287:2185-2195(2000).
DR EMBL: AEO03569; AAF50870.1; -;
FLYBase: FBgn0040648; CG11666.
SEQUENCE 8 AA: 1062 MW: ED11B5B044004376 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
2 w 2

RESULT 15
P82685 ID PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
DE [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta
americana*.";
RA Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 950 MW: 326365B449D5A774 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 16
P82686 ID PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
DE [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta
americana*.";
RA Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 856 MW: DC6365A5B9D5BDDA CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 17
P82687 ID PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
DE [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta*

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RT americana.;
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 909 MW; DC6365B449D5A76A CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 7 W 7

RESULT 18
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RA MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 7 W 7

RESULT 19
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE AND FUNCTION.

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RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 865 MW; C76365B449C0C775 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 7 W 7

RESULT 20
002831 PRELIMINARY; PRT; 8 AA.
ID 002831
AC 002831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Melsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL: S83371; ADD14433.1; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 1028 MW; B859C7272EA77371 CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 2 W 2

RESULT 21
O9TRV3 PRELIMINARY; PRT; 8 AA.
ID O9TRV3
AC O9TRV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;

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RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RL protein-6."
SL Mol. Endocrinol. 5:938-948(1991).
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
Db 5 w 5

RESULT 22
P82929 PRELIMINARY; PRT; 8 AA.
ID P82929;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
RL of the full complement ribosomal proteins present."
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
Db 2 w 2

RESULT 23
Q95213 PRELIMINARY; PRT; 8 AA.
ID Q95213;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE GERMLINE DH (DF) GENE (FRAGMENT).
DF.
GN Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F-I/RGM;
RA Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
RL Mol. Immunol. 0:0-0(0).
DR EMBL: U62585; AAB18735.1; -.
KW MHC.
FT NON_TER 1 1

FT NON_TER 8 8
SQ SEQUENCE 8 AA; 845 MW; 5CA861B5AB58677B CRC64;

Query Match 30.6%; Score 11; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 yxg 8
Db 1 ypg 3

RESULT 24
Q9TD02 PRELIMINARY; PRT; 8 AA.
ID Q9TD02;
AC Q9TD02;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Teranatos dolichopterus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxId=61836;
RN [1]
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective."
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AF03041.1; -.
KW Mitochondrion.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DDA4056 CRC64;

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
Db 6 w 6

RESULT 25
Q9T4Y2 PRELIMINARY; PRT; 8 AA.
ID Q9T4Y2;
AC Q9T4Y2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Asterina pectinifera (Starfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxId=7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89354669; PubMed=2766382;
RA Jacobs H.T., Asakawa S., Ataki T., Muira K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA."
RL Curr. Genet. 15:193-206(1989).
DR EMBL: X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1114 MW; F0C9D36415B736D6 CRC64;

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 w 1
|
Db 6 w 6

Search completed: January 14, 2002, 07:53:45
Job time: 725 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:16 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1b
Perfect score: 36
Sequence: 1 wkxxxyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_1101:*

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2: /SID52/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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20: /SID52/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	77.8	8	21	AA06419
2	28	77.8	8	21	AA06479
3	27	75.0	8	21	AA06764
4	27	75.0	8	21	AA06814
5	27	75.0	8	21	AA06916
6	26	72.2	8	21	AA06521
7	26	72.2	8	21	AA06574
8	25	69.4	8	4	AA030170
9	25	69.4	8	21	AA06426
10	25	69.4	8	21	AA06512
11	25	69.4	8	21	AA06823

12	25	69.4	8	21	AA06876	Claudin-7 cyclic c
13	25	69.4	8	21	AA06917	Claudin-7 cell adh
14	24	66.7	8	21	AA06583	Claudin-3 cell adh
15	24	66.7	8	21	AA06636	Claudin-3 cyclic c
16	24	66.7	8	21	AA06645	Claudin-4 cell adh
17	24	66.7	8	21	AA06698	Claudin-4 cyclic c
18	22	61.1	6	21	AA06418	Claudin-1 cell adh
19	22	61.1	6	21	AA06477	Claudin-1 cyclic c
20	22	61.1	6	21	AA06762	Claudin-6/9 cell a
21	22	61.1	6	21	AA06812	Claudin-6/9 cyclic
22	22	61.1	7	21	AA06478	Claudin-1 cell adh
23	22	61.1	7	21	AA06763	Claudin-1 cyclic c
24	22	61.1	7	21	AA06813	Claudin-6/9 cell a
25	22	61.1	7	21	AA06834	Claudin-6/9 cyclic
26	22	61.1	8	21	AA06443	Claudin-1 cyclic c
27	22	61.1	8	21	AA06452	Claudin-1 cyclic c
28	22	61.1	8	21	AA06452	Claudin-1 cyclic c
29	22	61.1	8	21	AA06461	Claudin-1 cyclic c
30	22	61.1	8	21	AA06470	Claudin-1 cyclic c
31	22	61.1	8	21	AA06770	Claudin-6/9 cyclic
32	22	61.1	8	21	AA06779	Claudin-6/9 cyclic
33	22	61.1	8	21	AA06787	Claudin-6/9 cyclic
34	22	61.1	8	21	AA06796	Claudin-6/9 cyclic
35	22	61.1	8	21	AA06804	Claudin-6/9 cyclic
36	21	58.3	6	7	AA061337	Sequence of novel
37	21	58.3	6	21	AA06519	Claudin-2 cell adh
38	21	58.3	6	21	AA06572	Claudin-2 cyclic c
39	21	58.3	7	21	AA06520	Claudin-2 cell adh
40	21	58.3	7	21	AA06573	Claudin-2 cyclic c
41	21	58.3	8	21	AA06528	Claudin-2 cyclic c
42	21	58.3	8	21	AA06546	Claudin-2 cyclic c
43	21	58.3	8	21	AA06555	Claudin-2 cyclic c
44	21	58.3	8	21	AA06564	Claudin-2 cyclic c
45	21	58.3	8	21	AA06564	Claudin-2 cyclic c
46	20	55.6	6	19	AA015938	Cyclo(Tyr-Lys-Orn-
47	20	55.6	6	20	AA042901	Cyclic hexapeptide
48	20	55.6	6	20	AA042902	Linear intermediate
49	20	55.6	6	21	AA058399	Cyclic peptide mim
50	20	55.6	6	21	AA059400	Cyclic peptide mim

ALIGNMENTS

RESULT 1

AA06419 standard; peptide: 8 AA.

XX

AC AAB06419:

XX

DT 28-SEP-2000 (first entry)

XX

DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.

XX

KW Claudin-1 modulating agent; cell adhesion recognition sequence;

KW Cdk sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection.

XX

OS Mammalia.

XX

PN WO200026360-A1.

PD

PD 11-MAY-2000.

XX

XX

PF 03-NOV-1999; 99WO-CA01029.

XX

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

XX

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PA

PI Blaschuck OW, Symonds JM, Gour BJ;

XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
| | : | |
Db 1 wklysyag 8

RESULT 2
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
DE
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
| | : | |
Db 1 wklysyag 8

RESULT 3
AAB06764
ID AAB06764 standard; peptide; 8 AA.
XX
AC AAB06764;
XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.
DE
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 70; Page 103; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
| | : | |
Db 1 wkvtatlg 8

RESULT 4
ID AAB06814 standard; peptide: 8 AA.
AC AAB06814:
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
XX inflammatory disease; cancer; graft rejection; cyclic.
XX Mammalia.
XX OS
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 73: Page 104; 121pp: English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
XX are cadherins, which are membrane glycoproteins involved in cell
XX adhesion. In some situations, cell adhesion occurs at abnormal levels,
XX and these peptides can be used to modulate these levels, and thus treat
XX autoimmune diseases, inflammatory diseases and cancer, and aid wound
XX healing and implant adhesion. In addition, they can also be used to
XX facilitate drug delivery to the desired target site. The present
XX sequence has a cyclic conformation.
XX
XX Sequence 8 AA:
SQ

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wkxxayxg 8
II I: I
DB 1 wkvtaflg 8

RESULT 5
ID AAB06916 standard; protein: 8 AA.
XX
XX AAB06916:
XX
XX 05-OCT-2000 (first entry)
XX
XX Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
XX Claudin modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX

OS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX FT /note= "N-terminal acetyl"
XX FT 8
XX FT Modified-site 8
XX FT /note= "C-terminal amide"
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 71: Page 103; 121pp: English.
XX
XX The present sequence is a peptide which can be used in a claudin-mediated
XX cell adhesion modulator. The claudin group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and this peptide
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, it can also be used to facilitate drug delivery
XX to the desired target site.
XX
XX Sequence 8 AA:
SQ

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wkxxayxg 8
II I: I
DB 1 wkvtaflg 8

RESULT 6
ID AAB06521 standard; peptide: 8 AA.
XX
XX AAB06521:
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
XX Mammalia.
XX OS
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX 03-NOV-1998; 98US-0185908.
XX

PR 30-MAR-1999; 990S-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
SQ Sequence 8 AA;
XX

Query Match 72.2%; Score 26; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxaxyg 8
| : | |
Db 1 wrtsyyvg 8

RESULT 7
AAB06574
ID AAB06574 standard; peptide; 8 AA.
XX
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX
XX 30-MAR-1999; 99US-0282029.
XX
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC

CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
XX
XX
SQ Sequence 8 AA;
XX

Query Match 72.2%; Score 26; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxaxyg 8
| : | |
Db 1 wrtsyyvg 8

RESULT 8
AAP30170
ID AAP30170 standard; peptide; 6 AA.
XX
AC AAP30170;
XX
DT 30-JUL-1992 (first entry)
XX
XX
DE Sequence of a cyclic peptide which is a somatostatin analogue.
XX
XX
XX Somatostatin analogue; glucagon release inhibitor; growth hormone;
KW insulin; acromegaly therapy; diabetes; diabetic retinopathy;
KW cyclic peptide.
XX
XX
XX Key Location/Qualifiers
FH Modified-site 1 /label= D-W
FT Modified-site 5 /label= N-Me-A
FT
XX
XX EP70021-A.
XX
XX 19-JAN-1983.
XX
XX
XX 10-JUL-1982; 82EP-0106205.
XX
XX 15-JUL-1981; 81US-0283404.
XX
XX (MERI) MERCK & CO INC.
XX
XX Nutt RF;
XX
XX WPI; 1983-10097K/05 (10097K).
XX
XX
XX Cyclic hexa:peptide somatostatin analogue prepn. - by cyclisation
PT of linear hexa:peptide in soln. in DMF or DMSO in presence of
PT base and cyclising agent
XX
XX
XX Claim 1; Page 1; 25pp; English.
XX
XX
XX The inventors claim a method for the preparation of the cyclic
CC peptide of the sequence in AAP30170. The method is the cyclisation of
CC a linear permutation of AAP30170 in soln. in DMF or DMSO in the
CC presence a base and a cyclising agent. The cyclisation occurs with
CC more rapid reaction kinetics than are observed in many peptide
CC cyclisations. So the reaction can be carried out in a much more
CC cond. state (10-100 times more cond.) than is used in normal
CC cyclisations. Therefore the reaction vol. used for a given amt. of
CC the linear peptides used in the prepn. of cyclic AAP30170 is greatly
CC reduced.
XX
XX
XX Sequence 6 AA;
SQ

Query Match 69.4% Score 25; DB 4; Length 6;
Best Local Similarity 66.7% Pred. NO. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxay 6
1111
Db 1 wkvfay 6

RESULT 9
AAB06426
ID AAB06426 standard; peptide: 8 AA.
XX
AC AAB06426;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA:

Query Match 69.4% Score 25; DB 21; Length 8;
Best Local Similarity 37.5% Pred. NO. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wxxxayxg 8
11111
Db 1 wrlfysyag 8
RESULT 10
AAB06512
ID AAB06512 standard; peptide: 8 AA.
XX

AC AAB06512;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA:

Query Match 69.4% Score 25; DB 21; Length 8;
Best Local Similarity 37.5% Pred. NO. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wxxxayxg 8
11111
Db 1 wrlfysyag 8

RESULT 11
AAB06823
ID AAB06823 standard; peptide: 8 AA.
XX
AC AAB06823;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-7 cell adhesion recognition sequence SEQ ID NO: 394.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX

PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 76; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wxxxayxg 8
1 : | |
Db 1 wqmsyag 8

RESULT 12
AAB06876
ID AAB06876 standard; peptide; 8 AA.
XX
AC AAB06876;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT

PT and across the skin -
XX
PS Claim 79; Page 105; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wxxxayxg 8
1 : | |
Db 1 wqmsyag 8

RESULT 13
AAB06917
ID AAB06917 standard; Protein; 8 AA.
XX
AC AAB06917;
XX
DT 05-OCT-2000 (first entry)
XX
DE Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Synthetic.
XX
XX

Key Location/Qualifiers
FH Modified-site 1 /note="N-terminal acetyl"
FT Modified-site 8 /note="C-terminal amide"
FT
FT
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
XX
XX

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 77; Page 104; 121pp; English.
XX
CC The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide

CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.

XX Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
I: | |
Db 1 wqmsyag 8

RESULT 14
AAB06583
ID AAB06583 standard; peptide; 8 AA.

AC AAB06583;
XX
DT 28-SEP-2000 (first entry)

XX Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.

DE Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 52; Page 99; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

XX Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
I: | |
Db 1 wvrsafig 8

RESULT 15
AAB06636
ID AAB06636 standard; peptide; 8 AA.

AC AAB06636;

XX 28-SEP-2000 (first entry)

XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.

DE Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 55; Page 100; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxayxg 8
I: | |
Db 1 wvrsafig 8

RESULT 16
AAB06645
ID AAB06645 standard; peptide; 8 AA.

AC AAB06645;

XX 28-SEP-2000 (first entry)

XX Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.

DE Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
PT
XX
XX Claim 61; Page 101; 121pp; English.
PS
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 8 AA;
SQ
Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 wxxxayxg 8
|: |: |
Db 1 wrwtatfg 8
RESULT 18
AAB06417
AAB06417 standard; peptide; 6 AA.
XX
XX AAB06417;
AC
XX
DT 28-SEP-2000 (first entry)
XX
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 32.
DE
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
FN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PE
XX 03-NOV-1998; 98US-0185908.
PR
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
PT
XX
XX Claim 39; Page 95; 121pp; English.
PS
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 8 AA;
SQ

CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

XX Sequence 6 AA;

Query Match 61.1%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 wkxxy 6
11 : 1
1 wklysy 6

RESULT 19
AAB06477 standard; peptide; 6 AA.

XX AAB06477;

XX 28-SEP-2000 (first entry)

XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 108.

DE Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -

XX Claim 43; Page 97; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.

XX Sequence 6 AA;

Query Match 61.1%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 wkxxy 6
11 : 1

DB 1 wklysy 6

RESULT 20
AAB06762 standard; peptide; 6 AA.

XX AAB06762;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 333.

XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -

XX Claim 70; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
XX are cadherins, which are membrane glycoproteins involved in cell
XX adhesion. In some situations, cell adhesion occurs at abnormal levels,
XX and these peptides can be used to modulate these levels, and thus treat
XX autoimmune diseases, inflammatory diseases and cancer, and aid wound
XX healing and implant adhesion. In addition, they can also be used to
XX facilitate drug delivery to the desired target site.

XX Sequence 6 AA;

Query Match 61.1%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 wkxxy 6
11 : 1
1 wklysy 6

RESULT 21
AAB06812 standard; peptide; 6 AA.

XX AAB06812;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 383.

XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;

XX inflammatory disease; cancer; graft rejection; cyclic.
XX Mammalia.
XX WO200026360-A1.
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are adherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
XX Sequence 6 AA;
SQ

Query Match 61.1%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxxx 6
11 :1
1 :1
Db 1 wkvtaf 6
1 :1

RESULT 22
AAB06418
ID AAB06418 standard; peptide; 7 AA.
XX
XX AAB06418;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 33.
DE
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA

XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 39; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 7 AA;
SQ

Query Match 61.1%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxxx 6
11 :1
1 :1
Db 1 wklysy 6
1 :1

RESULT 23
AAB06478
ID AAB06478 standard; peptide; 7 AA.
XX
XX AAB06478;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 109.
DE
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 43; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX Sequence 7 AA:

Query Match 61.1%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
11 1;
Db 1 wklyy 6

RESULT 24

AAB06763 ID AAB06763 standard; peptide; 7 AA.

XX AAB06763;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 334.

XX Claudin-6 modulating agent; claudin-9 modulating agent;

KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 70; Page 103; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.

XX Sequence 7 AA:

Query Match 61.1%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
11 1;

Db 1 wkvtaf 6

RESULT 25

AAB06813 ID AAB06813 standard; peptide; 7 AA.

XX AAB06813;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 384.

XX Claudin-6 modulating agent; claudin-9 modulating agent;

KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 73; Page 104; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.

XX Sequence 7 AA:

Query Match 61.1%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxy 6
11 1;
Db 1 wkvtaf 6

Search completed: January 14, 2002, 07:43:16
Job time: 427 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:35 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1b
Perfect score: 36
Sequence: 1 wxxxxxxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	55.6	6	1	US-08-338-890B-2
2	20	55.6	6	1	US-08-338-890B-3
3	20	55.6	6	2	US-08-340-208B-2
4	20	55.6	6	2	US-08-340-208B-3
5	20	55.6	6	3	US-08-997-263-2
6	20	55.6	6	3	US-08-997-263-3
7	19	52.8	6	1	US-08-338-890B-4
8	19	52.8	6	1	US-08-338-890B-5
9	19	52.8	6	2	US-08-340-208B-4
10	19	52.8	6	2	US-08-340-208B-5
11	19	52.8	6	3	US-08-997-263-4
12	19	52.8	6	3	US-08-997-263-5
13	19	52.8	7	1	US-08-321-625-86
14	19	52.8	7	1	US-08-500-956-2
15	19	52.8	7	2	US-08-495-508-3
16	19	52.8	7	4	US-09-181-083-86
17	18	50.0	5	1	US-08-240-511-1
18	18	50.0	8	2	US-08-687-219B-36
19	18	50.0	8	3	US-08-335-733D-23
20	18	50.0	8	3	US-08-335-733D-24
21	18	50.0	8	3	US-08-335-733D-25
22	17	47.2	5	1	US-08-190-802A-263
23	17	47.2	5	4	US-08-477-346-263
24	17	47.2	6	1	US-08-428-488-29
25	17	47.2	6	1	US-08-428-488-79
26	17	47.2	6	1	US-08-428-488-80
27	17	47.2	6	1	US-08-428-488-81

28	17	47.2	6	1	US-08-428-488-87	Sequence 87, Appl
29	17	47.2	6	1	US-08-428-488-89	Sequence 89, Appl
30	17	47.2	6	1	US-08-428-488-90	Sequence 90, Appl
31	17	47.2	6	1	US-08-428-488-91	Sequence 91, Appl
32	17	47.2	6	4	US-09-196-934-16	Sequence 16, Appl
33	17	47.2	7	1	US-08-428-488-83	Sequence 83, Appl
34	17	47.2	7	1	US-08-428-488-84	Sequence 84, Appl
35	17	47.2	7	1	US-08-428-488-85	Sequence 85, Appl
36	17	47.2	7	1	US-08-428-488-86	Sequence 86, Appl
37	17	47.2	7	1	US-08-428-488-88	Sequence 88, Appl
38	17	47.2	7	1	US-08-428-488-104	Sequence 104, App
39	17	47.2	7	1	US-08-428-488-105	Sequence 105, App
40	17	47.2	7	1	US-08-428-488-106	Sequence 106, App
41	17	47.2	7	1	US-08-428-488-107	Sequence 107, App
42	17	47.2	8	2	US-08-687-219B-34	Sequence 34, Appl
43	17	47.2	8	2	US-08-687-219B-37	Sequence 37, Appl
44	16	44.4	3	4	US-09-461-697-405	Sequence 405, App
45	16	44.4	4	1	US-08-079-445-3	Sequence 3, Appl1
46	16	44.4	4	1	US-07-840-077A-7	Sequence 7, Appl1
47	16	44.4	4	1	US-08-454-950-7	Sequence 7, Appl1
48	16	44.4	4	1	US-08-434-761-3	Sequence 3, Appl1
49	16	44.4	4	1	US-08-338-890B-1	Sequence 1, Appl1
50	16	44.4	4	1	US-08-454-949-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-338-890B-2
; Sequence 2, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spavevillo, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905Fris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn 38,788
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: OPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2-3, Xaa at line 72
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /notes="an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary

OTHER INFORMATION: amino group", Xaa=Orn
US-08-338-890B-2

Query Match 55.6%; Score 20; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxay 6
1111
Db 1 WXXFPY 6

RESULT 2
US-08-338-890B-3
; Sequence 3, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nult, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905Fris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1-3
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /note="an amine protecting group or a solid
; support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
; NAME/KEY: Modified-site
; LOCATION: 6, Xaa at line 100
; OTHER INFORMATION: /label=protecting2
; OTHER INFORMATION: /note="a carboxyl protecting group can be
; present or absent on the hydroxyl group", Xaa=Orn
US-08-338-890B-3

Query Match 55.6%; Score 20; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxay 6

Db 11111
1 WXXFPY 6

RESULT 3
US-08-340-208B-2
; Sequence 2, Application US/08340208B
; Patent No. 5965694
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
; TITLE OF INVENTION: Methods Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694Fris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,208B
; FILING DATE: NOV. 16, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2-3, Xaa at line 72
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /notes="an amine protecting group or a solid
; support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
US-08-340-208B-2

Query Match 55.6%; Score 20; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxay 6
11111
Db 1 WXXFPY 6

RESULT 4
US-08-340-208B-3
; Sequence 3, Application US/08340208B
; Patent No. 5965694
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
; TITLE OF INVENTION: Methods Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:


```

ADDRESSRE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 59656941is
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3, Xaa at Line 100
OTHER INFORMATION: /label=protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-340-208B-3

Query Match      55.6%; Score 20; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 wxxxay 6
      1 11111
      1 WKXFPY 6

RESULT 5
US-08-997-263-2
; Sequence 2, Application US/08997263
; Patent No. 6001960
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 60019601is
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788

```

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; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/338,890
; FILING DATE: NOV. 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2-3, Xaa at Line 72
; OTHER INFORMATION: /label=protecting1
; OTHER INFORMATION: /note="an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary
; OTHER INFORMATION: amino group", Xaa=Orn
US-08-997-263-2

Query Match      55.6%; Score 20; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 wxxxay 6
      1 11111
      1 WKXFPY 6

RESULT 6
US-08-997-263-3
; Sequence 3, Application US/08997263
; Patent No. 6001960
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanevello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 60019601is
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/338,890
; FILING DATE: NOV. 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788

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; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1-3
;   OTHER INFORMATION: /label=protecting1
;   OTHER INFORMATION: /note="an amine protecting group or a solid
;   OTHER INFORMATION: support can be present or absent on the primary
;   OTHER INFORMATION: amino group", Xaa=-Orn
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 6, Xaa at line 100
;   OTHER INFORMATION: /label=protecting2
;   OTHER INFORMATION: /note="a carboxyl protecting group can be
;   OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
; US-08-997-263-3
;
; Query Match          55.6%; Score 20; DB 3; Length 6;
; Best Local Similarity 66.7%; Pred. No. 1.6e+05;
; Matches. 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 wkxxay 6
   |||
Db 1 WKXFPY 6
;
; RESULT 7
; US-08-338-890B-4
; Sequence 4, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
;   APPLICANT: Hirschmann, Ralph
;   APPLICANT: Spanevello, Rolando
;   APPLICANT: Nutt, Ruth
;   TITLE OF INVENTION: Synthetic Somatostatin Mimics
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905r1s
;   STREET: One Liberty Place, 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19103
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: MS-DOS/WINDOWS
;   SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/338,890B
;   FILING DATE: NOV. 14, 1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Malinoski, Lynn
;   REGISTRATION NUMBER: 38,788
;   REFERENCE/DOCKET NUMBER: UPN-2040
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (215)568-3100
;   TELEFAX: (215)568-3439
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 6
;   TYPE: amino acid
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Modified-site

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; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1,2,4
;   OTHER INFORMATION: /label=protecting1
;   OTHER INFORMATION: /note="an amine protecting group or a solid
;   OTHER INFORMATION: support can be present or absent on the primary
;   OTHER INFORMATION: amino group"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 5
;   OTHER INFORMATION: /label= methyl
;   OTHER INFORMATION: /note="a methyl group is present on the amino
;   OTHER INFORMATION: group"
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 6
;   OTHER INFORMATION: /label= protecting3
;   OTHER INFORMATION: /notes="a hydroxyl protecting group can be
;   OTHER INFORMATION: present or absent on the hydroxyl group"
; US-08-338-890B-4
;
; Query Match          52.8%; Score 19; DB 1; Length 6;
; Best Local Similarity 50.0%; Pred. No. 1.6e+05;
; Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1 wkxxay 6
   |||
Db 1 WKXFPY 6
;
; RESULT 8
; US-08-338-890B-5
; Sequence 5, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
;   APPLICANT: Hirschmann, Ralph
;   APPLICANT: Spanevello, Rolando
;   APPLICANT: Nutt, Ruth
;   TITLE OF INVENTION: Synthetic Somatostatin Mimics
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;   ADDRESSSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905r1s
;   STREET: One Liberty Place, 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19103
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: MS-DOS/WINDOWS
;   SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/338,890B
;   FILING DATE: NOV. 14, 1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Malinoski, Lynn
;   REGISTRATION NUMBER: 38,788
;   REFERENCE/DOCKET NUMBER: UPN-2040
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (215)568-3100
;   TELEFAX: (215)568-3439
;   INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 6
;   TYPE: amino acid
;   TOPOLOGY: circular
;   MOLECULE TYPE: peptide
;   FEATURE:
;   NAME/KEY: Modified-site

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LOCATION: 2, 4 /label- protecting1
OTHER INFORMATION: /note- "an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label- methyl
OTHER INFORMATION: /note- "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label- protecting3
OTHER INFORMATION: /note- "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-338-890B-5

Query Match 52.8%; Score 19; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wkxxay 6
1 1
1 1
Db 1 WKVKFY 6

RESULT 9
US-08-340-208B-4
; Sequence 4, Application US/08340208B
; Patent No. 5965694
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,208B
; FILING DATE: NOV. 16, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; TELECOMMUNICATION INFORMATION: UPN-2041
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1,2,4
; OTHER INFORMATION: /label- protecting1
; OTHER INFORMATION: /note- "an amine protecting group or a solid

OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label- methyl
OTHER INFORMATION: /note- "a methyl group is present on the amino
OTHER INFORMATION: group"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label- protecting3
OTHER INFORMATION: /note- "a hydroxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-340-208B-4

Query Match 52.8%; Score 19; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wkxxay 6
1 1
1 1
Db 1 WKVKFY 6

RESULT 10
US-08-340-208B-5
; Sequence 5, Application US/08340208B
; Patent No. 5965694
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; TITLE OF INVENTION: Somatostatin Mimics And Synthetic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694aris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,208B
; FILING DATE: NOV. 16, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; TELECOMMUNICATION INFORMATION: UPN-2041
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2, 4
; OTHER INFORMATION: /label- protecting1
; OTHER INFORMATION: /note- "an amine protecting group or a solid
; OTHER INFORMATION: support can be present or absent on the primary
; OTHER INFORMATION: amino group"

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: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /label= methyl
: OTHER INFORMATION: /note= "a methyl group is present on the amino
: OTHER INFORMATION: group"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: /label= protecting3
: OTHER INFORMATION: /note= "a hydroxyl protecting group can be
: OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-208B-5

Query Match          52.8%; Score 19; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wkxay 6
   1 1
   1 1
Db 1 WKVKFY 6

RESULT 11
US-08-997-263-4
: Sequence 4, Application US/08997263
: Patent No. 6001960
: GENERAL INFORMATION:
: APPLICANT: Hirschmann, Ralph
: APPLICANT: Spanevello, Rolando
: APPLICANT: Nutt, Ruth
: TITLE OF INVENTION: Synthetic Somatostatin Mimics
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960-15
: STREET: One Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/WINDOWS
: SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,263
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/338,890
: FILING DATE: NOV. 14, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Malinoski, Lynn
: REGISTRATION NUMBER: 38,788
: REFERENCE/DOCKET NUMBER: UPN-2040
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215)568-3100
: TELEFAX: (215)568-3439
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1,2,4
: OTHER INFORMATION: /label= protecting1
: OTHER INFORMATION: /note= "an amine protecting group or a solid
: OTHER INFORMATION: support can be present or absent on the primary
: OTHER INFORMATION: amino group"
: FEATURE:

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: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /label= methyl
: OTHER INFORMATION: /note= "a methyl group is present on the amino
: OTHER INFORMATION: group"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: /label= protecting3
: OTHER INFORMATION: /note= "a hydroxyl protecting group can be
: OTHER INFORMATION: present or absent on the hydroxyl group"
US-08-997-263-4

Query Match          52.8%; Score 19; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wkxay 6
   1 1
   1 1
Db 1 WKVKFY 6

RESULT 12
US-08-997-263-5
: Sequence 5, Application US/08997263
: Patent No. 6001960
: GENERAL INFORMATION:
: APPLICANT: Hirschmann, Ralph
: APPLICANT: Spanevello, Rolando
: APPLICANT: Nutt, Ruth
: TITLE OF INVENTION: Synthetic Somatostatin Mimics
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960-15
: STREET: One Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS/WINDOWS
: SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,263
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/338,890
: FILING DATE: NOV. 14, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Malinoski, Lynn
: REGISTRATION NUMBER: 38,788
: REFERENCE/DOCKET NUMBER: UPN-2040
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215)568-3100
: TELEFAX: (215)568-3439
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6
: TYPE: amino acid
: TOPOLOGY: circular
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 2, 4
: OTHER INFORMATION: /label= protecting1
: OTHER INFORMATION: /note= "an amine protecting group or a solid
: OTHER INFORMATION: support can be present or absent on the primary
: OTHER INFORMATION: amino group"
: FEATURE:

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NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: /label= methyl
 OTHER INFORMATION: /note= "a methyl group is present on the amino
 OTHER INFORMATION: group"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /label= protecting3
 OTHER INFORMATION: /note= "a hydroxyl protecting group can be
 OTHER INFORMATION: present or absent on the hydroxyl group"
 US-08-997-263-5

Query Match 52.8%; Score 19; DB 3; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1.6e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxxy 6
 || |
 DB 1 WKVXY 6

RESULT 13

US-08-321-625-06
 ; Sequence 86, Application US/08321625
 ; Patent No. 5639860

GENERAL INFORMATION:

APPLICANT: TANAKA, Takeo
 APPLICANT: MORISHITA, Yoshikazu
 APPLICANT: MAKINO, Mika
 APPLICANT: CHIBA, Shigeru
 APPLICANT: KAMAMOTO, Isao
 APPLICANT: TSUKUDA, Eiji
 APPLICANT: YOSHIDA, Mayumi
 APPLICANT: BANDO, Chieko
 APPLICANT: YAMAGUCHI, Kazuo
 APPLICANT: MATSUDA, Yuzuru
 TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
 NUMBER OF SEQUENCES: 92
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
 STREET: 1300 NO. 5639860th Seventeenth Street, Suite 1800
 CITY: Arlington
 STATE: VA
 COUNTRY: USA
 ZIP: 22209

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/321,625
 FILING DATE: 12-OCT-1994
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: TERRY, David T.
 REGISTRATION NUMBER: 20,178
 REFERENCE/DOCKET NUMBER: 506.32366PX1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-312-6600
 TELEFAX: 703-312-6666

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal

US-08-321-625-86

Query Match 52.8%; Score 19; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.6e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxa 5
 || |
 DB 3 WKCTA 7

RESULT 14

US-08-500-956-2
 ; Sequence 2, Application US/08500956
 ; Patent No. 5650269

GENERAL INFORMATION:

APPLICANT: STEFAS, ELIE
 APPLICANT: RUCHETON, MARCEL
 APPLICANT: GRAFAND, HUBERT
 TITLE OF INVENTION: METHOD FOR DETECTING VIRAL COMPOUNDS
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN, IP GROUP OF
 ADDRESSEE: PILLSBURY MADISON &
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/500,956
 FILING DATE: 09-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B J
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 60649/219388
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/861-3000
 TELEFAX: 202/822-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-500-956-2

Query Match 52.8%; Score 19; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.6e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxa 5
 || |
 DB 2 WKSDA 6

RESULT 15

US-08-495-508-3
 ; Sequence 3, Application US/08495508
 ; Patent No. 5859213

GENERAL INFORMATION:

APPLICANT: STEFAS, ELIE
 APPLICANT: RUCHETON, MARCEL

APPLICANT: GRAAFLAND, HUBERT
TITLE OF INVENTION: AQUEOUS PROTEIN COMPOSITION,
TITLE OF INVENTION: GLYCOPROTEIN CONTAINED THEREIN, PREPARATION METHOD
TITLE OF INVENTION: THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,508
FILING DATE: 23-OCT-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/01399
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00143
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 219390/LA-112117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-495-508-3

Query Match 52.8%; Score 19; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
|||
Db 2 WKSDA 6

RESULT 16
US-09-181-083-86
Sequence 86, Application US/09181083
Patent No. 6194195
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Ei-ji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:

ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. 6194195th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,083
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-181-083-86

Query Match 52.8%; Score 19; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
|||
Db 3 WKGTA 7

RESULT 17
US-08-240-511-1
Sequence 1, Application US/08240511
Patent No. 5643722
GENERAL INFORMATION:
APPLICANT: ROTHSCCHILD, Kenneth J.
APPLICANT: SONAR, Sanjay M.
TITLE OF INVENTION: METHODS FOR THE DETECTION AND ISOLATION OF PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,511
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 16865-0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-240-511-1

Query Match 50.0%; Score 18; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
DB 1 WKYVA 5

RESULT 18

US-08-687-219B-36
Sequence 36, Application US/08687219B
Patent No. 5985341

GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVE & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: Beridgc, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: MPB 38526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-36

Query Match 50.0%; Score 18; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 kxxayxg 8
DB 1 KASSYLG 7

RESULT 19

US-08-335-733D-23
Sequence 23, Application US/08335733D
Patent No. 6042831

GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botz, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCY-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-335-733D-23

Query Match 50.0%; Score 18; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxay 6
DB 3 WRSELY 8

RESULT 20

US-08-335-733D-24
; Sequence 24, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-24

Query Match 50.0%; Score 18; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxay 6
1: |
Db 2 WRSELY 7

RESULT 21
US-08-335-733D-25
; Sequence 25, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.

ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-25

Query Match 50.0%; Score 18; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxay 6
1: |
Db 1 WRSELY 6

RESULT 22
US-08-190-802A-263
; Sequence 263, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-190-802A-263

Query Match 47.2%; Score 17; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxa 5
1: 1
Db 1 WRTAA 5

RESULT 23
US-08-477-346-263
Sequence 263, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: WRTAA peptide
US-08-477-346-263

Query Match 47.2%; Score 17; DB 4; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxa 5
1: 1
Db 1 WRTAA 5

RESULT 24
US-08-428-488-29
Sequence 29, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-428-488-29

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ayxq 8
1: 1
Db 1 AYAG 4

RESULT 25
US-08-428-488-79
Sequence 79, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Burns, Doane, Swecker & Mathis
3 STREET: P.O. Box 1404
4 CITY: Alexandria
5 STATE: Virginia
6 COUNTRY: United States
7 ZIP: 22113-1404
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: PatentIn Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/428,488
15 FILING DATE: 27-Apr-1995
16 CLASSIFICATION: 514
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Baumeister, Mary Katherine
19 REGISTRATION NUMBER: 26,254
20 REFERENCE/DOCKET NUMBER: 028724-087
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (703) 836-6620
23 TELEFAX: (703) 836-2021
24 INFORMATION FOR SEQ ID NO: 79:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 6 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: peptide
31 FEATURE:
32 NAME/KEY: Modified-site
33 LOCATION: 1
34 OTHER INFORMATION: /note= "Position 1 = Nicotinoyl-Ala."
35 FEATURE:
36 NAME/KEY: Modified-site
37 LOCATION: 3
38 OTHER INFORMATION: /note= "Position 3 = D-Ala."
39 FEATURE:
40 NAME/KEY: Modified-site
41 LOCATION: 6
42 OTHER INFORMATION: /note= "Position 6 = D-Leu-Cholesteryl ester."
43 US-08-428-488-79

Query Match 47.28; Score 17; DB 1; Length 6;
Best Local Similarity 75.08; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ayyg 8
|||
Db 1 AYAG 4

Search completed: January 14, 2002, 07:41:36
Job time: 457 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:21 ; Search time 43.28 seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1c
Perfect score: 35
Sequence: 1 wkxxsfxg 8

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	51.4	7	2	S33244	neuromodulatory pe
2	18	51.4	7	2	S33246	neuromodulatory pe
3	16	45.7	8	2	A38887	T-cell receptor ga
4	15	42.9	7	2	S33245	neuromodulatory pe
5	15	42.9	8	2	A42057	fibroblast growth
6	13	37.1	8	2	S13661	polygalacturonase
7	12	34.3	5	2	PT0308	Ig heavy chain CRD
8	12	34.3	6	2	S66195	alcohol dehydrogen
9	12	34.3	6	2	A31263	dihydrofolate redu
10	12	34.3	6	2	B31263	cerebellar degener
11	12	34.3	6	2	B35640	variant surface gl
12	12	34.3	8	2	C61512	variant surface gl
13	12	34.3	3	2	D61512	bradykinin-potentl
14	11	31.4	3	2	F37196	RPCH-related neuro
15	11	31.4	4	2	A34562	T-cell receptor be
16	11	31.4	4	2	B53284	T-cell receptor be
17	11	31.4	4	2	PT0661	cholecystokinin-5
18	11	31.4	5	2	A32516	neuropeptide - sea
19	11	31.4	5	2	A60803	gut pentapeptide -
20	11	31.4	5	2	JH0253	bradykinin-potentl
21	11	31.4	5	2	G37196	Ig heavy chain CRD
22	11	31.4	5	2	PT0281	T-cell receptor be
23	11	31.4	5	2	PT0729	T-cell receptor be
24	11	31.4	5	2	PT0580	T-cell receptor be
25	11	31.4	6	2	B34835	dnad protein - pse
26	11	31.4	6	2	A61068	locustakinin - mig
27	11	31.4	6	2	PT0629	T-cell receptor be
28	11	31.4	6	2	PT0532	T-cell receptor be
29	11	31.4	6	2	PT0519	T-cell receptor be

30	11	31.4	6	2	PT0637	T-cell receptor be
31	11	31.4	6	2	PT0641	T-cell receptor be
32	11	31.4	6	2	PT0726	T-cell receptor be
33	11	31.4	6	2	F41946	T-cell receptor ga
34	11	31.4	6	2	PD0028	pev-kinin 2 - pena
35	11	31.4	6	4	I79564	hypothetical TCL3
36	11	31.4	7	2	S21230	dermorphin (Trp-4,
37	11	31.4	7	2	A58512	venom heptapeptide
38	11	31.4	7	2	A61081	tryptophyllin, bas
39	11	31.4	7	2	S57274	trilacylglycerol 11
40	11	31.4	7	2	S09652	hypothetical prote
41	11	31.4	7	2	PN0649	alpha-dextrin endo
42	11	31.4	7	2	PO0727	H2 class I protein
43	11	31.4	7	2	H33058	180K exoantigen -
44	11	31.4	7	2	S33567	tubulin beta-3 cha
45	11	31.4	7	2	E48394	glycoprotein compo
46	11	31.4	7	2	PH1602	Ig H chain V-D-J r
47	11	31.4	7	2	E33932	Ig mu chain D regl
48	11	31.4	7	2	PT0526	T-cell receptor be
49	11	31.4	7	2	PT0628	T-cell receptor be
50	11	31.4	7	2	PT0642	T-cell receptor be

ALIGNMENTS

RESULT 1
S33244 neuromodulatory peptide Wwamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 51.4%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxs 5
|| |
Db 1 WKEMS 5

RESULT 2
S33246 neuromodulatory peptide Wwamide-3 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33246
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 51.4%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxs 5
|| |

Db 1 WKQMS 5

RESULT 3
A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <NHE>
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 45.7%; Score 16; DB 2; Length 8;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 wkxxsf 6
Db 3 WDSSGF 8

RESULT 4
S33245
neuromodulatory peptide Wwamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A:Reference number: S33244; MUID:93265912
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match
Best Local Similarity 42.9%; Score 15; DB 2; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxsf 5
Db 1 WREMS 5

RESULT 5
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor r
A:Reference number: A42057; MUID:92107200
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <MER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match
42.9%; Score 15; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 sfxg 8
Db 5 SFLG 8

RESULT 6
S13661
polygalacturonase (EC 3.2.1.15) isoform pg2 - fungus (Sclerotinia sclerotiorum) (frag
N:Alternate names: endopolylgalacturonase; pectin depolymerase; pectinase
C:Species: Sclerotinia sclerotiorum
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S13661
R:Waksman, G.; Keon, J.P.R.; Turner, G.
Biochim. Biophys. Acta 1073, 43-48, 1991
A:Title: Purification and characterization of two endopolylgalacturonases from Sclerot
A:Reference number: S13661; MUID:91120822
A:Accession: S13661
A:Molecule type: protein
A:Residues: 1-8 <WAK>
C:Function:
A:Description: involved in pectin degradation
C:Keywords: glycosidase; hydrolase

Query Match
Best Local Similarity 37.1%; Score 13; DB 2; Length 8;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 sfxg 8
Db 5 TFSG 8

RESULT 7
PT0308
Ig heavy chain CDR3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 34.3%; Score 12; DB 2; Length 5;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
Db 2 WE 3

RESULT 8
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fra
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltnyst, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases
nzyme.
A:Reference number: S66191; MUID:95331382

A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HCE>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 5 WE 6

RESULT 9
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 3 WE 4

RESULT 10
B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886
A:Accession: B31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 3 WE 4

RESULT 11
B35640
cerebellar degeneration-related protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993

C:Accession: B35640
R:Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal
A:Reference number: A35640; MUID:90222173
A:Accession: B35640
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6 <CHE>

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 2 WE 3

RESULT 12
C61512
variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C:Accession: C61512
R:Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te
A:Reference number: A61512; MUID:81172836
A:Accession: C61512
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Keywords: glycoprotein

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 1 WE 2

RESULT 13
D61512
variant surface glycoprotein MITat 1.6 - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C:Accession: D61512
R:Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te
A:Reference number: A61512; MUID:81172836
A:Accession: D61512
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Keywords: glycoprotein

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
DB 1 WE 2

RESULT 14

F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C>Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196
R:Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557
A:Accession: F37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 3 W 3

RESULT 15
A34626
RPCII-related neuropeptide - ferruginous spindle
C:Species: Fustinus ferrugineus (ferruginous spindle)
C>Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuraki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:9019762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 4 W 4

RESULT 16
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and
A:Reference number: A53284; MUID:91342695
A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60738)
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 2 W 2

RESULT 17
PT0661
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0661
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEED>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 3 W 3

RESULT 18
A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A:Reference number: A32516; MUID:87153871
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SHI>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
Db 2 W 2

RESULT 19
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Iu-Arg-Tyr-NH-2, a novel neuropeptide from sea anemone
A:Reference number: A60803; MUID:88222764

A:Accession: A60803
A:Molecule type: Protein
A:Residues: 1-5 <GRA>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 5 w 5

RESULT 20

gnt pentapeptide - Japanese eel
JH0253
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253

R:Usaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113

A:Accession: JH0253
A:Molecule type: Protein
A:Residues: 1-5 <UES>

A:Experimental source: gut
A:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
and of the circular muscle of the gastro-intestinal junction.

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 21

bradykinin-potentiating peptide 7 - island jarraraca
G37196
C:Species: Bothrops insularis (Island Jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196

R:Cluiter, A.C.O.; Vleijer, C.A.; Gijljo, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557

A:Accession: G37196
A:Status: Preliminary
A:Molecule type: Protein
A:Residues: 1-5 <CIN>

C:Keywords: pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 22

PT0281

Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337

A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; Immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 4 w 4

RESULT 23

PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0640; PT0685; PT0729

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601

A:Accession: PT0640
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>

A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE3>

A:Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
A:Accession: PT0580
A:Status: translation not shown

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 5 w 5

RESULT 24

PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0580
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
Db 4 W 4

RESULT 25

B34835
dnaa protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A:Reference number: A34835; MUID:90160310
A:Accession: B34835
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-6 <YEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PTD:g151421
C:Keywords: DNA binding

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
Db 6 W 6

Search completed: January 14, 2002, 07:44:22
Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds
(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1c
Perfect score: 35
Sequence: 1 wkxxxxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	51.4	7 1 WMA2_ACHFU	P35920 aechatina fu
2	18	51.4	7 1 WMA3_ACHFU	P35921 aechatina fu
3	15	42.9	7 1 WMA1_ACHFU	P35919 aechatina fu
4	11	31.4	5 1 BPP7_BOTIN	P30425 botchrops in
5	11	31.4	5 1 TPIS_CANFA	P54714 canis famill
6	11	31.4	5 1 UF01_MOUSE	P38639 mus musculu
7	11	31.4	6 1 LOK1_LOCOMI	P41491 locusta mig
8	11	31.4	8 1 ACT1_THUAL	P18691 thunnus alb
9	11	31.4	8 1 AKH6_GRYBI	P14086 gryllus bim
10	11	31.4	8 1 AKH_LIBAU	P25418 libellula a
11	11	31.4	8 1 AKH_MELML	P25423 melolontha
12	11	31.4	8 1 AKH_TABAT	P14595 tabanus atr
13	11	31.4	8 1 CCKK_MACEU	P30369 macropus eu
14	11	31.4	8 1 HTP1_PERAM	P04548 periplaneta
15	11	31.4	8 1 HTP2_PERAM	P05419 tenebrio mo
16	11	31.4	8 1 HTP_TENMO	P25419 tenebrio mo
17	11	31.4	8 1 LCK1_LEUMA	P21140 leucophaea
18	11	31.4	8 1 LCK2_LEUMA	P21141 leucophaea
19	11	31.4	8 1 LCK3_LEUMA	P21142 leucophaea
20	11	31.4	8 1 LCK4_LEUMA	P21143 leucophaea
21	11	31.4	8 1 LCK5_LEUMA	P19987 leucophaea
22	11	31.4	8 1 LCK6_LEUMA	P19988 leucophaea
23	11	31.4	8 1 LCK7_LEUMA	P19989 leucophaea
24	11	31.4	8 1 LCK8_LEUMA	P19990 leucophaea
25	11	31.4	8 1 PLP_BRANA	P81707 brassica na
26	11	31.4	8 1 RPCH_PANBO	P08939 pandanus ho
27	10	28.6	5 1 ALI4_CARMA	P81817 carcinus ma
28	10	28.6	5 1 MSLC_SALTY	P35446 salmoneila
29	10	28.6	8 1 ALI5_CARMA	P81818 carcinus ma
30	10	28.6	8 1 ALI7_CARMA	P81820 carcinus ma
31	10	28.6	8 1 ALI8_CARMA	P81821 carcinus ma
32	10	28.6	8 1 ALI3_CYPPO	P81854 cydia pomon
33	10	28.6	8 1 ALI4_CALVO	P41840 calliphora

ALIGNMENTS

RESULT 1	WMA2_ACHFU	STANDARD:	PRT:	7 AA.
ID	WMA2_ACHFU			
AC	P35920;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1994 (Rel. 30, Last annotation update)			
DE	WMA2IDE-2.			
OS	Achatina fulica (Giant African snail).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;			
OC	Achatinacea; Achatinidae; Achatina.			
OX	NCBI_TaxID=6530;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=ganglion;			
RX	MEDLINE=93265912; PubMed=8495720;			
RA	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;			
RT	"Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from			
RL	ganglia of the African giant snail, Achatina fulica.";			
KW	FEBS Lett. 323:104-108(1993).			
FT	Neuropeptide; Amidation.			
MOD_RES	7			
SEQUENCE	7 AA: 964 MW: 7362DSB686D32310 CRC64:			
Query Match	51.4%;	Score 18:	DB 1:	Length 7;
Best Local Similarity	60.0%;	Pred. No. 1e+05:		
Matches	3;	Conservative	0;	Mismatches
			2;	Indels
				Gaps
				0;
QY	1 wkxxxx 5			
	11			
	11			
DB	1 WKXMS 5			
RESULT 2	WMA3_ACHFU	STANDARD:	PRT:	7 AA.
ID	WMA3_ACHFU			
AC	P35921;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1994 (Rel. 30, Last annotation update)			
DE	WMA3IDE-3.			
OS	Achatina fulica (Giant African snail).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;			
OC	Achatinacea; Achatinidae; Achatina.			
OX	NCBI_TaxID=6530;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=ganglion;			
RX	MEDLINE=93265912; PubMed=8495720;			
RA	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;			

RT "Mwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.",
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 51.4%; Score 18; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxs 5
1 1
Db 1 WKEMS 5

RESULT 3
WMA1_ACHFV STANDARD; PRT; 7 AA.

AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_Taxid=6530;
RN [1]
RP SEQUENCE.

RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Mwakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR: S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD_RES
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 42.9%; Score 15; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxs 5
1 1
Db 1 WKEMS 5

RESULT 4
BPP7_BOTIN STANDARD; PRT; 5 AA.

AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_Taxid=8723;
RN [1]
RP SEQUENCE.

RC TISSUE=Venom;
AC MEDLINE=90351557; PubMed=2386615;

RA Cintira A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1 w 3
Db 3 W 3

RESULT 5
TPIS_CANFA STANDARD; PRT; 5 AA.

ID TPIS_CANFA
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN TPIL.

OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE.

RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-

CC ACETONE PHOSPHATE.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro: IPR000652; Trioseph. isomase.

DR PROSITE: PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER
FT NON_TER
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 fxg 8
1 1
Db 1 FVG 3

RESULT 6
UF01_MOUSE STANDARD; PRT; 5 AA.

ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)

01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID:10090;
[1]
SEQUENCE:
RC TISSUE=Fibroblast;
RC MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
-1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
Db 1 W 1

RESULT 7
ID LOK1_LOCM1 STANDARD; PRT; 6 AA.
AC PA1491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridoidea; Acrididae; Locusta.
NCBI_TaxID:7004;
[1]
SEQUENCE:
RC TISSUE=Corpora cardiaca;
RC MEDLINE=92262851; PubMed=1585017;
RX Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
-1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
CC TUBULES.
CC PIR: A61068; A61068.
DR Neuropeptide; Amidation.
KW MOD_RES 6 6
FT SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
Db 5 W 5

RESULT 8
ACI_THUAL STANDARD; PRT; 8 AA.
ID ACI_THUAL

AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE ANGIOTENSIN-CONVERTING ENZYME INHIBITOR
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI_TaxID=8236;
[1]
SEQUENCE:
RC TISSUE=Muscle;
RC MEDLINE=88326322; PubMed=3415688;
RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
Db 6 W 6

RESULT 9
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus.
NCBI_TaxID=6999, 7007;
[1]
SEQUENCE:
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426615;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
[2]
SEQUENCE:
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=99145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
-1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / RPTH / RPCH FAMILY.
CC PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1
FT PIRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 8 W 8

RESULT 10

AKH_LIBAU STANDARD; PRT; 8 AA.
ID AKH_LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly."
RT Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
CC PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 8 W 8

RESULT 11

AKH_MEML STANDARD; PRT; 8 AA.
ID AKH_MEML
AC P23423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer).
OC Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]

RP SEQUENCE.
RC SPECIES=Melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;

RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."
RT Biochem. J. 275:671-677(1991).
RN [2]

RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."
RT Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
CC PIR: S15422; S15422.
DR PIR: S21663; S21663.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 8 W 8

RESULT 12

AKH_TABAT STANDARD; PRT; 8 AA.
ID AKH_TABAT
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I) (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."
RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1. Flight.
KW Neuropeptide; Amidation; Filiglit.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

RESULT 13
CCKN_MACEU STANDARD; PRT: 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLECYSTOKININ (CCK).
CN CCK.
OS Macropus eugenii (Tammur wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.

RT TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
FA Fan Z. W., Eng J., Shaw G., Yalow R. S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
maiusupials";
RL Peptides 9:429-431(1988).
-1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR PIR: PQ0012; PQ0012.
DR InterPro: IPR001651; Gastrin.

DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA6837876B5A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 14
HTF1_PERAM STANDARD; PRT: 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-1) (PERIPLANETIN CC-1)
DE (PER-CAN-1) (LED-CC-1) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach).
OS Leptoclausa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.

RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Wilten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.

RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.

RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RT beetle and the American cockroach are identical";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.

RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L., Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphodrhina portenosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).

CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05169; A05169.

DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

RESULT 15
HTF2_PERAM STANDARD; PRT: 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
DE (PEA-GAH-II) (LED-CC-II) (HYPERREHALOSAEMIC NEUROPEPTIDE II).
OS Periplaneta americana (American cockroach),
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattidae; Blattellidae; Periplaneta.
ON NCBI_Taxid=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rhinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardiocceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Keilner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rhinehart K.L., Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE AKH / HATH / RPCH FAMILY).
CC -1- SIMILARITY: BELONGS TO THE AKH / HATH / RPCH FAMILY.
DR PIR; A05170; A05170.
DR PIR; S08996; S08996.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
HTF_TENMO
ID HTF_TENMO STANDARD; PRT; 8 AA.
AC P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERREHALOSAEMIC FACTOR (HOTH) (HYPERREHALOSAEMIC NEUROPEPTIDE).
OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebrio.
ON NCBI_Taxid=7067, 7075;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; PubMed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrehalosemic neuropeptide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:455-459(1990).
CC -1- FUNCTION: HYPERREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HATH / RPCH FAMILY.
DR PIR; A43976; A43976.
DR PIR; B43976; B43976.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
Db 8 w 8
RESULT 17
LCK1_LEUMA
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
ON NCBI_Taxid=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyolotroplins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDD76A CRC64;

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Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 7 w 7

RESULT 18
LCK2_LEUMA          STANDARD; PRT; 8 AA.
ID LCK2_LEUMA
AC P21141:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
   from Leucophaea maderae: members of a new family of
   Cephalomyotroplins."
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
   ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 7 w 7

RESULT 19
LCK3_LEUMA          STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC P21142:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
   from Leucophaea maderae: members of a new family of
   Cephalomyotroplins."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
   ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
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SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 7 w 7

RESULT 20
LCK4_LEUMA          STANDARD; PRT; 8 AA.
ID LCK4_LEUMA
AC P21143:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
   from Leucophaea maderae: members of a new family of
   Cephalomyotroplins."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
   ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD8A CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 7 w 7

RESULT 21
LCK5_LEUMA          STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
   myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
   ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
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CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C86588 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 22
LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR: JS0316; JS0316.
KM Neuropeptide; Amidation.
FT MOD_RES 1
PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8
AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 23
LCK7_LEUMA STANDARD; PRT; 8 AA.
ID LCK7_LEUMA
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;

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RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinins VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0317; JS0317.
KM Neuropeptide; Amidation.
FT MOD_RES 8
AMIDATION.
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CCDC76A CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 24
LCK8_LEUMA STANDARD; PRT; 8 AA.
ID LCK8_LEUMA
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinins VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0318; JS0318.
KM Neuropeptide; Amidation.
FT MOD_RES 8
AMIDATION.
SQ SEQUENCE 8 AA; 902 MW; 736365A5B9CAADD8 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 25
PLP_BRANA STANDARD; PRT; 8 AA.
ID PLP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLASTIDIAL LIPID-ASSOCIATED PROTEIN (FRAGMENT).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC euruside II; Brassicales; Brassicaceae; Brassica.
 OK NCBI_TaxID:3708;
 RN (1)
 RP SEQUENCE.
 RC STRAIN-CV. TOPAZ; TISSUE:Tapetum;
 RX MEDLINE:99349136; PubMed:10420651;
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
 RA Murphy D.J.;
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the
 RT pollen coat of Brassica napus.";
 RL Planta 208:588-598(1999).
 CC -1- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
 CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.
 CC -1- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.
 FT NON_TER 8
 SQ SEQUENCE 8 AA: 989 MW: 9D7B1AA452CA042 CRC64;

Query Match 31.48; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 DB 8 W 8

Search completed: January 14, 2002, 07:52:04
 Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:45 : Search time 80.15 Seconds
(without alignments)
14.600 Million cell updates/sec

Title: 09-185908-1c
Perfect score: 35
Sequence: 1 wkxxsfxy 8

Scoring table: BIOSUM62
Gap 10.0, Gapext 0.5
Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 50 summaries

- Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	45.7	7	8	Q95945	Q95945 saccharomyc
2	16	45.7	8	11	Q62721	Q62721 rattus norv
3	14	40.0	8	6	P82929	P82929 bos taurus
4	12	34.3	8	2	O09258	O09258 synecococc
5	12	34.3	8	11	P70243	P70243 mus musculu
6	12	34.3	8	11	Q9QVD3	Q9QVD3 rattus sp.
7	11	31.4	6	13	P82096	P82096 litorea rub
8	11	31.4	7	10	O49223	O49223 glycine max
9	11	31.4	7	13	P82065	P82065 litorea bu
10	11	31.4	8	2	O85406	O85406 coxiella bu
11	11	31.4	8	4	O15888	O15888 homo sapien
12	11	31.4	8	4	O15890	O15890 homo sapien
13	11	31.4	8	5	O9VRD2	O9VRD2 drosophila
14	11	31.4	8	5	P82685	P82685 periplaneta
15	11	31.4	8	5	P82686	P82686 periplaneta
16	11	31.4	8	5	P82687	P82687 periplaneta
17	11	31.4	8	5	P82688	P82688 periplaneta
18	11	31.4	8	5	P82689	P82689 periplaneta
19	11	31.4	8	6	O02831	O02831 oryctolagus

20	11	31.4	8	6	Q9TRV3	Q9TRV3 sus sp. ins
21	11	31.4	8	8	Q9TD02	Q9TD02 terranatos
22	11	31.4	8	8	Q9T4Y2	Q9T4Y2 asterlina pe
23	11	31.4	8	11	O35835	O35835 rattus norv
24	11	31.4	8	11	P82598	P82598 rattus norv
25	11	31.4	8	11	O9ETI8	O9ETI8 mus spreus
26	11	31.4	8	11	O9ETI7	O9ETI7 mus caroll
27	11	31.4	8	11	O9ETI6	O9ETI6 mesocricetu
28	11	31.4	8	11	Q99MN0	Q99MN0 mus musculu
29	11	31.4	8	13	P79940	P79940 xenopus lae
30	11	31.4	8	13	Q98TU5	Q98TU5 xenopus lae
31	10	28.6	7	2	O07354	O07354 synecococc
32	10	28.6	8	2	O9R5R0	O9R5R0 shigella dy
33	10	28.6	8	2	P87225	P87225 saccharomyc
34	10	28.6	8	4	Q9HCQ0	Q9HCQ0 homo sapien
35	9	25.7	8	8	Q9GD00	Q9GD00 mascola mad
36	9	25.7	8	11	Q9QVF4	Q9QVF4 rattus sp.
37	8	22.9	8	2	O56759	O56759 xanthobacte
38	8	22.9	8	2	O9R9E0	O9R9E0 bacillus su
39	8	22.9	8	5	Q9TWH6	Q9TWH6 perlinereis
40	8	22.9	8	6	Q9TRX8	Q9TRX8 bos taurus
41	7	20.0	7	4	O15903	O15903 homo sapien
42	7	20.0	7	8	O98866	O98866 spinacia ol
43	7	20.0	8	2	O56140	O56140 streptococc
44	7	20.0	8	2	O45889	O45889 clostridium
45	7	20.0	8	2	Q9S6D5	Q9S6D5 escherichia
46	7	20.0	8	2	Q9S443	Q9S443 pseudomonas
47	7	20.0	8	2	Q9R5L7	Q9R5L7 clostridium
48	7	20.0	8	4	O15898	O15898 homo sapien
49	7	20.0	8	7	O95213	O95213 oryctolagus
50	7	20.0	8	8	Q34909	Q34909 locusta mlg

ALIGNMENTS

RESULT 1
Q95945 ID AC Q95945 PRELIMINARY: PRT: 7 AA.
AC Q95945;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSIDE INTRON 5 (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81069885; PubMed=6254986;
RX Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL: V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 7 AA: 859 MW: 7587232362DC460 CRC64;

Query Match 45.7%; Score 16; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
Db 4 wk 5
RESULT 2

Q62721
ID 062721 PRELIMINARY; PRT; 8 AA.
AC 062721
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT Prohibitin-encoding genes."
RL Gene 158:291-294(1995).
DR EMBL, U17178; AAA86692.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 45.7%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
DB 6 wk 7
RESULT 3
P82929 PRELIMINARY; PRT; 8 AA.
AC P82929
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
RT of the full complement ribosomal proteins present."
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 40.0%; Score 14; DB 6; Length 8;
Best Local Similarity 33.3%; Pred. No. 4.7e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxsf 6
DB 2 WCLTF 7
RESULT 4
009258

ID 009258 PRELIMINARY; PRT; 8 AA.
AC 009258;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NTFH (FRAGMENT).
GN NTFH.
OS Synecococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxId=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RA Chen H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF001780; AAC33369.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 sfxxg 8
DB 5 AFYG 8

RESULT 5
P70243 PRELIMINARY; PRT; 8 AA.
ID P70243
AC P70243;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Ophoff R.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL, X98325; CAA66969.1; -.
KW Calcium channel.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
DB 7 WQ 8

RESULT 6
Q9QVD3 PRELIMINARY; PRT; 8 AA.
ID Q9QVD3
AC Q9QVD3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCB1_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takaya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M., Matsunabe Y., Ozaki S., Yoshida M., Koga T.,
RA "Putative Inositol 1,4,5-trisphosphate binding proteins in rat brain
cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA; 1047 MW; D72415BB06C37041 CRC64;

Query Match 34.4%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
DB 3 WO 4

RESULT 7
P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCB1_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RT Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 8
O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCB1_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, ESSEX; TISSUE=ROOTS;
RX MEDLINE=91367679; PubMed=1891369;
```

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RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins.";
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047050; AAC03556.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 31.4%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 9
P82065 PRELIMINARY; PRT; 7 AA.
AC P82065;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE TRYPHOXYLLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCB1_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1
FT MOD_RES 7
FT MOD_RES 1
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 4 W 4

RESULT 10
O85406 PRELIMINARY; PRT; 8 AA.
AC O85406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
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OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NINE MILE PHASE I;
RA Williams H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
   Coxiella burnetii."
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 4 w 4

RESULT 11
ID 015888 PRELIMINARY; PRT; 8 AA.
AC 015888.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL, L32069; AAA73878.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 12
ID 015890 PRELIMINARY; PRT; 8 AA.
AC 015890.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
```

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RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL, L32083; AAA73880.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 975 MW; 605EAC65BEA5A2D3 CRC64;

Query Match 31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 1 w 1

RESULT 13
ID 09VRD2 PRELIMINARY; PRT; 8 AA.
AC 09VRD2.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AF03569; AAF0870.1; -.
DR Flybase: FBgn0040648; CG11666.
SQ SEQUENCE 8 AA; 1062 MW; ED1B5B044004376 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 5; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 2 w 2

RESULT 14
P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=9978;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE:98010462; PubMed-9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
RL -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropetide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 5; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 7 w 7

RESULT 15
P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=9978;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE:98010462; PubMed-9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
```

```
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
RL -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropetide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 5; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 7 w 7

RESULT 16
P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=9978;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE:98010462; PubMed-9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
RL -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropetide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 5; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 7 w 7

RESULT 17
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=9978;
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RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 18
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-5 (PEA-k-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 865 MW; C76365B449CD775 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 19
C002831 PRELIMINARY; PRT; 8 AA.
AC C002831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PRO ALMA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).

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OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metseranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
FT SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 2 w 2

RESULT 20
Q9TRY3 PRELIMINARY; PRT; 8 AA.
AC Q9TRY3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
RL SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 5 w 5

RESULT 21
Q9TDD2 PRELIMINARY; PRT; 8 AA.
AC Q9TDD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Teranatos dolichopterus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Teranatos.
OX NCBI_TaxID=61836;
RN [1]

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RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RL (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AAF03041.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DD44056 CRC64;

Query Match 31.4%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 22
O9T4Y2 PRELIMINARY; PRT; 8 AA.
ID O9T4Y2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Asterina pecliniifera (Starfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID:7594;
[1]
RN SEQUENCE FROM N.A.
RA MEDLINE:8935469; PubMed:2763382;
RA Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL Curr. Genet. 15:193-206(1989).
DR EMBL: X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 1114 MW; F0C9D36415B736D6 CRC64;

Query Match 31.4%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 23
O35835 PRELIMINARY; PRT; 8 AA.
ID O35835;
AC O35835;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORF1 PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-TESTIS;
RX MEDLINE:98008057; PubMed:9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
```

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RT NRD convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL: X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EALB1ADC5A5B6 CRC64;

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 24
P82598 PRELIMINARY; PRT; 8 AA.
ID P82598;
AC P82598;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 38KDA NON-ARGINASE GROWTH INHIBITORY FACTOR (NAGIF)(FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
[1]
RN SEQUENCE.
RP STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE:20198203; PubMed:10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -!- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON_TER
SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 25
Q9ET18 PRELIMINARY; PRT; 8 AA.
ID Q9ET18;
AC Q9ET18;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity Orls identified in an intercross between the NZO
RT (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (JUL-2000) to the EMBL/Genbank/DBD databases.
DR EMBL: AF286200; AAG01474.1; -.
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FT NON_TER 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred.No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
Db 8 W 8

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:16 : Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1c
Perfect score: 35
Sequence: 1 wxxxxfxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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A.Geneseq_1101.*
1: /SIDs2/gcgdata/geneseq/genesqp/AA1980.DAT:*
2: /SIDs2/gcgdata/geneseq/genesqp/AA1981.DAT:*
3: /SIDs2/gcgdata/geneseq/genesqp/AA1982.DAT:*
4: /SIDs2/gcgdata/geneseq/genesqp/AA1983.DAT:*
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22: /SIDs2/gcgdata/geneseq/genesqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	27	77.1	8	21	AAB06419	Claudin-1 cell adh
2	27	77.1	8	21	AAB06479	Claudin-1 cyclic c
3	27	77.1	8	21	AAB06764	Claudin-1 cell a
4	27	77.1	8	21	AAB06814	Claudin-6/9 cyclic
5	27	77.1	8	21	AAB06916	Claudin cell adhes
6	25	71.4	8	21	AAB06521	Claudin-2 cell adh
7	25	71.4	8	21	AAB06574	Claudin-2 cyclic c
8	24	68.6	8	21	AAB06426	Claudin-1 cell adh
9	24	68.6	8	21	AAB06512	Claudin-1 cyclic c
10	24	68.6	8	21	AAB06583	Claudin-3 cell adh
11	24	68.6	8	21	AAB06636	Claudin-3 cyclic c

12	24	68.6	8	21	AAB06645	Claudin-4 cell adh
13	24	68.6	8	21	AAB06698	Claudin-4 cyclic c
14	24	68.6	8	21	AAB06823	Claudin-7 cell adh
15	24	68.6	8	21	AAB06876	Claudin-7 cyclic c
16	24	68.6	8	21	AAB06917	Claudin-7 cell adh
17	22	62.9	6	21	AAB06762	Claudin-6/9 cell a
18	22	62.9	6	21	AAB06812	Claudin-6/9 cyclic
19	22	62.9	7	21	AAB06763	Claudin-6/9 cell a
20	22	62.9	7	21	AAB06813	Claudin-6/9 cyclic
21	22	62.9	8	21	AAB06770	Claudin-6/9 cyclic
22	22	62.9	8	21	AAB06779	Claudin-6/9 cyclic
23	22	62.9	8	21	AAB06787	Claudin-6/9 cyclic
24	22	62.9	8	21	AAB06796	Claudin-6/9 cyclic
25	22	62.9	8	21	AAB06804	Claudin-6/9 cyclic
26	21	60.0	6	6	AAP50739	Somatostatin analog
27	21	60.0	6	6	AAP50741	Somatostatin analog
28	21	60.0	6	7	AAP61336	Sequence of novel
29	21	60.0	6	21	AAB06417	Claudin-1 cell adh
30	21	60.0	6	21	AAB06477	Claudin-1 cyclic c
31	21	60.0	7	21	AAB06418	Claudin-1 cell adh
32	21	60.0	7	21	AAB06478	Claudin-1 cyclic c
33	21	60.0	8	21	AAB06434	Claudin-1 cyclic c
34	21	60.0	8	21	AAB06443	Claudin-1 cyclic c
35	21	60.0	8	21	AAB06452	Claudin-1 cyclic c
36	21	60.0	8	21	AAB06461	Claudin-1 cyclic c
37	21	60.0	8	21	AAB06470	Claudin-1 cyclic c
38	20	57.1	6	20	AA101577	Antigenic peptide
39	20	57.1	6	21	AAB06519	Claudin-2 cell adh
40	20	57.1	6	21	AAB06572	Claudin-2 cyclic c
41	20	57.1	7	21	AAB06520	Claudin-2 cell adh
42	20	57.1	7	21	AAB06573	Claudin-2 cyclic c
43	20	57.1	8	21	AAB06528	Claudin-2 cyclic c
44	20	57.1	8	21	AAB06537	Claudin-2 cyclic c
45	20	57.1	8	21	AAB06546	Claudin-2 cyclic c
46	20	57.1	8	21	AAB06555	Claudin-2 cyclic c
47	20	57.1	8	21	AAB06564	Claudin-2 cyclic c
48	19	54.3	6	21	AAB06581	Claudin-3 cell adh
49	19	54.3	6	21	AAB06634	Claudin-3 cyclic c
50	19	54.3	6	21	AAB06643	Claudin-4 cell adh

ALIGNMENTS

RESULT 1
ID AAB06419 standard; peptide; 8 AA.
XX
AC AAB06419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsfxg 8
11111111
1 wklysyag 8
Db

RESULT 2
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsfxg 8
11111111
1 wklysyag 8
Db

RESULT 3
AAB06764
ID AAB06764 standard; peptide; 8 AA.
XX
AC AAB06764;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 70; Page 103; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wxxsfxg 8
11111111
1 wklysyag 8
Db

RESULT 4
AAB06814
ID AAB06814 standard; peptide: 8 AA.
XX
AC AAB06814;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.
XX
KM Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KM Inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA:

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
II : | |
DB 1 wkvtafig 8

RESULT 5
AAB06916
ID AAB06916 standard; protein: 8 AA.
XX
AC AAB06916;
XX
DT 05-OCT-2000 (first entry)
XX
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
KM Claudin modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
XX
FT Modified-site 1
FT Modified-site /note= "N-terminal acetyl"
FT Modified-site 8
FT /note= "C-terminal amide"
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
DR 03-NOV-1999; 99WO-CA01029.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 71; Page 103; 121pp; English.
XX
CC The present sequence is a peptide which can be used in a claudin-mediated
XX cell adhesion modulator. The claudin group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and this peptide
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, it can also be used to facilitate drug delivery
XX to the desired target site.
XX
SQ Sequence 8 AA:

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
II : | |
DB 1 wkvtafig 8

RESULT 6
AAB06521
ID AAB06521 standard; peptide: 8 AA.
XX
AC AAB06521;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX
KM Claudin-2 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX 03-NOV-1998; 98US-0185908.
XX

PR	30-MAR-1999;	99US-0282029.
XX	(ADHE-) ADHEREX TECHNOLOGIES INC.	
PA	Blaschuck OW, Symonds JM, Gour BJ;	
XX	WPI; 2000-365610/31.	
XX		
DR		
XX	Antibody modulation of claudin-mediated cell adhesion for increasing	
PT	vasopermeability, for delivering drugs to tumors and the nervous system	
PT	and across the skin -	
XX		
PS	Claim 46; Page 97; 121pp; English.	
CC	The present invention relates to the use of peptides as claudin-mediated	
CC	cell adhesion modulators. The claudin-2 group of proteins are cadherins,	
CC	which are membrane glycoproteins involved in cell adhesion. In some	
CC	situations, cell adhesion occurs at abnormal levels, and these peptides	
CC	can be used to modulate these levels, and thus treat autoimmune diseases,	
CC	inflammatory disorders and cancer, and aid wound healing and implant	
CC	adhesion. In addition, they can also be used to facilitate drug delivery	
CC	to the desired target site.	
XX		
SQ	Sequence 8 AA:	
OY	Query Match	71.4%; Score 25; DB 21; Length 8;
	Best Local Similarity	37.5%; Pred. No. 4.3e+05;
Matches	3; Conservative	2; Mismatches 3; Indels 0; Gaps 0
DB	1 wxxsfxg 8	
	1 : 1 : 1	
	1 wrtsyvg 8	
RESULT 7		
AAB06574		
ID	AAB06574 standard; peptide; 8 AA.	
AC	AAB06574;	
XX		
DT	28-SEP-2000 (first entry)	
DE	Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.	
XX		
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;	
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW	graft rejection; cyclic.	
XX		
OS	Mammalia.	
XX		
PN	WO200026360-A1.	
XX		
PD	11-MAY-2000.	
XX		
PE	03-NOV-1999; 99WO-CA01029.	
XX		
PR	03-NOV-1998; 98US-0185908.	
PR	30-MAR-1999; 99US-0282029.	
XX		
FA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
XX		
P1	Blaschuck OW, Symonds JM, Gour BJ;	
XX	WPI; 2000-365610/31.	
DR		
XX	Antibody modulation of claudin-mediated cell adhesion for increasing	
PT	vasopermeability, for delivering drugs to tumors and the nervous system	
PT	and across the skin -	
XX		
PS	Claim 49; Page 98; 121pp; English.	
CC	The present invention relates to the use of peptides as claudin-mediated	

```

CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
CC
XX Sequence 8 AA:
SQ
Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wxsfxg 8
||:|:|
Db 1 wrssyvg 8
RESULT 8
AAB06426
ID AAB06426 standard; peptide; 8 AA.
XX
XX AAB06426;
XX
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
XX
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site.
XX
XX Sequence 8 AA:
SQ
Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

OY 1 wxxxxfxg 8
I: I: I
DB 1 wrlysyug 8

RESULT 9
ID AAB06512 standard; peptide: 8 AA.
AC AAB06512;
XX
XX 28-SEP-2000 (first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection; cyclic.
XX
XX Mammalia.
OS
PN WO200026360-A1.
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 43; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
SQ Sequence 8 AA:

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
I: I: I
DB 1 wrlysyug 8

RESULT 10
ID AAB06583 standard; peptide: 8 AA.
AC AAB06583;
XX
XX 28-SEP-2000 (first entry)
XX

DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 52; Page 99; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
SQ Sequence 8 AA:

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
I: I: I
DB 1 wrvsafig 8

RESULT 11
ID AAB06636 standard; peptide: 8 AA.
AC AAB06636;
XX
XX
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.
DE
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection; cyclic.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR

PR 30-MAR-1999; 99US-0282029.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuck OM, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 wxxsfxg 8
| : | |
Db 1 wvrsafig 8

RESULT 12
AAB06645
ID AAB06645 standard; peptide; 8 AA.
XX
AC AAB06645;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.
XX
XX Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 58; Page 100; 121pp; English.
XX

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 wxxsfxg 8
| : | |
Db 1 wvrsafig 8

RESULT 13
AAB06698
ID AAB06698 standard; peptide; 8 AA.
XX
AC AAB06698;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
QY 1 wkxxsfxy 8	
1 : 1 1	
DB 1 wrvtatfg 8	
RESULT 14	
AAB06823	
ID AAB06823 standard; peptide: 8 AA.	
XX AAB06823;	
AC	
XX 28-SEP-2000 (first entry)	
DT	
XX Claudin-7 cell adhesion recognition sequence SEQ ID NO: 394.	
DE	
XX	
XX Claudin-7 modulating agent; cell adhesion recognition sequence;	
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KM graft rejection.	
XX	
XX Mammalia.	
OS	
XX WO200026360-A1.	
PN	
XX 11-MAY-2000.	
PD	
XX 03-NOV-1999; 99WO-CA01029.	
PE	
XX 03-NOV-1998; 98US-0185908.	
PR	
XX 30-MAR-1999; 99US-0282029.	
PA	
XX (ADHE-) ADHEREX TECHNOLOGIES INC.	
PI	
XX Blaschuck OW, Symonds JM, Gour BJ;	
DR	
XX WPI: 2000-365610/31.	
PT	
XX Antibody modulation of claudin-mediated cell adhesion for increasing	
PT vasopermeability, for delivering drugs to tumors and the nervous system	
PT and across the skin -	
PS	
XX Claim 76; Page 104; 121pp; English.	
PS	
XX The present invention relates to the use of peptides as claudin-mediated	
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,	
CC which are membrane glycoproteins involved in cell adhesion. In some	
CC situations, cell adhesion occurs at abnormal levels, and these peptides	
CC can be used to modulate these levels, and thus treat autoimmune diseases,	
CC inflammatory diseases and cancer, and aid wound healing and implant	
CC adhesion. In addition, they can also be used to facilitate drug delivery	
CC to the desired target site.	
CC	
XX	
XX Sequence 8 AA;	

DE	Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.
XX	
KW	Claudin-7 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW	graft rejection; cyclic.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PE	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
PI	
XX	Blaschuck OW, Symonds JM, Gour BJ;
DR	
XX	WPI: 2000-365610/31.
PT	
XX	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 79; Page 105; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site. The present sequence has a cyclic
CC	conformation.
XX	
XX	
XX	Sequence 8 AA;
Query Match	
Best Local Similarity 68.6%; Score 24; DB 21; Length 8;	
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
QY 1 wkxxsfxy 8	
1 : 1 1	
DB 1 wqmsyag 8	
RESULT 16	
AAB06917	
ID AAB06917 standard; Protein: 8 AA.	
XX AAB06917;	
AC	
XX 05-OCT-2000 (first entry)	
DT	
XX Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.	
DE	
XX	
XX Claudin-7 modulating agent; cell adhesion recognition sequence;	
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW graft rejection.	
XX	
XX Synthetic.	
OS	
XX	
XX Key	Location/Qualifiers
XX	1
FT	Modified-site
FT	/note= "N-terminal acetyl"
FT	8
FT	Modified-site
FT	/note= "C-terminal amide"
XX	

PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 77; Page 104; 121pp; English.
XX
XX The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;
XX
XX
XX Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 wkxxsfxg 8
| : |
Db 1 wqmsyag 8
XX
RESULT 17
AAB06762
ID AAB06762 standard; peptide; 6 AA.
XX
AC AAB06762;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 333.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
OS Mammalia.
OS
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI; 2000-365610/31.
XX

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 70; Page 103; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
XX
SQ Sequence 6 AA;
XX
XX
XX Query Match 62.9%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wkxxsf 6
| : |
Db 1 wkvtaf 6
XX
RESULT 18
AAB06812
ID AAB06812 standard; peptide; 6 AA.
XX
AC AAB06812;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 383.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
OS
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.

XX Sequence 6 AA:
SQ
Query Match 62.9%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxsf 6
11 : 1
Db 1 wkvtaf 6
RESULT 19
AAB06763 standard; peptide; 7 AA.
ID AAB06763
AC AAB06763;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 334.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
XX Mammalia.
OS
PN WO200026360-A1.
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 70; Page 103; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
XX
SQ Sequence 7 AA:
Query Match 62.9%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxsf 6
11 : 1
Db 1 wkvtaf 6
RESULT 20
AAB06813

ID AAB06813 standard; peptide; 7 AA.
XX
AC AAB06813;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 384.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 7 AA:
Query Match 62.9%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wkxxsf 6
11 : 1
Db 1 wkvtaf 6
RESULT 21
AAB06770
ID AAB06770 standard; peptide; 8 AA.
XX
AC AAB06770;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 341.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX

PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ
XX
DR WPI, 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 103; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

Query Match 62.9%; Score 22; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxf 6
| | : |
Db 2 wkvtaf 7

RESULT 22
AAB06779 AAB06779 standard; peptide; 8 AA.
XX
AC AAB06779;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 350.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI, 2400-365610/31.

XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 103; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

Query Match 62.9%; Score 22; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxf 6
| | : |
Db 2 wkvtaf 7

RESULT 23
AAB06787 AAB06787 standard; peptide; 8 AA.
XX
AC AAB06787;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 358.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI, 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to

CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

Query Match 62.9%; Score 22; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxf 6
11 : 1
Db 2 wkvtaf 7

RESULT 24
AAB06796
ID AAB06796 standard; peptide: 8 AA.
XX
AC AAB06796;

XX 28-SEP-2000 (first entry)
XX

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 367.
XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.

XX WO200026360-A1.
XX

XX 11-MAY-2000.
XX

XX 03-NOV-1999; 99WO-CA01029.
XX

XX 03-NOV-1998; 98US-0185908.
XX

XX 30-MAR-1999; 99US-0282029.
XX

XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX

XX Blaschuck OW, Symonds JM, Gour BJ;
XX

XX WPI; 2000-365610/31.
XX

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 73; Page 104; 121pp; English.
XX

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX

XX Sequence 8 AA;
XX

Query Match 62.9%; Score 22; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxf 6
11 : 1
Db 2 wkvtaf 7

RESULT 25
AAB06804
ID AAB06804 standard; peptide: 8 AA.
XX
AC AAB06804;

XX 28-SEP-2000 (first entry)
XX

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 375.
XX

XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.

XX WO200026360-A1.
XX

XX 11-MAY-2000.
XX

XX 03-NOV-1999; 99WO-CA01029.
XX

XX 03-NOV-1998; 98US-0185908.
XX

XX 30-MAR-1999; 99US-0282029.
XX

XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX

XX Blaschuck OW, Symonds JM, Gour BJ;
XX

XX WPI; 2000-365610/31.
XX

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 73; Page 104; 121pp; English.
XX

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX

XX Sequence 8 AA;
XX

Query Match 62.9%; Score 22; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxf 6
11 : 1
Db 2 wkvtaf 7

Search completed: January 14, 2002, 07:43:16
Job time: 427 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:36 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1c
Perfect score: 35
Sequence: 1 wkxxsfxxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues 43125
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/p1odaca/2/1aa/5A.COMB.pep:*
2: /cgn2_6/p1odaca/2/1aa/5B.COMB.pep:*
3: /cgn2_6/p1odaca/2/1aa/6A.COMB.pep:*
4: /cgn2_6/p1odaca/2/1aa/6B.COMB.pep:*
5: /cgn2_6/p1odaca/2/1aa/PCNUS.COMB.pep:*
6: /cgn2_6/p1odaca/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	51.4	7	4	US-09-258-754-268	Sequence 268, App
2	18	51.4	7	4	US-09-042-107-268	Sequence 268, App
3	17	48.6	6	2	US-08-484-458-25	Sequence 25, Appl
4	17	48.6	7	1	US-07-980-520-2	Sequence 2, Appl
5	17	48.6	7	2	US-08-680-634-2	Sequence 2, Appl
6	17	48.6	7	4	US-08-977-680-2	Sequence 36, Appl
7	17	48.6	8	2	US-08-687-219B-36	Sequence 2, Appl
8	17	48.6	8	3	US-08-467-472C-2	Sequence 2, Appl
9	17	48.6	8	3	US-08-467-472C-3	Sequence 3, Appl
10	17	48.6	8	3	US-08-467-472C-4	Sequence 4, Appl
11	17	48.6	8	4	US-09-384-061-2	Sequence 2, Appl
12	17	48.6	8	4	US-09-384-061-3	Sequence 3, Appl
13	17	48.6	8	4	US-09-384-061-4	Sequence 4, Appl
14	16	45.7	3	4	US-09-461-697-405	Sequence 405, App
15	16	45.7	4	1	US-08-079-445-3	Sequence 3, Appl
16	16	45.7	4	1	US-07-840-077A-7	Sequence 7, Appl
17	16	45.7	4	1	US-08-454-950-7	Sequence 7, Appl
18	16	45.7	4	1	US-08-434-761-3	Sequence 1, Appl
19	16	45.7	4	1	US-08-338-890B-1	Sequence 7, Appl
20	16	45.7	4	1	US-08-454-949-7	Sequence 8, Appl
21	16	45.7	4	2	US-08-671-467A-8	Sequence 1, Appl
22	16	45.7	4	2	US-08-340-208B-1	Sequence 2, Appl
23	16	45.7	4	2	US-08-651-179B-2	Sequence 3, Appl
24	16	45.7	4	2	US-08-651-179B-3	Sequence 4, Appl
25	16	45.7	4	3	US-08-997-263-1	Sequence 5, Appl
26	16	45.7	4	3	US-09-315-861-5	Sequence 25, Appl
27	16	45.7	4	3	US-08-981-122-25	Sequence 25, Appl

28	16	45.7	4	4	US-08-435-568A-19	Sequence 19, Appl
29	16	45.7	4	4	US-08-682-767-29	Sequence 29, Appl
30	16	45.7	4	4	US-08-682-767-30	Sequence 30, Appl
31	16	45.7	5	1	US-07-657-769B-36	Sequence 36, Appl
32	16	45.7	5	1	US-08-068-947-1	Sequence 1, Appl
33	16	45.7	5	1	US-08-068-947-3	Sequence 3, Appl
34	16	45.7	5	1	US-07-973-235A-19	Sequence 19, Appl
35	16	45.7	5	1	US-08-332-071B-1	Sequence 1, Appl
36	16	45.7	5	1	US-08-332-071B-2	Sequence 2, Appl
37	16	45.7	5	1	US-08-240-511-1	Sequence 1, Appl
38	16	45.7	5	1	US-08-486-057B-22	Sequence 22, Appl
39	16	45.7	5	1	US-07-789-184-97	Sequence 97, Appl
40	16	45.7	5	1	US-08-416-007-1	Sequence 1, Appl
41	16	45.7	5	1	US-08-416-007-5	Sequence 5, Appl
42	16	45.7	5	1	US-07-902-935-1	Sequence 1, Appl
43	16	45.7	5	1	US-08-475-263-97	Sequence 97, Appl
44	16	45.7	5	1	US-08-485-886-97	Sequence 2, Appl
45	16	45.7	5	2	US-08-465-764-2	Sequence 2, Appl
46	16	45.7	5	2	US-08-475-751-1	Sequence 1, Appl
47	16	45.7	5	2	US-08-475-751-5	Sequence 5, Appl
48	16	45.7	5	2	US-08-470-932-1	Sequence 1, Appl
49	16	45.7	5	2	US-08-467-025-1	Sequence 1, Appl
50	16	45.7	5	2	US-08-477-362-97	Sequence 97, Appl

ALIGNMENTS

RESULT 1
US-09-258-754-268
; Sequence 268, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslathi, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 268
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-268

Query Match 51.4%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxs 5
Db 1 WKPAS 5

RESULT 2
US-09-042-107-268
; Sequence 268, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslathi, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892

;; CURRENT APPLICATION NUMBER: US/09/042,107
;; CURRENT FILING DATE: 1998-03-13
;; NUMBER OF SEQ ID NOS: 436
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 268
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-268

Query Match 51.4%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
| | |
Db 1 WKPAS 5

RESULT 3
US-08-484-438-25
; Sequence 25, Application US/08484438
; Patent No. 5811098 5780031
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plozman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegal, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,165
; FILING DATE: 24-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misticok, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; * TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-484-438-25

Query Match 48.6%; Score 17; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxsf 6
| | : |
Db 1 WELMTF 6

RESULT 4
US-07-980-520-2
; Sequence 2, Application US/07980520
; Patent No. 5582862
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Haber, Edgar
; APPLICANT: Matsueda, Gary R.
; TITLE OF INVENTION: Antibodies That Bind to '2-Antiplasmin
; TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 5582862 Inhibit Plasma
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/980,520
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,003
; FILING DATE: 27-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/177,222
; FILING DATE: 04-APR-1988
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 833-7533
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-980-520-2

Query Match 48.6%; Score 17; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
| | |
Db 2 WKPAS 6

RESULT 5
US-08-680-634-2
; Sequence 2, Application US/08680634

Patent No. 5831031
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
APPLICANT: Haber, Edgar
APPLICANT: Matsuda, Gary R.
TITLE OF INVENTION: Antibodies That Bind To '2-Antiplasma
TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 5831031 Inhibit Plasma
TITLE OF INVENTION: '2-Antiplasma
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,634
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,520
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/943,372
FILING DATE: 10-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/589,003
FILING DATE: 27-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/177,222
FILING DATE: 04-APR-1988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-680-634-2

Query Match 48.6%; Score 17; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
DB 2 WPKGS 6

RESULT 6
US-08-977-680-2
Sequence 2, Application US/08977680
Patent No. 6280730
GENERAL INFORMATION:
APPLICANT: Reed, Guy L.
APPLICANT: Haber, Edgar
APPLICANT: Matsuda, Gary R.
TITLE OF INVENTION: Antibodies That Bind To '2-Antiplasma
TITLE OF INVENTION: Crosslinked To Fibrin Which Do No. 6280730 Inhibit Plasma
TITLE OF INVENTION: '2-Antiplasma
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,680
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/680,634
FILING DATE: 16-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,520
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/943,372
FILING DATE: 10-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/589,003
FILING DATE: 27-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/177,222
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.1450006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-977-680-2

Query Match 48.6%; Score 17; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxs 5
DB 2 WPKGS 6

RESULT 7
US-08-687-219B-36
Sequence 36, Application US/08687219B
Patent No. 598541
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIVE & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687, 219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-36

Query Match 48.6%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 kxxsfxxg 8
| | : |
Db 1 KASSYLIG 7

RESULT 8
US-08-467-472C-2
Sequence 2, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467, 472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742, 908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021, 606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
JOURNAL: TANDEN MASS SPECTROMETRY
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
US-08-467-472C-2

Query Match 48.6%; Score 17; DB 3; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wkxxs 5
| | :
Db 4 WKTST 8

RESULT 9
US-08-467-472C-3
Sequence 3, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 357-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
VOLUME: SYMPOSIUM
JOURNAL: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIDA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
JOURNAL: TANDEN MASS SPECTROMETRY
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-3

Query Match 48.6%; Score 17; DB 3; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxs 5
Db 4 WKTST 8

RESULT 10
US-08-467-472C-4
Sequence 4, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908

FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
JOURNAL: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
VOLUME: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:

PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-4
Query Match 48.6%; Score 17; DB 3; Length 8;
Best local similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 wxxxs 5
DB 4 WKTST 8
RESULT 11
US-09-384-061-2
Sequence 2, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER

LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -5- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEN MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 2: CYS-SER
US-09-384-061-2
Query Match 48.6%; Score 17; DB 4; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 WXXX 5
DB 4 WKTST 8
RESULT 12
US-09-384-061-3
Sequence 3, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY

STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -5- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 3: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-3

Query Match 48.6%; Score 17; DB 4; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxxx 5
11 :
Db 4 WKTST 8

RESULT 13
US-09-384-061-4
Sequence 4, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC., 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-4

Query Match 48.6%; Score 17; DB 4; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 wkxs 5
 11 :
 Db 4 WKTST 8

RESULT 14
 US-09-461-697-405
 ; Sequence 405, Application US/09461697
 ; Patent No. 6277974
 ; GENERAL INFORMATION:
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.
 ; APPLICANT: Lo, Donald C.
 ; APPLICANT: Barney, Shawn
 ; APPLICANT: Thomas, Mary Beth
 ; APPLICANT: Portbury, Stuart D.
 ; APPLICANT: Putnam, Kasurti
 ; APPLICANT: Katz, Lawrence C.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 ; FILE REFERENCE: 10001-005-999
 ; CURRENT APPLICATION NUMBER: US/09/461,697
 ; CURRENT FILING DATE: 1999-12-14
 ; NUMBER OF SEQ ID NOS: 466
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 405
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-461-697-405

Query Match 45.7%; Score 16; DB 4; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wk 2
 11 :
 Db 2 WK 3

RESULT 15
 US-08-079-445-3
 ; Sequence 3, Application US/08079445
 ; Patent No. 5440016
 ; GENERAL INFORMATION:
 ; APPLICANT: Biodelle, Sylvia E.
 ; APPLICANT: Pinilla, Clemencia
 ; APPLICANT: Elchler, Jutta
 ; APPLICANT: Houghten, Richard A.
 ; TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
 ; TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CAMPBELL AND FLORES
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/079,445
 ; FILING DATE: 18-JUN-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-HP 9648
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /label= Xaa
 OTHER INFORMATION: /note= "Xaa=Kfmoc"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /label= Xaa
 OTHER INFORMATION: /note= "Xaa-any amino acid"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: /note= "C-terminal amino acid is
 OTHER INFORMATION: amidated"
 US-08-079-445-3

Query Match 45.7%; Score 16; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 wk 2
 11 :
 Db 2 WK 3

RESULT 16
 US-07-840-077A-7
 ; Sequence 7, Application US/07840077A
 ; Patent No. 5443816
 ; GENERAL INFORMATION:
 ; APPLICANT: Zamora, Paul O.
 ; APPLICANT: Rhodes, Buck A.
 ; TITLE OF INVENTION: Peptide-metal ion
 ; TITLE OF INVENTION: Pharmaceutical Preparation and Method
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Rhomed Incorporated
 ; STREET: 4261 Ballroom Park
 ; CITY: Albuquerque
 ; STATE: NM
 ; COUNTRY: U.S.A.
 ; ZIP: 87109-5802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM PC/XT/AT, IBM PS/2 or
 ; OPERATING SYSTEM: compatibles
 ; SOFTWARE: Wordperfect 6.0a for Windows
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/840,077A
 ; FILING DATE: 20-FEB-1992
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/816,477
 ; FILING DATE: 03-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deborah A. Peacock
 ; REGISTRATION NUMBER: 31,649
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-840-077A-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
Db 2 wk 3

RESULT 17
US-08-454-950-7
Sequence 7, Application US/08454950
Patent No. 5690905
GENERAL INFORMATION:
APPLICANT: Zamora, Paul O.
APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Peptide-Metal Ion
TITLE OF INVENTION: Pharmaceutical Preparation and Method
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomed Incorporated
STREET: 4261 Balloon Park
CITY: Albuquerque
STATE: NM
COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordperfect 6.0a for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,950
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-454-950-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
Db 2 wk 3

RESULT 18
US-08-434-761-3
Sequence 3, Application US/08434761
Patent No. 5698673
GENERAL INFORMATION:
APPLICANT: Blondelle, Sylvie E.
APPLICANT: Pinilla, Clemencia
APPLICANT: Eichler, Jutta
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,761
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,445
FILING DATE: 18-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-HP 9648
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= "xaa"
OTHER INFORMATION: /note= "xaa=Krmoc"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= "xaa"
OTHER INFORMATION: /note= "xaa-any amino acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "C-terminal amino acid is
OTHER INFORMATION: amidated"
US-08-434-761-3

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
Db 2 wk 3

RESULT 19
US-08-338-890B-1
Sequence 1, Application US/08338890B
Patent No. 5700905
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905Rris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-890B-1

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
Db 2 wk 3

RESULT 20
US-08-454-949-7
Sequence 7, Application US/08454949
Patent No. 5759516
GENERAL INFORMATION:
APPLICANT: Zamora, Paul O.
APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Peptide-Metal Ion
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomco Incorporated
STREET: 4261 Balloun Park
CITY: Albuquerque
STATE: NM

COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: WordPerfect 6.0a for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,949
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dedorah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-454-949-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
Db 2 wk 3

RESULT 21
US-08-671-487A-8
Sequence 8, Application US/08671487A
Patent No. 5955577
GENERAL INFORMATION:
APPLICANT: MAYO, KEVIN H.
TITLE OF INVENTION: SYNTHETIC APPROACH TO DESIGNED CHEMICAL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: METTING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
STREET: 203 TEXTILE BUILDING, 119 NORTH FOURTH STREET
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,487A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, MYRA H.
REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 110.00330101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1225
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-671-487A-8

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
Db 2 wk 3

RESULT 22
US-08-340-208B-1
Sequence 1, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
TITLE OF INVENTION: Methods Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-208B-1

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
Db 2 wk 3

RESULT 23
US-08-651-179B-2
Sequence 2, Application US/08651179B
Patent No. 5985240
GENERAL INFORMATION:
APPLICANT: Zamora, Paul O.; Rhodes, Buck A.; Marek,
APPLICANT: Michael J.
TITLE OF INVENTION: Peptide Radiopharmaceutical
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dardy & Dardy P.C.
STREET: 805 Third Ave.
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,179B
FILING DATE: 21-MAY-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/447,453
FILING DATE: 23-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADDA C. COCORIS
REGISTRATION NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-651-179B-2

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
Db 2 wk 3

RESULT 24
US-08-651-179B-3
Sequence 3, Application US/08651179B
Patent No. 5985240
GENERAL INFORMATION:
APPLICANT: Zamora, Paul O.; Rhodes, Buck A.; Marek,
APPLICANT: Michael J.
TITLE OF INVENTION: Peptide Radiopharmaceutical
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dardy & Dardy P.C.
STREET: 805 Third Ave.
CITY: New York

STATE: NY
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch, 720 KB
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPATIBLES
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,179B
FILING DATE: 21-MAY-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/447,453
FILING DATE: 23-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADDA C. GOGORIS
REGISTRATION NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-651-179B-3

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
||
Db 2 wk 3

RESULT 25
US-08-997-263-1
Sequence 1, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338,890
FILING DATE: NOV. 14, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-997-263-1

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
||
Db 2 wk 3

Search completed: January 14, 2002, 07:41:36
Job time: 457 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:22 ; Search time 43.28 Seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1D
Perfect score: 35
Sequence: 1 wxxxxfxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	7	2	S33244
2	16	45.7	7	2	S33246
3	16	45.7	8	2	A38887
4	14	40.0	8	2	C61512
5	14	40.0	8	2	A46306
6	13	37.1	7	2	S33245
7	12	34.3	5	2	PT0308
8	12	34.3	6	2	S66195
9	12	34.3	6	2	A31263
10	12	34.3	6	2	B31263
11	12	34.3	6	2	B35640
12	12	34.3	8	2	S13661
13	12	34.3	8	2	D61512
14	12	34.3	8	2	A42057
15	11	31.4	3	2	F37196
16	11	31.4	4	2	A34626
17	11	31.4	4	2	B53284
18	11	31.4	4	2	PT0661
19	11	31.4	5	2	A32516
20	11	31.4	5	2	A60803
21	11	31.4	5	2	JH0253
22	11	31.4	5	2	G37196
23	11	31.4	5	2	PT0281
24	11	31.4	5	2	PT0729
25	11	31.4	5	2	PT0580
26	11	31.4	6	2	B34835
27	11	31.4	6	2	A61068
28	11	31.4	6	2	PT0629
29	11	31.4	6	2	PT0532

30	11	31.4	6	2	PT0519	T-cell receptor be
31	11	31.4	6	2	PT0637	T-cell receptor be
32	11	31.4	6	2	PT0641	T-cell receptor be
33	11	31.4	6	2	PT0726	T-cell receptor be
34	11	31.4	6	2	F41946	T-cell receptor ga
35	11	31.4	6	2	PD0028	pev-kinin 2 - pena
36	11	31.4	6	4	I79564	hypothetical TGL3
37	11	31.4	7	2	S21230	dermorphin (trp-4,
38	11	31.4	7	2	A58512	venom heptapeptide
39	11	31.4	7	2	A61081	tryptophyllin, bas
40	11	31.4	7	2	S57274	triacetylglucosyl 11
41	11	31.4	7	2	S09652	hypothetical prote
42	11	31.4	7	2	PN0649	alpha-dextrin endo
43	11	31.4	7	2	PQ0727	H2 class I protein
44	11	31.4	7	2	H33098	180k exoantigen -
45	11	31.4	7	2	S33567	tubulin beta-3 cha
46	11	31.4	7	2	E48394	glycoprotein compo
47	11	31.4	7	2	PH1602	Ig H chain V-D-J r
48	11	31.4	7	2	E33932	Ig mu chain D regl
49	11	31.4	7	2	PT0526	T-cell receptor be
50	11	31.4	7	2	PT0628	T-cell receptor be

ALIGNMENTS

RESULT 1
S33244
neuromodulatory peptide Wwamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A>Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 45.7%: Score 16: DB 2: Length 7;
Best Local Similarity 100.0%: Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
DB 1 wk 2

RESULT 2
S33246
neuromodulatory peptide Wwamide-3 - giant African snail
C:Species: Achatina fulica (giant African snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33246
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A>Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 45.7%: Score 16: DB 2: Length 7;
Best Local Similarity 100.0%: Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wk 2

Db 1 WK 2

RESULT 3

A38887

T-cell receptor gamma chain (5t.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A38887

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33245

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of

A:Reference number: S33244; MUID:93265912

A:Accession: S33245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 45.7%; Score 16; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 wkxxaf 6

I: |

Db 3 WDSSGF 8

RESULT 4

C61512

variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: C61512

R:Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termi

A:Reference number: A61512; MUID:81172836

A:Accession: C61512

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Keywords: glycoprotein

Query Match 40.0%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxaf 5

I: |

Db 1 WENNA 5

RESULT 5

A46306

spasmodogenic toxin PNV1 - spider (Phoneutria nigriventer) (fragment)

C:Species: Phoneutria nigriventer

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

C:Accession: A46306

R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.

Toxicol. 31, 377-384, 1993

A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide

A:Reference number: A46306; MUID:93276438

A:Accession: A46306

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 40.0%; Score 14; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 wkxxaf 6

I: |

Db 3 WDSSGF 8

RESULT 6

C61512

variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: C61512

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 afxg 8

I: |

Db 2 APFG 5

neuroendocrine peptide Wamide-2 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33245

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o

A:Reference number: S33244; MUID:93265912

A:Accession: S33245

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 37.1%; Score 13; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2

I: |

Db 1 WR 2

RESULT 7

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0308

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0308

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 34.3%; Score 12; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2

I: |

Db 2 WE 3

RESULT 8

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fra

C:Species: Gadus sp. (cod)

C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998

C:Accession: S66195

R:Helmgvist, U.; Hackett, M.; Shafigat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.

FEBS Lett. 367, 237-240, 1995

A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases

A:Reference number: S66191; MUID:95331382

A:Accession: S66195

A:Molecule type: protein

A:Residues: 1-6 <HUE>

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
Db 5 WE 6

RESULT 9

A31263

dhidrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum

C:Species: Plasmodium falciparum

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996

C:Accession: A31263

R:Peterson, D.S.; Walliker, D.; Wellem, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A:Title: Evidence that a point mutation in dhidrofolate reductase-thymidylate synthase

A:Reference number: A94217; MUID:89057886

C:Accession: A31263

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <PEP>

C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
Db 3 WE 4

RESULT 10

B31263

dhidrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum

C:Species: Plasmodium falciparum

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996

C:Accession: B31263

R:Peterson, D.S.; Walliker, D.; Wellem, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A:Title: Evidence that a point mutation in dhidrofolate reductase-thymidylate synthase

A:Reference number: A94217; MUID:89057886

C:Accession: B31263

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <PEP>

C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
Db 3 WE 4

RESULT 11

B35640

cerebellar degeneration-related protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993

C:Accession: B35640

R:Chen, Y.T.; Retilly, W.J.; Yennamandra, A.K.; Kozak, C.A.; Chaganli, R.S.K.; Posner, J.E.

Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990

A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal man

A:Reference number: A35640; MUID:90222173
A:Accession: B35640
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-6 <CHD>

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
Db 2 WE 3

RESULT 12

S13661

polygalacturonase (EC 3.2.1.15) isoform PG2 - fungus (Sclerotinia sclerotiorum) (frag

N:Alternate names: endopolgalacturonase; pectin depolymerase; pectinase

C:Species: Sclerotinia sclerotiorum

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C:Accession: S13661

R:Waksman, G.; Keon, J.P.R.; Turner, G.

Biochim. Biophys. Acta 1073, 43-48, 1991

A:Title: Purification and characterization of two endopolgalacturonases from Sclerot

A:Reference number: S13661; MUID:91120822

C:Accession: S13661

A:Molecule type: protein

A:Residues: 18 <WAK>

C:Function:

A:Description: Involved in pectin degradation

C:Keywords: glycosidase; hydrolase

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 fxg 8
1:
Db 6 FSG 8

RESULT 13

D61512

variant surface glycoprotein MITR 1.6 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: D61512

R:Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-ter

A:Reference number: A61512; MUID:81172836

C:Accession: D61512

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Keywords: glycoprotein

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
1:
Db 1 WE 2

RESULT 14

A42057

fibroblast growth factor receptor 1, secreted - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A42057
Mol. Cell. Biol. 12, 82-88, 1992
A;Title: Differential splicing in the extracellular region of fibroblast growth factor
A;Reference number: A42057; MUID:92107200
A;Accession: A42057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <MER>
A;Cross-references: GB:M80363
C;Keywords: growth factor receptor

Query Match 34.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 afxg 8
| |
Db 5 SFLG 8

RESULT 15
F37196
bradykinin-potentiating peptide 6 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: F37196
R;Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557
A;Accession: F37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <GIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 3 w 3

RESULT 16
A34626
RPCH-related neuropeptide - ferruginous spindle
C;Species: Fustinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762
A;Accession: A34626
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <KUR>
C;Keywords: neuropeptide

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1

Db 4 w 4

RESULT 17
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an
A;Reference number: A53284; MUID:91342695
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:q233916; PIDN:AAB19518.1; PID:q233918
A;Note: sequence extracted from NCBI backbone (NCBIT:60737, NCBI:P:60738)
C;Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 2 w 2

RESULT 18
PT0661
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0661
R;Feeney, A.J.
J. exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0661
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEF>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 3 w 3

RESULT 19
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>

C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecyst
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
DB 2 W 2

RESULT 20
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)

C:Species: Anthopleura elegantissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.
A:Reference number: A60803; MUID:88222764
A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GRA>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
DB 5 W 5

RESULT 21
JH0253

gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113
A:Accession: JH0253
A:Molecule type: protein
A:Residues: 1-5 <UES>
A:Experimental source: gut
C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastr
, and of the circular muscle of the gastro-intestinal junction.

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
DB 3 W 3

RESULT 22
G37196
bradykinin-potentiating peptide 7 - island jararaca
C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptide
A:Reference number: A37196; MUID:90351557
A:Accession: G37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
DB 3 W 3

RESULT 23
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
DB 4 W 4

RESULT 24

PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0640; PT0685; PT0729
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0640
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE2>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE3>

A:Experimental source: newborn thymus, strain BALB/c, clone 135-1A6
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 5 W 5

RESULT 25

PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0580
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PFE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 4 W 4

Search completed: January 14, 2002, 07:44:22
Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds

(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1d
Perfect score: 35
Sequence: 1 wxxxxfxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	16	45.7	7 1 WMA2_ACHFU	P35920 achatina fu
2	16	45.7	7 1 WMA3_ACHFU	P35921 achatina fu
3	13	37.1	7 1 WMA1_ACHFU	P35919 achatina fu
4	12	34.3	7 1 MNPI_LEPDE	P42984 lepliotars
5	11	31.4	5 1 BPP7_BOTIN	P30425 botriops in
6	11	31.4	5 1 TPIS_CANFA	P54714 canis famil
7	11	31.4	5 1 UF01_MOUSE	P38639 mus musculu
8	11	31.4	6 1 LOK1_LOCOMI	P41491 locusta mig
9	11	31.4	8 1 ACL_THUAL	P16691 thunnus alb
10	11	31.4	8 1 AKHG_GRTBI	P14086 gryllus blm
11	11	31.4	8 1 AKH_LIBAV	P25418 libellula a
12	11	31.4	8 1 AKH_MELML	P25423 melolontha
13	11	31.4	8 1 AKH_TABAT	P14595 tabanus aur
14	11	31.4	8 1 CCKN_MACEU	P30369 macropus eu
15	11	31.4	8 1 HTE1_PERAM	P04548 periplaneta
16	11	31.4	8 1 HTE2_PERAM	P04549 periplaneta
17	11	31.4	8 1 HTE_TENMO	P25419 tenebrio mo
18	11	31.4	8 1 LCK1_LEUMA	P21140 leucophaea
19	11	31.4	8 1 LCK2_LEUMA	P21141 leucophaea
20	11	31.4	8 1 LCK3_LEUMA	P21142 leucophaea
21	11	31.4	8 1 LCK4_LEUMA	P21143 leucophaea
22	11	31.4	8 1 LCK5_LEUMA	P19987 leucophaea
23	11	31.4	8 1 LCK6_LEUMA	P19988 leucophaea
24	11	31.4	8 1 LCK7_LEUMA	P19989 leucophaea
25	11	31.4	8 1 LCK8_LEUMA	P19990 leucophaea
26	11	31.4	8 1 PUP_BRANA	P81707 brassica na
27	11	31.4	8 1 PPH_C_PANBO	P08939 pandanus bo
28	10	28.6	7 1 ALL2_CARMA	P81805 carcinus ma
29	10	28.6	7 1 ALL3_CARMA	P81806 carcinus ma
30	10	28.6	7 1 ALL4_CARMA	P81807 carcinus ma
31	10	28.6	7 1 ALL5_CARMA	P81808 carcinus ma
32	10	28.6	7 1 ALL6_CARMA	P81815 carcinus ma
33	10	28.6	8 1 ALL7_CARMA	P81809 carcinus ma

34	10	28.6	8 1 ALL8_CARMA	P81811 carcinus ma
35	10	28.6	8 1 ALL9_CARMA	P81812 carcinus ma
36	10	28.6	8 1 NS3_MYCTU	P81152 mycobacteri
37	10	28.6	8 1 ORMY_ORCLI	P82455 orconectes
38	10	28.6	8 1 RSL_ERWCH	P37985 erwina chr
39	9	25.7	7 1 UC24_MAIZE	P80630 zea mays (m
40	8	22.9	7 1 FARS_HIRME	P42564 hirudo medl
41	7	20.0	5 1 AL14_CARMA	P81817 carcinus ma
42	7	20.0	6 1 OVM_LEPDE	P42985 lepliotars
43	7	20.0	7 1 ALL7_CYDPO	P82158 cydia pomon
44	7	20.0	7 1 FAR3_HAECCO	P81298 haemochus
45	7	20.0	7 1 FAR3_PANRE	P41874 panagrellus
46	7	20.0	7 1 HY7_PIG	P01153 sus scrofa
47	7	20.0	7 1 MSCL_SALTY	P39446 salmoneilla
48	7	20.0	8 1 AL15_CARMA	P81818 carcinus ma
49	7	20.0	8 1 AL17_CARMA	P81820 carcinus ma
50	7	20.0	8 1 AL18_CARMA	P81821 carcinus ma

ALIGNMENTS

RESULT 1
WMA2_ACHFU STANDARD; PRT: 7 AA.
ID WMA2_ACHFU
AC P35920:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA2IDE-2
OS Achatina fulica (Giant African snail).
OC Euharyota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
the ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Oy 1 wk 2
Db 1 wk 2

RESULT 2
WMA3_ACHFU STANDARD; PRT: 7 AA.
ID WMA3_ACHFU
AC P35921:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA3IDE-3
OS Achatina fulica (Giant African snail).
OC Euharyota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;

```
RT "Mwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
KM Neuropeptide; Amidation.
FT MOD_RES 7 AA; 965 MW; 7362D5B69B132310 CRC64;
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
DB 1 WK 2

RESULT 3
MMAL_ACHFV STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE MWAMIDE-1
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93263912; PubMed=8495720;
RX Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR: S33245; S33245.
KM Neuropeptide; Amidation.
FT MOD_RES 7 AA; 993 MW; 7362D5B69B041310 CRC64;
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 2
DB 1 WK 2

RESULT 4
MMPL_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytognaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;

RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Ieuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KM Neuropeptide; Amidation.
FT MOD_RES 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 afxg 8
DB 1 AYNG 4

RESULT 5
BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintera A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KM Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WK 1
DB 3 WK 3

RESULT 6
TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN Tpi1.
OS Canis familiaris (Dog).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID:9615;
RN [1]
RP SEQUENCE.
RC TISSUE:Heart;
RX MEDLINE:98163340; PubMed:9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE -> DIHYDROXY-
ACETONE PHOSPHATE.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE: P54714; DOG.
DR InterPro: IPR000652; Trioseph. isomerase.
DR PROSITE: PS00171; TIM. PARTIAL.
KM Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA: 550 MW: 64444862C9A00000 CRC64:

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 fvg 8
DB 1 fvg 3

RESULT 7
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE.
RC TISSUE:Fibroblast;
RX MEDLINE:95009907; PubMed:7523108;
RA Merrick B.A., Patterson R.M., Wilcher L.L., He C., Selick J.K.;
RT "Separation and sequencing of filillar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
RT PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON_TER 5 5
SQ SEQUENCE 5 AA: 717 MW: 73640870A3100000 CRC64:

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 1 w 1

RESULT 8
LOK1_LOCM1 STANDARD; PRT; 6 AA.
ID LOK1_LOCM1

AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID:7004;
RN [1]
RP SEQUENCE.
RC TISSUE:Corpora cardiaca;
RX MEDLINE:92262851; PubMed:1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.R.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
TUBULES.
DR PIR: A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA: 654 MW: 686365A5B9CDB000 CRC64:

Query Match 31.4%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 5 w 5

RESULT 9
AC1_THUVAL STANDARD; PRT; 8 AA.
ID AC1_THUVAL
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE ANGIOGENSIN-CONVERTING ENZYME INHIBITOR.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID:8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE:88326322; PubMed:3415688;
RA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Minura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA: 953 MW: 6AA863733051F1B7 CRC64:

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 10

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AKHG_GRYBI          STANDARD;          PRT;          8 AA.
ID AKHG_GRYBI
PI4086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RL the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RL the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 11
ID AKH_LIBAU          STANDARD;          PRT;          8 AA.
AKH_LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Palaepodera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";

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RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

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Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 12
ID AKH_MEML          STANDARD;          PRT;          8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21663; S21663.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB344736 CRC64;

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Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 |
 DB 8 W 8

RESULT 13
 AKH_TABAT
 ID AKH_TABAT STANDARD; PRT: 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)
 DE (DCC I).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
 OC Tabanidae; Tabanus.
 OX NCBI_TaxId=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE:90046758; PubMed:2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HTH / RPCH FAMILY.
 CC PIR: A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 |
 DB 8 W 8

RESULT 14
 CCKN_MACEU
 ID CCKN_MACEU STANDARD; PRT: 8 AA.
 AC P30369;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CHOLECYSTOKININ (CCK).
 DE CCK.
 GN CCK.
 OS Macropus eugenii (Tamar wallaby), and
 OS Dasyurus viverrinus (Southeastern quoll).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxId=9315, 9279;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 |
 DB 5 W 5

RESULT 15
 HTFL_PERAM
 ID HTFL_PERAM STANDARD; PRT: 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSEMIC FACTOR I (NEUROPEPTIDE M-1) (PERIPLANETIN CC-I)
 DE (PRA-CAH-1) (UED-CC-1) (HYPERTREHALASEMIC NEUROPEPTIDE I).
 OS Periplaneta americana (American cockroach).
 OS Lepidoptera decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxId=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Wilten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry";
 RT Blochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kallish F., Kramer S.J., McInroe G.A.,
 RA Miller C.R., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.

RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; Pubmed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.
DR Interpro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
DR Neuropeptide; Amidation.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1 1
Db 8 w 8

RESULT 16
HTF2_PERAM STANDARD; PRT; 8 AA.
ID HTF2_PERAM
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
(PER-CAH-II) (LED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
OS Periplaneta americana (American cockroach),
Leptinotarsa decemlineata (Colorado potato beetle), and
Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
[1]
NN SEQUENCE.
RP SPECIES=P.americana;
RX MEDLINE=85046530; Pubmed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
[2]
NN SEQUENCE.
RP SPECIES=P.americana;
RX MEDLINE=84298179; Pubmed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEntoe G.A.,
Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
[3]
NN SEQUENCE.
RP SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; Pubmed=2576128;

RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
[4]
NN SEQUENCE.
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; Pubmed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05170; A05170.
DR PIR: S08996; S08996.
DR PIR: B44960; B44960.
DR PIR: B49823; B49823.
DR Interpro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
DR Neuropeptide; Amidation.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1 1
Db 8 w 8

RESULT 17
HTF_TENMO STANDARD; PRT; 8 AA.
ID HTF_TENMO
AC P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR (HOTN) (HYPERTREHALOSEMIC NEUROPEPTIDE).
OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067, 7075;
[1]
NN SEQUENCE.
RP TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; Pubmed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrehalosemic neuropeptide from
tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:455-459(1990).
CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A43976; A43976.
DR PIR: B43976; B43976.
DR Interpro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
DR Neuropeptide; Amidation.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;


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Query Match      31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
   |
DB 8 w 8

RESULT 18
LCK1_LEUMA STANDARD; PRT: 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID:6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
CC KM Neuropeptide; Amidation.
CC MOD_RES 8
CC FT SEQUENCE 8 AA; 893 MW; DC6365B449C64;

Query Match      31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
   |
DB 7 w 7

RESULT 19
LCK2_LEUMA STANDARD; PRT: 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID:6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.

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KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match      31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
   |
DB 7 w 7

RESULT 20
LCK3_LEUMA STANDARD; PRT: 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID:6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
CC KM Neuropeptide; Amidation.
CC MOD_RES 8
CC FT SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match      31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
   |
DB 7 w 7

RESULT 21
LCK4_LEUMA STANDARD; PRT: 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID:6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).

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CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 906 MW; DC635B1E9D5BDDA CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 22
ICK5_LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C665B8 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 23
ICK6_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
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RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation.
FT MOD.RES 1
FT MOD.RES 8
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 24
ICK7_LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CD76A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 25
ICK8_LEUMA STANDARD; PRT; 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
```

CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC PIR: JS0318; JS0318.
 DR Neuropeptide; Amidation.
 KW Neuropeptide; Amidation.
 FT MOD.RES 8
 SO SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 1
 Db 7 W 7

Search completed: January 14, 2002, 07:52:04
 Job time: 679 sec

GenCore version 4.5
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CM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:46 ; Search time 80.15 Seconds
(without alignments)
14.600 Million cell updates/sec

Title: 09-185908-1D
Perfect score: 35
Sequence: 1 wkxxafxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

- Database :
- 1: SPRENBL_17:*
 - 2: sp_archaea:*
 - 3: sp_bacteria:*
 - 4: sp_fungi:*
 - 5: sp_human:*
 - 6: sp_invertebrate:*
 - 7: sp_mammal:*
 - 8: sp_mhc:*
 - 9: sp_organelle:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	7	8	Q95945
2	16	45.7	8	11	Q62721
3	15	42.9	8	2	O09258
4	13	37.1	8	6	P82929
5	12	34.3	8	6	O02831
6	12	34.3	8	11	P70243
7	12	34.3	8	11	O9QVD3
8	11	31.4	6	13	P82096
9	11	31.4	7	10	O49223
10	11	31.4	7	13	P82065
11	11	31.4	8	2	O85406
12	11	31.4	8	4	O15888
13	11	31.4	8	4	O15890
14	11	31.4	8	5	O9VRD2
15	11	31.4	8	5	P82685
16	11	31.4	8	5	P82686
17	11	31.4	8	5	P82687
18	11	31.4	8	5	P82688
19	11	31.4	8	5	P82689

20	11	31.4	8	6	O9TRY3	O9TRY3 sus sp. ins
21	11	31.4	8	8	O9TD02	O9TD02 terranatos
22	11	31.4	8	8	O9T4Y2	O9T4Y2 asterina pe
23	11	31.4	8	11	O35835	O35835 rattus norv
24	11	31.4	8	11	P82598	P82598 rattus norv
25	11	31.4	8	11	O9ET18	O9ET18 mus spreus
26	11	31.4	8	11	O9ET17	O9ET17 mus caroli
27	11	31.4	8	11	O9ET16	O9ET16 mesocricetu
28	11	31.4	8	11	O9PMN0	O9PMN0 mus musculu
29	11	31.4	8	13	P79940	P79940 xenopus lae
30	11	31.4	8	13	O98RT5	O98RT5 xenopus lae
31	10	28.6	7	4	O15903	O15903 homo sapien
32	10	28.6	8	2	O56759	O56759 xanthobacte
33	10	28.6	8	11	O9JLD7	O9JLD7 mesocricetu
34	10	28.6	8	12	O98YK9	O98YK9 human immun
35	8	22.9	8	2	O9S443	O9S443 pseudomonas
36	8	22.9	8	4	O15900	O15900 homo sapien
37	8	22.9	8	5	O9TWH6	O9TWH6 perliretis
38	8	22.9	8	6	O9TRX8	O9TRX8 bos taurus
39	7	20.0	7	2	O07354	O07354 synechococc
40	7	20.0	8	2	O9R5R0	O9R5R0 shigella dy
41	7	20.0	8	3	P87225	P87225 saccharomyc
42	7	20.0	8	4	O9HC00	O9HC00 homo sapien
43	7	20.0	8	7	O9S213	O9S213 oryctolagus
44	7	20.0	8	10	P82324	P82324 pistum setiv
45	7	20.0	8	12	O83977	O83977 influenza a
46	6	17.1	5	13	P82070	P82070 litoria rub
47	6	17.1	5	13	P82071	P82071 litoria rub
48	6	17.1	5	13	P82072	P82072 litoria rub
49	6	17.1	5	13	P82073	P82073 litoria rub
50	6	17.1	5	13	P82099	P82099 litoria rub

ALIGNMENTS

RESULT 1
ID Q95945 PRELIMINARY: PRT: 7 AA.
AC O95945:
DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE INSIDE INTRON 5 (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8106985; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL: V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B723262CDC460 CRC64;

Query Match 45.7%; Score 16; DB 8; Length 7;
Best local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
Db 4 wk 5
RESULT 2

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Q62721
ID 062721 PRELIMINARY; PRT; 8 AA.
AC 062721:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17178; AAA86692.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match
Best Local Similarity 45.7%; Score 16; DB 11; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
Db 6 wk 7

RESULT 3
009258 PRELIMINARY; PRT; 8 AA.
ID 009258:
AC 009258:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NIFH (FRAGMENT).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RA Chen H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001780; AAC33369.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; F1B859CDD046C406 CRC64;

Query Match
Best Local Similarity 42.9%; Score 15; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 afxg 8
Db 5 AFYG 8

RESULT 4
P82929 PRELIMINARY; PRT; 8 AA.
ID P82929:
AC P82929:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
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DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremull L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
RT of the full complement ribosomal proteins present.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match
Best Local Similarity 37.1%; Score 13; DB 6; Length 8;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 wkxxaf 6
Db 2 WGIITLF 7

RESULT 5
002831 PRELIMINARY; PRT; 8 AA.
ID 002831:
AC 002831:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metcaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match
Best Local Similarity 34.3%; Score 12; DB 6; Length 8;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 wkxxaf 6
Db 2 WPCILIF 7

RESULT 6
P70243 PRELIMINARY; PRT; 8 AA.
ID P70243:
AC P70243:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129;
RA Ophiot R.A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X98325; CAA66969.1; -.
KW Calcium channel.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 865 MW: D9C37DD81861ADDE CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 2
DB 7 W 8

RESULT 7
O9QVD3 PRELIMINARY; PRT; 8 AA.
AC O9QVD3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RT Iwanaga S., Hirata M.;
RT "Purative Inositol 1,4,5-trisphosphate binding proteins in rat brain cytosol."
RT J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA: 1047 MW: D72415B806C37041 CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 2
DB 3 W 4

RESULT 8
P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Mahlitz P.A., Boyle J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog

RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA: 792 MW: 6683704772C9A000 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 9
O49223 PRELIMINARY; PRT; 7 AA.
ID O49223
AC O49223;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
RX MEDLINE=91367679; PubMed=1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins."
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047050; AAC03556.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA: 850 MW: 6AAAAB378637810 CRC64;

Query Match 31.4%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 10
P82065 PRELIMINARY; PRT; 7 AA.
ID P82065
AC P82065;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TRYPOPHYLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;

RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Iltoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians";
RL Aust. J. Chem. 49:955-963(1996).
CC -I- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUOTRASMITTER.
CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -I- MASS SPECTROMETRY: MW=965; METHOD-FAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 983 MW: 7401E9D3676046B0 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 4 w 4

RESULT 11
ID 085406 PRELIMINARY; PRT; 8 AA.
AC 085406.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
ON NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NINE MILE PHASE I;
RA Williams H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
RT Coxiella burnetii.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 993 MW: 046B5AA453772727 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 4 w 4

RESULT 12
ID 015888 PRELIMINARY; PRT; 8 AA.
AC 015888.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;

RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coobbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32069; AAA73878.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 1068 MW: 0315A37EAB5B0763 CRC64;

Query Match 31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 6 w 6

RESULT 13
ID 015890 PRELIMINARY; PRT; 8 AA.
AC 015890.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA.
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coobbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 975 MW: 605EAC65BEA5A2D3 CRC64;

Query Match 31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 1 w 1

RESULT 14
ID 09VRD2 PRELIMINARY; PRT; 8 AA.
AC 09VRD2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazetj R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson G.R., Milos G.L.G.,
RA Abril J.F., Agbayan A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballow R.Y., Basu A.C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhanderi D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL:AE003569; AAF50870.1; -
SQ Flybase: FBgn0040648; CG11666;
SEQUENCE 8 AA: 1062 MW: ED11B5B044004376 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 w 1
Db 2 w 2
RESULT 15
P82685 PRELIMINARY: PRT: 8 AA.
AC P82685; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattellidae; Periplaneta.
NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 950 MW: 326365B449D5A774 CRC64;
Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 w 1
Db 7 w 7
RESULT 16
P82686 PRELIMINARY: PRT: 8 AA.
AC P82686; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattellidae; Periplaneta.
NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- MYOTROPIC ACTIVITY).
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 856 MW: DC6365A5B9D5BD4A CRC64;
Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 w 1
Db 7 w 7
RESULT 17
P82687 PRELIMINARY: PRT: 8 AA.
AC P82687; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattellidae; Periplaneta.
NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE-CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RT Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

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RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RL americana.";
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA; 909 MW; DC6365B449D5A76A CRC64;
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 18
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blattioidea; Blattidae; Periplaneta.
OX NCBI_TaxId-6978;

RN
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RL americana.";
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA; 839 MW; 736365A5B9DDDD8 CRC64;
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9DDDD8 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 19
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blattioidea; Blattidae; Periplaneta.
OX NCBI_TaxId-6978;

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RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RL americana.";
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA; 865 MW; C76365B449DC775 CRC64;
SQ SEQUENCE 8 AA; 865 MW; C76365B449DC775 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 20
Q9TR3 PRELIMINARY; PRT; 8 AA.
ID Q9TR3;
AC Q9TR3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBR-6.
OS Sus sp.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId-9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; Pubmed=1719383;
RA Shimasaki S., Gao L., Shimomaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 5 w 5

RESULT 21
Q9TD2 PRELIMINARY; PRT; 8 AA.
ID Q9TD2;
AC Q9TD2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Teranatos dolichopterus.
CC Mitochondrion.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
CC Cyprinodontiformes; Aplocheilidae; Rivulinae; Teranatos.
OX NCBI_TaxId-61836;
RN [1]

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RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AAF03041.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA: 1084 MW; F0C9D3640DD44056 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 8; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 22
O9T4Y2 PRELIMINARY; PRT; 8 AA.
AC O9T4Y2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Astionia pectinifera (Starfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asteriinae; Asteroidea.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89354669; PubMed=2766382;
RA Jacobs H.T., Asakawa S., Arai T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL Curr. Gene. 15:193-206(1989).
DR EMBL: X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA: 1114 MW; F0C9D36415B736D6 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 8; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 23
O35835 PRELIMINARY; PRT; 8 AA.
AC O35835:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORF1 PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-TESTIS;
RC MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Jonlie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
```

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RT NRP convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL: X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA: 886 MW; EA7EAIADDC5A5B6 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 11; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 24
P82598 PRELIMINARY; PRT; 8 AA.
AC P82598:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 38KDA NON-ARGINASE GROWTH INHIBITORY FACTOR (NAGIF)(FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA MEDLINE=20198203; PubMed=10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -I- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC -I- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON_TER
SQ SEQUENCE 8 AA: 914 MW; 80A3676B02D76B1D CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 11; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 25
Q9ET18 PRELIMINARY; PRT; 8 AA.
AC Q9ET18:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RT (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF286200; AAG01474.1; -.
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FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 8 w 8

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:16 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1D
Perfect score: 35
Sequence: 1 wkxxafxg 8

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: /_Geneseq_1101:*
2: /SIDS2/gcgdata/geneseq/AA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/AA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/AA1983.DAT:*
6: /SIDS2/gcgdata/geneseq/AA1984.DAT:*
7: /SIDS2/gcgdata/geneseq/AA1985.DAT:*
8: /SIDS2/gcgdata/geneseq/AA1986.DAT:*
9: /SIDS2/gcgdata/geneseq/AA1987.DAT:*
10: /SIDS2/gcgdata/geneseq/AA1988.DAT:*
11: /SIDS2/gcgdata/geneseq/AA1989.DAT:*
12: /SIDS2/gcgdata/geneseq/AA1990.DAT:*
13: /SIDS2/gcgdata/geneseq/AA1991.DAT:*
14: /SIDS2/gcgdata/geneseq/AA1992.DAT:*
15: /SIDS2/gcgdata/geneseq/AA1993.DAT:*
16: /SIDS2/gcgdata/geneseq/AA1994.DAT:*
17: /SIDS2/gcgdata/geneseq/AA1995.DAT:*
18: /SIDS2/gcgdata/geneseq/AA1996.DAT:*
19: /SIDS2/gcgdata/geneseq/AA1997.DAT:*
20: /SIDS2/gcgdata/geneseq/AA1998.DAT:*
21: /SIDS2/gcgdata/geneseq/AA1999.DAT:*
22: /SIDS2/gcgdata/geneseq/AA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	30	85.7	8	21	AA06764
2	30	85.7	8	21	AA06814
3	30	85.7	8	21	AA06916
4	27	77.1	8	21	AA06583
5	27	77.1	8	21	AA06636
6	27	77.1	8	21	AA06645
7	27	77.1	8	21	AA06688
8	25	71.4	6	21	AA06762
9	25	71.4	6	21	AA06812
10	25	71.4	7	21	AA06763
11	25	71.4	7	21	AA06813

12	25	71.4	8	21	AA06770	Claudin-6/9 cyclic
13	25	71.4	8	21	AA06779	Claudin-6/9 cyclic
14	25	71.4	8	21	AA06787	Claudin-6/9 cyclic
15	25	71.4	8	21	AA06796	Claudin-6/9 cyclic
16	25	71.4	8	21	AA06804	Claudin-6/9 cyclic
17	24	68.6	8	21	AA06819	Claudin-1 cell adh
18	24	68.6	8	21	AA06847	Claudin-1 cell adh
19	22	62.9	6	21	AA06581	Claudin-3 cell adh
20	22	62.9	6	21	AA06634	Claudin-3 cyclic c
21	22	62.9	6	21	AA06643	Claudin-3 cyclic c
22	22	62.9	6	21	AA06696	Claudin-4 cell adh
23	22	62.9	7	21	AA06582	Claudin-4 cyclic c
24	22	62.9	7	21	AA06635	Claudin-3 cell adh
25	22	62.9	7	21	AA06644	Claudin-3 cyclic c
26	22	62.9	7	21	AA06697	Claudin-4 cell adh
27	22	62.9	8	21	AA06521	Claudin-4 cyclic c
28	22	62.9	8	21	AA06574	Claudin-2 cell adh
29	22	62.9	8	21	AA06590	Claudin-2 cyclic c
30	22	62.9	8	21	AA06599	Claudin-3 cyclic c
31	22	62.9	8	21	AA06608	Claudin-3 cyclic c
32	22	62.9	8	21	AA06617	Claudin-3 cyclic c
33	22	62.9	8	21	AA06626	Claudin-3 cyclic c
34	22	62.9	8	21	AA06652	Claudin-4 cyclic c
35	22	62.9	8	21	AA06661	Claudin-4 cyclic c
36	22	62.9	8	21	AA06670	Claudin-4 cyclic c
37	22	62.9	8	21	AA06679	Claudin-4 cyclic c
38	22	62.9	8	21	AA06688	Claudin-4 cyclic c
39	22	62.9	8	21	AA06697	Claudin-8 cell adh
40	22	62.9	8	21	AA06897	Claudin-8 cyclic c
41	22	62.9	8	21	AA06918	Claudin-8 cell adh
42	21	60.0	6	4	AA030170	Sequence of a cycl
43	21	60.0	6	6	AA050739	Somatostatin analo
44	21	60.0	6	6	AA050741	Somatostatin analo
45	21	60.0	6	7	AA061336	Sequence of novel
46	21	60.0	6	21	AA06704	Claudin-5 cell adh
47	21	60.0	6	21	AA06754	Claudin-5 cyclic c
48	21	60.0	7	21	AA06705	Caludin-5 cell adh
49	21	60.0	7	21	AA06755	Claudin-5 cyclic c
50	21	60.0	8	21	AA06426	Claudin-1 cell adh

ALIGNMENTS

RESULT 1	
AA06764	standard; peptide; 8 AA.
ID	
XX	
AC	AA06764;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.
XX	
KW	Claudin-6 modulating agent; claudin-9 modulating agent;
KW	cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW	inflammatory disease; cancer; graft rejection.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 70; Page 103; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.
CC
SQ Sequence 8 AA:

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxafxg 8
111111
1 wkvtatfig 8
Db

RESULT 2
AAB06814
ID AAB06814 standard; peptide: 8 AA.
XX
AC AAB06814;
XX
DT 28-SEP-2000 (first entry)
XX
XX
DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.
XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 73; Page 104; 121pp; English.
XX
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing, and implant adhesion. In addition, they can also be used to

CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA:

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxafxg 8
111111
1 wkvtatfig 8
Db

RESULT 3
AAB06916
ID AAB06916 standard; Protein; 8 AA.
XX
AC AAB06916;
XX
DT 05-OCT-2000 (first entry)
XX
XX
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
XX Claudin modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Synthetic.
XX
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT FT
FT Modified-site 8 /note= "C-terminal amide"
XX
XX
XX PN WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 71; Page 103; 121pp; English.
XX
XX
XX The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.
CC
SQ Sequence 8 AA:

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
11 11 1
DB 1 wkvtafig 8

RESULT 4
AAB06583

ID AAB06583 standard; peptide: 8 AA.

AC AAB06583;

DT 28-SEP-2000 (first entry)

XX Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 52; Page 99; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

SO Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
11 11 1
DB 1 wkvtafig 8

RESULT 5
AAB06636

ID AAB06636 standard; peptide: 8 AA.

AC AAB06636;

DT 28-SEP-2000 (first entry)

XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 55; Page 100; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SO Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxxfxg 8
11 11 1
DB 1 wkvtafig 8

RESULT 6
AAB06645

ID AAB06645 standard; peptide: 8 AA.

AC AAB06645;

DT 28-SEP-2000 (first entry)

XX Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.

XX Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 58; Page 100; 121pp: English.

XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX

SO Sequence 8 AA;

OY 1 wxxaxfxg 8
I: I I I
Db 1 wrwtafng 8

RESULT 7
AAB06698
ID AAB06698 standard; peptide; 8 AA.
XX
AC AAB06698;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OM, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 61; Page 101; 121pp: English.
XX
CC The present invention relates to the use of peptides as claudin-mediated

CC	cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site. The present sequence has a cyclic
CC	conformation.
CC	
XX	Sequence 8 AA:
SQ	
Query Match	77.1%; Score 27; DB 21; Length 8;
Best Local Similarity	50.0%; Pred. NO. 4.3e+05;
Matches 4; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
QY	1 wxxaxfxg 8
	1:
Db	1 wvrtafg 8
RESULT 8	
AAB06762	
ID AAB06762 standard; peptide: 6 AA.	
XX	AAB06762;
AC	
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 333.
XX	
KW	Claudin-6 modulating agent; claudin-9 modulating agent;
XX	cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KM	inflammatory disease; cancer; graft rejection.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
XX	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 70; Page 103; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC	are cadherins, which are membrane glycoproteins involved in cell
CC	adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC	and these peptides can be used to modulate these levels, and thus treat
CC	autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC	healing and implant adhesion. In addition, they can also be used to
CC	facilitate drug delivery to the desired target site.
XX	
SQ	Sequence 6 AA:
Query Match	71.4%; Score 25; DB 21; Length 6;
Best Local Similarity	66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
11 11
Db 1 wkvtaf 6

RESULT 9

ID AAB06812 standard; peptide: 6 AA.

AC AAB06812;

DT 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 383.

KW Claudin-6 modulating agent; claudin-9 modulating agent;

KM cell adhesion recognition sequence; CAR sequence; autoimmune disease;

XX Inflammatory disease; cancer; graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

CC Claim 73; Page 104; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins

CC are cadherins, which are membrane glycoproteins involved in cell

CC adhesion. In some situations, cell adhesion occurs at abnormal levels,

CC and these peptides can be used to modulate these levels, and thus treat

CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to

CC facilitate drug delivery to the desired target site. The present

CC sequence has a cyclic conformation.

XX Sequence 6 AA;

SO

XX

XX

XX

DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 334.
XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KM cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KM inflammatory disease; cancer; graft rejection.

XX Mammalia.

OS WO200026360-A1.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

CC Claim 70; Page 103; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins

CC are cadherins, which are membrane glycoproteins involved in cell

CC adhesion. In some situations, cell adhesion occurs at abnormal levels,

CC and these peptides can be used to modulate these levels, and thus treat

CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to

CC facilitate drug delivery to the desired target site.

XX Sequence 7 AA;

SO

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 384.
XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KM cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KM inflammatory disease; cancer; graft rejection; cyclic.

XX Mammalia.

OS WO200026360-A1.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

CC Claim 70; Page 103; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins

CC are cadherins, which are membrane glycoproteins involved in cell

CC adhesion. In some situations, cell adhesion occurs at abnormal levels,

CC and these peptides can be used to modulate these levels, and thus treat

CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to

CC facilitate drug delivery to the desired target site.

XX Sequence 7 AA;

SO

XX

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XX

XX

PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 7 AA:

Query Match 71.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
11 11
Db 1 wkvtaf 6

RESULT 12

AAB06770
ID AAB06770 standard; peptide: 8 AA.

XX AAB06770;

XX 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 341.

XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX

OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 103; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA:

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
11 11
Db 2 wkvtaf 7

RESULT 13

AAB06779
ID AAB06779 standard; peptide: 8 AA.

XX AAB06779;

XX 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 350.

XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX

OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA:

Query Match 71.4%; Score 25; DB 21; Length 8;

Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
1111
Db 2 wkvtaf 7

RESULT 14
AAB06787
ID AAB06787 standard; peptide; 8 AA.

AC AAB06787;

DT 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 358.
XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
XX cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.
OS
PN WO200026360-A1.

XX 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

PT WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vascopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 73; Page 104; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.

XX Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
1111
Db 2 wkvtaf 7

RESULT 15

AAB06796
ID AAB06796 standard; peptide; 8 AA.

XX AAB06796;

DT 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 367.

XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.
OS

PN WO200026360-A1.

XX 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

PT WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vascopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 73; Page 104; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.

XX Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxaf 6
1111
Db 2 wkvtaf 7

RESULT 16
AAB06804
ID AAB06804 standard; peptide; 8 AA.

XX AAB06804;

DT 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 375.

XX
XX Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection; cyclic.
XX
XX Mammalia.
OS

PN WO200026360-A1.

XX 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 73; Page 104; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxaf 6
1111
2 wkvtaf 7
Db

RESULT 17
AAB06419
ID AAB06419 standard; peptide; 8 AA.
XX
AC AAB06419;
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX
PS Claim 39; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wkxxafxg 8
11::1
1 wklysyag 8
Db

RESULT 18
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 wxxxxfxg 8
1 : : 1
DB 1 wklvysag 8

RESULT 19
AAB06581
ID AAB06581 standard; peptide: 6 AA.
XX AAB06581;
AC
XX 28-SEP-2000 (first entry)
XX
XX
XX Claudin-3 cell adhesion recognition sequence SEQ ID NO: 56.
DE
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 52; Page 99; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 6 AA;

Query Match 62.9%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wxxxxaf 6
1 : : 1
DB 1 wlvysaf 6
OY
RESULT 20
AAB06634
ID AAB06634 standard; peptide: 6 AA.
XX
XX AAB06634;
AC

XX 28-SEP-2000 (first entry)
DT
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 267.
DE
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 55; Page 100; 121pp; English.
PS
XX

The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation.
CC
CC
XX
XX Sequence 6 AA;

Query Match 62.9%; Score 22; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wxxxxaf 6
1 : : 1
DB 1 wlvysaf 6
OY
RESULT 21
AAB06643
ID AAB06643 standard; peptide: 6 AA.
XX
XX AAB06643;
AC
XX 28-SEP-2000 (first entry)
XX
XX Claudin-4 cell adhesion recognition sequence SEQ ID NO: 48.
DE
XX Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX
XX 11-MAY-2000.
PD

Query Match 62.9%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wxxxxaf 6
I: | |
Db 1 wrvsaf 6

RESULT 24
AAB06635
ID AAB06635 standard; peptide: 7 AA.

XX AAB06635;
XX 28-SEP-2000 (first entry)
XX
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 268.
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX Mammalia.
XX WO200026360-A1.
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 55: Page 100; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-3 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.
XX
XX Sequence 7 AA:
SQ

Query Match 62.9%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxaf 6
I: | |
Db 1 wrvsaf 6

RESULT 25
AAB06644
ID AAB06644 standard; peptide: 7 AA.

AC AAB06644;
XX
XX 28-SEP-2000 (first entry)
XX
XX
XX Claudin-4 cell adhesion recognition sequence SEQ ID NO: 49.
XX
XX Claudin-4 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
XX Mammalia.
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 58: Page 100; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-4 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site.
XX
XX Sequence 7 AA:
SQ

Query Match 62.9%; Score 22; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxxxaf 6
I: | |
Db 1 wrvtaf 6

Search completed: January 14, 2002, 07:43:16
Job time: 427 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:36 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1D

Perfect score: 35

Sequence: 1 WXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

43125

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 8
Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents.AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiletest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	54.3	7	1	US-08-321-625-86 Sequence 86, Appl
2	19	54.3	7	2	US-08-500-956-2 Sequence 2, Appl
3	19	54.3	7	2	US-08-495-508-3 Sequence 3, Appl
4	19	54.3	7	4	US-09-181-083-86 Sequence 86, Appl
5	18	51.4	5	1	US-08-240-511-1 Sequence 1, Appl
6	17	48.6	5	1	US-08-190-802A-263 Sequence 263, App
7	17	48.6	5	4	US-08-477-346-263 Sequence 263, App
8	16	45.7	3	4	US-09-461-697-405 Sequence 405, App
9	16	45.7	4	1	US-08-079-445-3 Sequence 3, Appl
10	16	45.7	4	1	US-07-840-077A-7 Sequence 7, Appl
11	16	45.7	4	1	US-08-454-950-7 Sequence 7, Appl
12	16	45.7	4	1	US-08-434-761-3 Sequence 3, Appl
13	16	45.7	4	1	US-08-338-890B-1 Sequence 1, Appl
14	16	45.7	4	1	US-08-454-949-7 Sequence 7, Appl
15	16	45.7	4	2	US-08-671-487A-8 Sequence 8, Appl
16	16	45.7	4	2	US-08-340-208B-1 Sequence 1, Appl
17	16	45.7	4	2	US-08-651-179B-2 Sequence 2, Appl
18	16	45.7	4	3	US-08-651-179B-3 Sequence 3, Appl
19	16	45.7	4	3	US-08-997-263-1 Sequence 1, Appl
20	16	45.7	4	3	US-09-315-861-5 Sequence 5, Appl
21	16	45.7	4	3	US-08-981-122-25 Sequence 25, Appl
22	16	45.7	4	4	US-08-435-568A-19 Sequence 19, Appl
23	16	45.7	4	4	US-08-682-767-29 Sequence 29, Appl
24	16	45.7	4	4	US-08-682-767-30 Sequence 30, Appl
25	16	45.7	5	1	US-07-657-769B-36 Sequence 36, Appl
26	16	45.7	5	1	US-08-068-947-1 Sequence 1, Appl
27	16	45.7	5	1	US-08-068-947-3 Sequence 3, Appl

28	16	45.7	5	1	US-07-973-235A-19 Sequence 19, Appl
29	16	45.7	5	1	US-08-332-071B-1 Sequence 1, Appl
30	16	45.7	5	1	US-08-332-071B-2 Sequence 2, Appl
31	16	45.7	5	1	US-08-486-057B-22 Sequence 22, Appl
32	16	45.7	5	1	US-07-789-184-97 Sequence 97, Appl
33	16	45.7	5	1	US-08-416-007-1 Sequence 1, Appl
34	16	45.7	5	1	US-08-416-007-5 Sequence 5, Appl
35	16	45.7	5	1	US-07-902-935-1 Sequence 1, Appl
36	16	45.7	5	1	US-08-475-263-97 Sequence 97, Appl
37	16	45.7	5	1	US-08-485-886-97 Sequence 97, Appl
38	16	45.7	5	2	US-08-465-764-2 Sequence 2, Appl
39	16	45.7	5	2	US-08-475-751-1 Sequence 1, Appl
40	16	45.7	5	2	US-08-475-751-5 Sequence 5, Appl
41	16	45.7	5	2	US-08-470-932-1 Sequence 1, Appl
42	16	45.7	5	2	US-08-467-025-1 Sequence 1, Appl
43	16	45.7	5	2	US-08-477-362-97 Sequence 97, Appl
44	16	45.7	5	2	US-08-462-720-19 Sequence 19, Appl
45	16	45.7	5	2	US-08-477-134-97 Sequence 97, Appl
46	16	45.7	5	2	US-08-347-397-2 Sequence 2, Appl
47	16	45.7	5	2	US-08-347-397-7 Sequence 7, Appl
48	16	45.7	5	2	US-08-347-397-8 Sequence 8, Appl
49	16	45.7	5	2	US-08-347-397-9 Sequence 9, Appl
50	16	45.7	5	2	US-08-347-397-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-321-625-86
Sequence 86, Application US/08321625
Patent No. 5639860
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mike
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Elji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 NO. 5639860th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.33366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO.: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-321-625-86

Query Match 54.3%; Score 19; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
111
Db 3 WKCTA 7

RESULT 2
US-08-500-956-2
Sequence 2, Application US/08500956
Patent No. 5650269
GENERAL INFORMATION:
APPLICANT: STEFAS, ELIE
APPLICANT: ROCHEFON, MARCEL
APPLICANT: GRAAFLAND, HUBERT
TITLE OF INVENTION: METHOD FOR DETECTING VIRAL COMPOUNDS
TITLE OF INVENTION: USING A VIRAL PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, IP GROUP OF
ADDRESSEE: PILLSBURY MADISON &
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500, 956
FILING DATE: 09-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 60649/219388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-500-956-2

Query Match 54.3%; Score 19; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
111
Db 2 WKSDA 6

RESULT 3
US-08-495-509-3

Sequence 3, Application US/08495508
Patent No. 5859213
GENERAL INFORMATION:
APPLICANT: STEFAS, ELIE
APPLICANT: ROCHEFON, MARCEL
APPLICANT: GRAAFLAND, HUBERT
TITLE OF INVENTION: AQUEOUS PROTEIN COMPOSITION,
TITLE OF INVENTION: GLYCOPROTEIN CONTAINED THEREIN, PREPARATION METHOD
TITLE OF INVENTION: THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495, 508
FILING DATE: 23-OCT-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/01399
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00143
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 219390/LA-112117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-495-508-3

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
111
Db 2 WKSDA 6

RESULT 4
US-09-181-083-86
Sequence 86, Application US/09181083
Patent No. 6194195
GENERAL INFORMATION:
APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshikazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao
APPLICANT: TSUKUDA, Elji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko

```

: APPLICANT: YAMAGUCHI, Kazuo
: APPLICANT: MATSUDA, Yuzuru
: TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
: NUMBER OF SEQUENCES: 92
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
: STREET: 1300 NO. 6194195th Seventeenth Street, Suite 1800
: CITY: Arlington
: STATE: VA
: COUNTRY: USA
: ZIP: 22209
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/181,083
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/321,625
: FILING DATE: 12-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: TERRY, David T.
: REGISTRATION NUMBER: 20,178
: REFERENCE/DOCKET NUMBER: 506.32366PX1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-312-6600
: TELEFAX: 703-312-6666
: INFORMATION FOR SEQ. ID NO.: 86:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: US-08-240-511-1

Query Match 54.3%: Score 19; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxa 5
Db 3 WKCTA 7

RESULT 5
US-08-240-511-1
: Sequence 1, Application US/08240511
: Patent No. 5643722
: GENERAL INFORMATION:
: APPLICANT: ROTHSCCHILD, Kenneth J.
: APPLICANT: SONAR, Sanjay M.
: TITLE OF INVENTION: METHODS FOR THE DETECTION AND ISOLATION OF PROTEINS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: BAKER & BOTTIS, L.L.P.
: STREET: 1299 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20004-2400
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/240,511
: FILING DATE: 11-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Remenick, James
: REGISTRATION NUMBER: 36,902
: REFERENCE/DOCKET NUMBER: 16865-0128
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-639-7700
: TELEFAX: 202-639-7890
: TELEX:
: INFORMATION FOR SEQ. ID NO.: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: US-08-240-511-1
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Query Match 51.4%: Score 18; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wkxxa 5
Db 1 WKYVA 5
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RESULT 6
US-08-190-802A-263
: Sequence 263, Application US/08190802A
: Patent No. 5519003
: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Daria
: APPLICANT: Ron, Dorit
: TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Dehlinger & Associates
: STREET: P.O. Box 60850
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306-0850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/190,802A
: FILING DATE: 01-FEB-1994
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Fadian, Gary R.
: REGISTRATION NUMBER: 33,875
: REFERENCE/DOCKET NUMBER: 8600-0139
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ. ID NO.: 263:
: SEQUENCE CHARACTERISTICS:
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LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-190-802A-263

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 40.0%; Pred No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
1: 1
Db 1 WRTAA 5

RESULT 7
US-08-477-346-263
; Sequence 263, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Kon, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTAA peptide
; US-08-477-346-263

Query Match 48.6%; Score 17; DB 4; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wkxxa 5
1: 1
Db 1 WRTAA 5

RESULT 8
US-09-461-697-405
; Sequence 405, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Putnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 405
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-405

Query Match 45.7%; Score 16; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
1: 1
Db 2 WK 3

RESULT 9
US-08-079-445-3
; Sequence 3, Application US/08079445
; Patent No. 5440016
; GENERAL INFORMATION:
; APPLICANT: Blondelle, Sylvie E.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Eichler, Julia
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
; TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/079,445
; FILING DATE: 18-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-HP 9648
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa-XKfmc"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa-any amino acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "C-terminal amino acid is
OTHER INFORMATION: amldated"
US-08-079-445-3

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
DB 2 wk 3

RESULT 10
US-07-840-077A-7
Sequence 7, Application US/07840077A
Patent No. 5443816
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Zamora, Paul O.
APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Peptide-Metal Ion
TITLE OF INVENTION: Pharmaceutical Preparation and Method
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomed Incorporated
STREET: 4261 Balloon Park
CITY: Albuquerque
STATE: NM
COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordperfect 6.0a for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/840,077A
FILING DATE: 20-FEB-1992
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:

TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: No
ANTI-SENSE: No
US-07-840-077A-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
DB 2 wk 3

RESULT 11
US-08-454-950-7
Sequence 7, Application US/08454950
Patent No. 5690905
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Zamora, Paul O.
APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Peptide-Metal Ion
TITLE OF INVENTION: Pharmaceutical Preparation and Method
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomed Incorporated
STREET: 4261 Balloon Park
CITY: Albuquerque
STATE: NM
COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordperfect 6.0a for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,950
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: No
ANTI-SENSE: No
US-08-454-950-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 2 WK 3

RESULT 12
US-08-434-761-3
; Sequence 3, Application US/08434761
; Patent No. 5698673
; GENERAL INFORMATION:
; APPLICANT: Blondelle, Sylvie E.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Eichler, Julia
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
; TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,761
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/079,445
; FILING DATE: 18-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-HP 9648
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Xaa=KfMOC"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa-any amino acid"
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "C-terminal amino acid is
; OTHER INFORMATION: amidated"
; US-08-434-761-3

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 2 WK 3

RESULT 13
US-08-338-890B-1
; Sequence 1, Application US/08338890B
; Patent No. 5700905
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spaveello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,890B
; FILING DATE: NOV. 14, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malinoski, Lynn
; REGISTRATION NUMBER: 38,788
; REFERENCE/DOCKET NUMBER: UPN-2040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)568-3100
; TELEFAX: (215)568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-338-890B-1

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 2 WK 3

RESULT 14
US-08-454-949-7
; Sequence 7, Application US/08454949
; Patent No. 5759516
; GENERAL INFORMATION:
; APPLICANT: Zamora, Paul O.
; APPLICANT: Rhodes, Buck A.
; TITLE OF INVENTION: Peptide-Metal Ion
; TITLE OF INVENTION: Pharmaceutical Preparation and Method
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhoad Incorporated
; STREET: 4261 Balloon Park
; CITY: Albuquerque
; STATE: NM

COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: WordPerfect 6.0a for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,949
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
TELEFAX: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-454-949-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wk 2
11
Db 2 wk 3

RESULT 15
US-08-671-487A-8
Sequence 8, Application US/08671487A
Patent No. 5955577
GENERAL INFORMATION:
APPLICANT: MAYO, KEVIN H.
TITLE OF INVENTION: SYNTHETIC APPROACH TO DESIGNED CHEMICAL
STRUCTURES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P. A.
STREET: 203 TEXTILE BUILDING, 119 NORTH FOURTH STREET
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,487A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, MYRA H.
REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 110.00330101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1225
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-671-487A-8

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wk 2
11
Db 2 wk 3

RESULT 16
US-08-340-208B-1
Sequence 1, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
METHODS THEREFOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694-15
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-208B-1

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wk 2
11
Db 2 wk 3

RESULT 17
US-08-651-179B-2
; Sequence 2, Application US/08651179B
; Patent No. 5985240
; GENERAL INFORMATION:
; APPLICANT: Zamora, Paul O.; Rhodes, Buck A.; Marek,
; APPLICANT: Michael J.
; TITLE OF INVENTION: Peptide Radiopharmaceutical
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Ave.
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
; COMPUTER: IBM PC/XT/AT, IBM PS/2 or
; OPERATING SYSTEM: PC-DOS or MS-DOS
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,179B
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/447,453
; FILING DATE: 23-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADDA C. GOGORIS
; REGISTRATION NUMBER: 29,714
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHEICAL: No
; ANTI-SENSE: No
; US-08-651-179B-2

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
Db 2 wk 3

RESULT 18
US-08-651-179B-3
; Sequence 3, Application US/08651179B
; Patent No. 5985240
; GENERAL INFORMATION:
; APPLICANT: Zamora, Paul O.; Rhodes, Buck A.; Marek,
; APPLICANT: Michael J.
; TITLE OF INVENTION: Peptide Radiopharmaceutical
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Ave.
; CITY: New York

STATE: NY
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,179B
FILING DATE: 21-MAY-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/447,453
FILING DATE: 23-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADDA C. GOGORIS
REGISTRATION NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: No
ANTI-SENSE: No
US-08-651-179B-3

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
Db 2 wk 3

RESULT 19
US-08-997-263-1
; Sequence 1, Application US/08997263
; Patent No. 6001960
; GENERAL INFORMATION:
; APPLICANT: Hirschmann, Ralph
; APPLICANT: Spanavello, Rolando
; APPLICANT: Nutt, Ruth
; TITLE OF INVENTION: Synthetic Somatostatin Mimics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960r1s
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/WINDOWS
; SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/338,890
; FILING DATE: NOV. 14, 1994

ATTN/AGENCY INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-997-263-1

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 2 WK 3

RESULT 20
US-09-315-861-5
Sequence 5, Application US/09315861
Patent No. 6114160
GENERAL INFORMATION:
APPLICANT: Rodney B. Croteau, Mark R. Willung
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TAXOL
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Donald L. Stephens Jr.
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,363
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Donald L. Stephens Jr.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-46842/DLS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acid residues
TYPE: amino acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-09-315-861-5

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 3 WK 4

RESULT 21
US-08-981-122-25
Sequence 25, Application US/08981122B
Patent No. 6127339
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981,122B
CURRENT FILING DATE: 1997-12-18
PRIOR FILING DATE: 1995-06-21
PRIOR APPLICATION NUMBER: PCT/JP96/01734
PRIOR FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 4
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of a peptide synthesized in Example 4 from L-form
Patent No. 6127339
OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide
OTHER INFORMATION: synthesizing system (Ramps)
US-08-981-122-25

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 3 WK 4

RESULT 22
US-08-435-568A-19
Sequence 19, Application US/08435568A
Patent No. 6143298
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
APPLICANT: Davis, Gary
TITLE OF INVENTION: Soluble Truncated Forms of ICAM-1
FILE REFERENCE: MCI 208,4C2D2
CURRENT APPLICATION NUMBER: US/08/435,568A
CURRENT FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 4
TYPE: PPT
ORGANISM: Homo sapiens
US-08-435-568A-19

Query Match 45.7%; Score 16; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wk 2
11
DB 1 WK 2

RESULT 23
US-08-682-767-29
; Sequence 29, Application US/08682767
; Patent No. 6291741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,767
; FILING DATE: 30-July-96
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 51735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-682-767-29

Query Match 45.7%; Score 16; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
DB 3 WK 4

RESULT 24
US-08-682-767-30
; Sequence 30, Application US/08682767
; Patent No. 6291741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,767
; FILING DATE: 30-July-96
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 51735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-682-767-30

Query Match 45.7%; Score 16; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wk 2
11
DB 3 WK 4

RESULT 25
US-07-657-769B-36
; Sequence 36, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-657-769B-36

4

Query Match 45.78; Score 16; DB 1; Length 5;
Best Local Similarity 100.08; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WK 2
DB 1 WK 2

Search completed: January 14, 2002, 07:41:36
Job time: 457 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:22 ; Search time 43.28 Seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1E
Perfect score: 36
Sequence: 1 wrxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: PIR_68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	50.0	7	2	S33245 neuromodulatory pe
2	15	41.7	7	2	S33244 neuromodulatory pe
3	15	41.7	7	2	S33246 neuromodulatory pe
4	13	36.1	8	2	S63493 dissimilatory sulf
5	12	33.3	5	2	B61445 Leu-enkephalin - b
6	12	33.3	5	2	A61445 Met-enkephalin - b
7	12	33.3	5	2	PT0278 Ig heavy chain CRD
8	12	33.3	6	2	A41946 T-cell receptor ga
9	12	33.3	7	2	A60224 Met-enkephalin-Arg
10	12	33.3	8	2	P00012 cholecystokinin -
11	12	33.3	8	2	A43001 cholecystokinin -
12	12	33.3	8	2	A42057 fibroblast growth
13	13	33.3	8	2	A38887 T-cell receptor ga
14	11	30.6	3	2	F37196 bradykinin-potenti
15	11	30.6	4	2	A37832 phenol 2-monooxyge
16	11	30.6	4	2	A34626 RPKC-related neuro
17	11	30.6	4	2	PT0240 Ig heavy chain CRD
18	11	30.6	4	2	B53284 T-cell receptor be
19	11	30.6	4	2	PT0661 T-cell receptor be
20	11	30.6	5	2	A32516 cholecystokinin-5
21	11	30.6	5	2	I40469 dnazx-like protein
22	11	30.6	5	2	A60803 neuropeptide - sea
23	11	30.6	5	2	JH0253 gut pentapeptide -
24	11	30.6	5	2	G37196 bradykinin-potenti
25	11	30.6	5	2	PT0281 Ig heavy chain CRD
26	11	30.6	5	2	PT0308 Ig heavy chain CRD
27	11	30.6	5	2	PT0729 T-cell receptor be
28	11	30.6	5	2	PT0580 T-cell receptor be
29	11	30.6	6	2	S66195 alcohol dehydrogen

30	11	30.6	6	2	B34835 dnaa protein - pse
31	11	30.6	6	2	A31263 dihydrofolate redu
32	11	30.6	6	2	B31263 dihydrofolate redu
33	11	30.6	6	2	A61068 locus-takinin - mig
34	11	30.6	6	2	B35640 cerebellar degener
35	11	30.6	6	2	PT0632 T-cell receptor be
36	11	30.6	6	2	PT0532 T-cell receptor be
37	11	30.6	6	2	PT0519 T-cell receptor be
38	11	30.6	6	2	PT0637 T-cell receptor be
39	11	30.6	6	2	PT0641 T-cell receptor be
40	11	30.6	6	2	PT0726 T-cell receptor be
41	11	30.6	6	2	F41946 T-cell receptor ga
42	11	30.6	6	2	PD0028 pev-kinin 2 - pena
43	11	30.6	6	4	I79564 hypothetical TGL3
44	11	30.6	7	1	NYPG7 hypothalamic hepta
45	11	30.6	7	2	A60139 fatty-acid synthas
46	11	30.6	7	2	S21230 dermorphin (Trp-4,
47	11	30.6	7	2	A58512 venom heptapeptide
48	11	30.6	7	2	A61081 tryptophyllin, bas
49	11	30.6	7	2	S57274 triacylglycerol 11
50	11	30.6	7	2	S09652 hypothetical prote

ALIGNMENTS

RESULT 1
S33245
neuromodulatory peptide Wmamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33245
A:Accession: S33244; MUID:93265912
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 50.0%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxs 5
DB 1 WREMS 5

RESULT 2
S33244
neuromodulatory peptide Wmamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 41.7%; Score 15; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxs 5
DB 1 WREMS 5

DB 1 WKMS 5

RESULT 3

S33246

neuromodulatory peptide Wwamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33246

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 41.7%; Score 15; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxs 5
| |
DB 1 WKQMS 5

RESULT 4

S63493

dissimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio

C:Species: Desulfovibrio desulfuricans

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S63493; S63494

R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A:Reference number: S63489; MUID:96085152

A:Accession: S63493

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STB>

A:Accession: S63494

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STB>

Query Match 36.1%; Score 13; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 syxg 8
| |
DB 4 TYKG 7

RESULT 5

B61445

Leu-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: B61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A:Reference number: A61445; MUID:84144823

A:Accession: B61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
DB 1 YGG 3

RESULT 6

A61445

Met-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: A61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A:Reference number: A61445; MUID:84144823

A:Accession: A61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
DB 1 YGG 3

RESULT 7

PT0278

Ig heavy chain CRD3 region (clone 4-88) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0278

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0278

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
| |
DB 1 YFG 3

RESULT 8

A41946

T-cell receptor gamma chain (1t.22) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A41946

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma

A:Reference number: A41946; MUID:92049316

A:Accession: A41946

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WH>
C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 1 YRG 3

RESULT 9
A60224

Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Modden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:title: Isolation and characterization of opioid peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91223680
A:Accession: A60224
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAD>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 1 YRG 3

RESULT 10
PQ0012

cholecystokinin - southeastern quoll
N:Alternate names: CCK
C:Species: Dasyurus viverrinus (southeastern quoll)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C:Accession: PQ0012
R:Pan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: PQ0012
A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 2 YMG 4

RESULT 11
A43001

cholecystokinin - tammar wallaby

N:Alternate names: CCK
C:Species: Macropus eugenii (tammar wallaby)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C:Accession: A43001; PQ0012
R:Pan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: A43001

A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 2 YMG 4

RESULT 12

fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:title: Differential splicing in the extracellular region of fibroblast growth facto
A:Reference number: A42057; MUID:92107200
A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <MER>
A:Cross-references: GB:M80363.
C:Keywords: growth factor receptor

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 syxg 8
| |
Db 5 SFLG 8

RESULT 13

A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whitsett, M.; Mosley, R.L.; Whitsett, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WH>
C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.2e+05;

Matches 1; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 wxsxy 6
|
:

Db 3 WDSGF 8

RESULT 14

F37196

bradykinin-potentiating peptide 6 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C:Accession: F37196

R:Cifra, A.C.O.; Vieira, G.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides 4

A:Reference number: A37196; MUID:90351557

A:Accession: F37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <GIN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
3 w 3

Db

RESULT 15

A37832

phenol 2-monooxygenase (EC 1.14.13.7) chain p5 - Pseudomonas sp. (strain CF600) (fragment

C:Species: Pseudomonas sp.

C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993

C:Accession: A37832

R:Powlowski, J.; Shingler, V.

J. Bacteriol. 172, 6834-6840, 1990

A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxyl

A:Reference number: A37832; MUID:91072231

A:Accession: A37832

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <POW>

C:Keywords: oxidoreductase

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sy 6
|
1 1
1 sy 2

Db

RESULT 16

A34626

RPGH-related neuropeptide - ferruginous spindle

C:Species: Fusinus ferrugineus (ferruginous spindle)

C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C:Accession: A34626

R:Kuraki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A:Title: A molluscan neuropeptide related to the crustacean hormone, RPGH.

A:Reference number: A34626; MUID:90179762

A:Accession: A34626

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
4 w 4

Db

RESULT 17

PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0240

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0240

A:Molecule type: DNA

A:Residues: 1-4 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; Immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxg 8
|
1 ypg 3

Db

RESULT 18

B53284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: B53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity an

A:Reference number: A53284; MUID:91342695

A:Accession: B53284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <HAR>

A:Cross-references: GB:S60737; NID:q233916; PIDN:AA19518.1; PID:q233918

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60738)

C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
2 w 2

Db

RESULT 19

PT0661

T-cell receptor beta chain V-D-J region (121-1Bv) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0661

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEF>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 20
A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eyssalein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest
A:Reference number: A32516; MUID:87153871
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SHI>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 21
I40469
dnaZx-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40469
R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A:Reference number: I40469; MUID:89218958
A:Accession: I40469
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: EMBL:X14796; NID:940130; PIDN:CAA32902.1; PID:94376204
C:Genetics:
A:start codon: GTC

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 sy 6
DB 2 sy 3

RESULT 22
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graft, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemone
A:Reference number: A60803; MUID:88222764
A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GRN>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 23
JH0253
gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113
A:Accession: JH0253
A:Molecule type: protein
A:Residues: 1-5 <UES>
A:Experimental source: gut
C:Comment: This peptide increased basal tone of the circular muscle of the esophagoga
, and of the circular muscle of the gastro-intestinal junction.

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 24
G37196
bradykinin-potentiating peptide 7 - island jaraaraca
C:Species: Bothrops insularis (island jaraaraca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196
R:Chintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptide
A:Reference number: A37196; MUID:90351557
A:Accession: G37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CIN>

C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 3 W 3

RESULT 25

PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 4 W 4

Search completed: January 14, 2002, 07:44:22
Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds
(without alignments)
9.889 Million coll updates/sec

Title: 09-185908-1e
Perfect score: 36
Sequence: 1 wrxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProtL39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	50.0	7	1	WMAL_ACHFU
2	15	41.7	7	1	WMA2_ACHFU
3	15	41.7	7	1	WMA3_ACHFU
4	13	36.1	7	1	NMP1_LEPDE
5	12	33.3	8	1	CCKN_MACEU
6	11	30.6	5	1	BPP7_BOTIN
7	11	30.6	5	1	UF01_MOUSE
8	11	30.6	6	1	LOK1_LOCAT
9	11	30.6	7	1	HY7_PIG
10	11	30.6	8	1	AC1_THUL
11	11	30.6	8	1	AKHG_GRYBI
12	11	30.6	8	1	AKH_LIBAU
13	11	30.6	8	1	AKH_MELML
14	11	30.6	8	1	AKH_TABAT
15	11	30.6	8	1	AL16_CARMA
16	11	30.6	8	1	GLUR_HUMAN
17	11	30.6	8	1	HTF1_PERAM
18	11	30.6	8	1	HTF2_PERAM
19	11	30.6	8	1	HTE_TENMO
20	11	30.6	8	1	LCK1_LEUMA
21	11	30.6	8	1	LCK2_LEUMA
22	11	30.6	8	1	LCK3_LEUMA
23	11	30.6	8	1	LCK4_LEUMA
24	11	30.6	8	1	LCK5_LEUMA
25	11	30.6	8	1	LCK6_LEUMA
26	11	30.6	8	1	LCK7_LEUMA
27	11	30.6	8	1	LCK8_LEUMA
28	11	30.6	8	1	PLP_BRANA
29	11	30.6	8	1	RPCH_PANBO
30	11	30.6	8	1	UPAA_HUMAN
31	9	25.0	8	1	ALL3_CYDPO
32	9	25.0	8	1	ALL4_CALVO
33	9	25.0	8	1	ALL4_CYDPO

ALIGNMENTS

RESULT 1					ALIGNMENTS				
WMAL_ACHFU	ID	WMAL_ACHFU	STANDARD:	PRT:	7	AA.			
AC	P35919;								
DT	01-JUN-1994 (Rel. 29, Created)								
DT	01-JUN-1994 (Rel. 29, Last sequence update)								
DT	01-OCT-1994 (Rel. 30, Last annotation update)								
DE	WMAMIDE-1.								
OS	Achatina fulica (Giant African snail).								
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;								
OC	Achatinacea; Achatinidae; Achatina.								
OX	NCBI_TaxID=6530;								
RN	[1]								
RP	SEQUENCE.								
RC	TISSUE=Ganglion;								
RX	MEDLINE=93265912; PubMed=8495720;								
RA	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;								
RT	"Wamide-1, -2 and -3, novel neuromodulatory peptides isolated from								
RT	ganglia of the African giant snail, Achatina fulica.";								
RL	FEBS Lett. 323:104-108(1993).								
CC	-I- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS								
CC	SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.								
DR	PIR: S33245; S33245.								
KW	Neuropeptide; Amidation.								
FT	MOD_RES								
SQ	SEQUENCE	7	AA;	993	MM;	7362D5B69B041310	CRC64;		
Query Match									
Best Local Similarity 50.0%; Score 18; DB 1; Length 7;									
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
OY	1	wrxs	5						
DB	1	wrxms	5						
RESULT 2									
WMAL_ACHFU	ID	WMAL_ACHFU	STANDARD:	PRT:	7	AA.			
AC	P35920;								
DT	01-JUN-1994 (Rel. 29, Created)								
DT	01-JUN-1994 (Rel. 29, Last sequence update)								
DT	01-OCT-1994 (Rel. 30, Last annotation update)								
DE	WMAMIDE-2.								
OS	Achatina fulica (Giant African snail).								
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;								
OC	Achatinacea; Achatinidae; Achatina.								
OX	NCBI_TaxID=6530;								
RN	[1]								
RP	SEQUENCE.								

```

RC TISSUE=ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
RW Neuropeptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B685D32310 CRC64;

Query Match
Best Local Similarity 41.7%; Score 15; DB 1; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxs 5
   1: 1
   1 WKQMS 5

RESULT 3
WMA3_ACHFU STANDARD; PRT; 7 AA.
ID WMA3_ACHFU
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE WMA3_ACHFU-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
RW Neuropeptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match
Best Local Similarity 41.7%; Score 15; DB 1; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wxxs 5
   1: 1
   1 WKQMS 5

RESULT 4
NMPL_LEPDE STANDARD; PRT; 7 AA.
ID NMPL_LEPDE
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Cucujiformia; Phytophaga; Coleoptera; Polyphaga;
OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;

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RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RX Grauwels L., van Luyven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RL a novel myotrophic neuropeptide in the Colorado potato beetle,
RL Leptinotarsa decemlineata."
RL Peptides 16:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5D0 CRC64;

Query Match
Best Local Similarity 36.1%; Score 13; DB 1; Length 7;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 yxxg 8
   1: 1
   1 AYNG 4

RESULT 5
CCKN_MACEU STANDARD; PRT; 8 AA.
ID CCKN_MACEU
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE CCKN_MACEU-3.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain; PubMed=3375140;
RX MEDLINE=88234141;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RL marsupials."
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR PIR: PQ0012; PQ0012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN: 1.
KW Amidation; Sulfation; Hormone.
FT MOD.RES 2
FT MOD.RES 2 SULFATION.
FT MOD.RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match
Best Local Similarity 33.3%; Score 12; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxxg 8
   1: 1
   2 YMG 4

RESULT 6
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE 55,2 (5A) (ANGIOTENSIN-CONVERTING
ENZYME INHIBITOR).
OS Bothrops insularis (Island Jararaca) (Quelma Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosteus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE:Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintru A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD.RES 1
SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 7
ID UF01_MOUSE STANDARD: PRT: 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE:Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RT Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON.TER 5
SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 1 W 1

RESULT 8
ID LOK1_LOCM1 STANDARD: PRT: 6 AA.

P41491.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schodis L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
TUBULES.
CC CC
CC PIR: A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD.RES 6
SQ SEQUENCE 6 AA: 654 MW: 686365A5B9CDB000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 9
ID HY7_PIG STANDARD: PRT: 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE HYPOTHALAMIC HEPTAPEPTIDE.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
ACTH-releasing activity from porcine hypothalamus.";
RL Horn. Metab. Res. 13:228-232(1981).
DR PIR: A01417; NYPG7.
SQ SEQUENCE 7 AA: 957 MW: 632845B1FB5059A0 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SY 6
DB 5 SY 6

RESULT 10
ID ACT1_THUAL STANDARD: PRT: 8 AA.

AC P18691;
DT 01-NOV-1990 (Rel. 16, Last Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE ANGIOTENSIN-CONVERTING ENZYME INHIBITOR.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle."
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 6 w 6

RESULT 11
AKHG_GRYBI STANDARD; PRT; 8 AA.
ID AKHG_GRYBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE ADIPOKINETIC HORMONE G (AKH-G) (RO 11).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus
NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetically from the corpora cardiaca of
the cricket Gryllus bimaculatus."
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1988).
RN [3]
RP FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
OS PIR: A28004; A28004.
DR InterPro: IP0002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1
SQ SEQUENCE 1
PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 8 w 8

RESULT 12
AKH_LIBAU STANDARD; PRT; 8 AA.
ID AKH_LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE ADIPOKINETIC HORMONE (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetically sequenced from a
dragonfly."
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
OS PIR: S10596; S10596.
DR InterPro: IP0002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1
FT MOD_RES 8
FT MOD_RES 1
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 8 w 8

RESULT 13
AKH_MELML STANDARD; PRT; 8 AA.
ID AKH_MELML
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer), and
OS Geotrupes stercorosus (Dor beetle).
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
NCBI_TaxID=7061, 7087, 7058;
RN [1]

RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; Pubmed=2039445;
RA Gaede G.;
RT "A unique charged lysosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginalata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; Pubmed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21653; S21653.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
FT SEQUENCE 8 AA: 1022 MW: 867AB75AB344736 CRC64:
SQ
Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 w 1
DB 8 w 8
RESULT 14
AKH_TABAT
ID AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I) (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae; Tabanus.
OX NCBI_TaxId=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; Pubmed=2813385;
RA Jaefe H., Raine A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
FT SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64:
SQ
Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 w 1
DB 8 w 8
RESULT 15
AL16_CARMA
ID AL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxId=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; Pubmed=9461295;
RA Dye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8 AMIDATION.
FT SEQUENCE 8 AA: 813 MW: 7C286BA45BA76878 CRC64:
SQ
Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 sy 6
DB 5 sy 6
RESULT 16
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; Pubmed=5126885;
RA Lote C.-J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).

-!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A SIMILAR STRUCTURE HAS ALSO BEEN FOUND.

DR PIR: A03188; XGH0U.

KW GLYCOPROTEIN. 1 S-LINKED (GAL. . .);
FT CARBOHYD 1
SQ SEQUENCE 8 AA; 855 MW; C2D87A1F5B1EB1E CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 syxg 8
DB 4 SHDG 7

RESULT 17
HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548; 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-I)
DE (PEA-CAH-I) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach).
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
Gromphodromina potentosa, Blatella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).

-!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

CC -!- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.

DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.

DR Interpro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.

FT MOD_RES 1
FT MOD_RES 8
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 18
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549; 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
DE (PEA-CAH-II) (LED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
OS Periplaneta americana (American cockroach).
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;

RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphodorrhin porticensis*, *Blattella germanica* and *Blatta orientalis*
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
RT atom bombardment mass spectrometry".
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05170; A05170.
DR PIR: S08996; S08996.
DR PIR: B44960; B44960.
DR PIR: B49823; B49823.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 1005 MW; 86745771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 19
HFE_TEMNO
ID HFE_TEMNO STANDARD; PRT; 8 AA.
AC P25419:
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR (HOFN) (HYPERTREHALOSEMIC NEUROPEPTIDE).
DE Tenebrio molitor (Yellow mealworm), and *Zophobas rugipes*.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cuculiformia; Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067, 7075;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE:90341081; Pubmed-2381871;
RA Gaede G., Koslinski G.;
RT "The primary structure of the hypertrehalosemic neuropeptide from
RT tenebrionid beetles: a novel member of the AKH/RPCH family."
RL Peptides 11:455-459(1990).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A43976; A43976.
DR PIR: B43976; B43976.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 1005 MW; 86745775B9C44736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 20
LCK1_LEUMA
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins".
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 893 MW; DC6365B449CD76A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 21
LCK2_LEUMA
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroplins".
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 852 MW; DC6365A5B9C8676A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 7 w 7

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 22
LCK3_LEUMA STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-II1).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 7 w 7

RESULT 23
LCK4_LEUMA STANDARD; PRT; 8 AA.
ID LCK4_LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD4A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;

QY 1 w 1
|
Db 7 w 7

Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24
LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE.
RP TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 7 w 7

RESULT 25
LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE.
RP TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR; JS0316; JS0316.

KV Neuropeptide: Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. NO. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

Search completed: January 14, 2002, 07:52:04
Job time: 679 sec

GenC version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:46 ; Search time 80.15 Seconds

(without alignments)
14.600 Million cell updates/sec

Title: 09-185908-1E
Perfect score: 36
Sequence: 1 wrxxyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

1: SPREMBL_17:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	44.4	8	11 Q62721	Q62721 rattus norv
2	14	38.9	8	10 Q95824	Q95824 spinacia ol
3	13	36.1	7	8 Q95945	Q95945 saccharomyc
4	12	33.3	8	2 O09258	O09258 synchococc
5	12	33.3	8	5 Q9TWH6	Q9TWH6 perineureis
6	12	33.3	8	11 P70243	P70243 mus musculu
7	12	33.3	8	11 Q9QVD3	Q9QVD3 rattus sp.
8	11	30.6	6	13 P82096	P82096 rattus sp.
9	11	30.6	7	10 O49223	O49223 rattus sp.
10	11	30.6	7	13 P82065	P82065 rattus sp.
11	11	30.6	8	2 O85406	O85406 rattus sp.
12	11	30.6	8	4 O15888	O15888 homo sapien
13	11	30.6	8	4 O15890	O15890 homo sapien
14	11	30.6	8	4 O15898	O15898 homo sapien
15	11	30.6	8	5 Q9VRD2	Q9VRD2 drosophila
16	11	30.6	8	5 P82685	P82685 periplaneta
17	11	30.6	8	5 P82686	P82686 periplaneta
18	11	30.6	8	5 P82687	P82687 periplaneta
19	11	30.6	8	5 P82688	P82688 periplaneta

20	11	30.6	8	5 P82689	P82689 periplaneta
21	11	30.6	8	6 O02831	O02831 oryctolagus
22	11	30.6	8	6 Q9TRY3	Q9TRY3 sus sp. ins
23	11	30.6	8	7 P82929	P82929 bos taurus
24	11	30.6	8	7 Q95213	Q95213 oryctolagus
25	11	30.6	8	8 Q34909	Q34909 locusta mig
26	11	30.6	8	8 Q9TD02	Q9TD02 terranatos
27	11	30.6	8	8 Q9T4Y2	Q9T4Y2 asterina pe
28	11	30.6	8	11 O35835	O35835 rattus norv
29	11	30.6	8	11 P82598	P82598 rattus norv
30	11	30.6	8	11 Q9ET18	Q9ET18 mus spreus
31	11	30.6	8	11 Q9ET17	Q9ET17 mus caroli
32	11	30.6	8	11 Q9ET16	Q9ET16 mesocricetu
33	11	30.6	8	11 Q9SMN0	Q9SMN0 mus musculu
34	11	30.6	8	13 P79940	P79940 xenopus lae
35	11	30.6	8	13 Q98TU5	Q98TU5 xenopus lae
36	9	25.0	7	12 Q9YVE3	Q9YVE3 human adeno
37	9	25.0	7	12 Q9YIR0	Q9YIR0 human adeno
38	9	25.0	7	12 Q9YIC9	Q9YIC9 human adeno
39	8	22.2	8	2 O52062	O52062 bacillus me
40	8	22.2	8	2 Q9S443	Q9S443 pseudomonas
41	8	22.2	8	2 Q9R9C2	Q9R9C2 borrelia bu
42	8	22.2	8	8 Q9GDD0	Q9GDD0 mescalita mad
43	8	22.2	8	10 P82324	P82324 pisum sativ
44	8	22.2	8	11 Q9QVF4	Q9QVF4 rattus sp.
45	7	19.4	7	2 O07354	O07354 synchococc
46	7	19.4	7	2 O50556	O50556 actinobacil
47	7	19.4	7	8 Q99182	Q99182 gnatholebia
48	7	19.4	7	12 Q9YQ10	Q9YQ10 porcine tra
49	7	19.4	7	13 P82101	P82101 litorea rub
50	7	19.4	8	2 Q56140	Q56140 streptococc

ALIGNMENTS

RESULT 1
ID Q62721 PRELIMINARY; PRT; 8 AA.
AC Q62721;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jue E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT Prohibitin-encoding genes";
RL Gene 158:291-294(1995).
DR EMBL: U17178; AAA86692.1; -;
FT NON_TER
SQ SEQUENCE 8 AA; 1150 MW; EPD237B05A41376 CRC64;

Query Match 44.4%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 2

Q9S8Z4
ID Q9S8Z4 PRELIMINARY; PRT; 8 AA.
AC Q9S8Z4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PHOTOSYSTEM I REACTION CENTER SUBUNIT IV, PSI-E.
OS Spinacia oleracea (Spinach)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=92249324; PubMed=1374333;
RA Lagoute B., Vallon O.;
RT "Purification and membrane topology of PSI-D and PSI-E, two subunits
of the photosystem I reaction center.";
RL Eur. J. Biochem. 205:1175-1185 (1992).
SQ SEQUENCE 8 AA; 1062 MW; 21458B1324069044 CRC64;

QY 2 rxxsy 6
| | |
Db 4 RRESY 8

RESULT 3
Q95945 PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DR 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INSIDE INTRON 5 (FRAGMENT).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
OG Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941 (1980).
DR EMBL; V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 36.1%; Score 13; DB 8; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
| |
Db 4 WK 5

RESULT 4
009258 PRELIMINARY; PRT; 8 AA.
AC 009258;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DR 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NIFH (FRAGMENT).
GN NIFH.
OS Synecococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RA Chen H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001780; AAC33369.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

QY 2 rxxsyxg 8
| | | |
Db 2 RQIAFYG 8

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 4.7e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 5
Q9TWH6 PRELIMINARY; PRT; 8 AA.
AC Q9TWH6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE BIOACTIVE PEPTIDE P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllodocta; Nereididae; Perinereis.
OX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95323338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.;
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
a polychaete annelid, Perinereis vancaurica.";
RL Comp. Biochem. Physiol. C,
Pharmacol. Toxicol. Endocrinol. 110:297-304 (1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CA87B0B59 CRC64;

Query Match 33.3%; Score 12; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 yxxg 8
| | | | |
Db 2 YEG 4

RESULT 6
P70243 PRELIMINARY; PRT; 8 AA.
AC P70243;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DR 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-ANG-1998 (TREMBLrel. 07, Last annotation update)
DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;

RA Ophoff R.A.:
DR Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
EMBL: X98325; CAA66969.1; -.
KW Calcium channel.
FT NON_TER 1 1
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 2
1:
Db 7 w 8

RESULT 7
O9QVD3 PRELIMINARY; PRT; 8 AA.
ID O9QVD3;
AC O9QVD3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INOSTITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE:
RA MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
cytosol."
RT J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA; 1047 MW; D72415BB06C37041 CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 2
1:
Db 3 w 4

RESULT 8
P82096 PRELIMINARY; PRT; 6 AA.
ID P82096
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE:
RC TISSUE SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella."
RT Aust. J. Chem. 52:0-0(1999).
RL Amphibian skin: Amidation.
FT MOD_RES 6 6 AMIDATION.

SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1:
Db 5 w 5

RESULT 9
O49223 PRELIMINARY; PRT; 7 AA.
ID O49223
AC O49223;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HMG-I-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=CV. ESSEX; TISSUE=ROOTS;
RC MEDLINE=91367679; PubMed=1891369;
RX "A plant DNA binding protein shares highly conserved sequence motifs
with HMG-box proteins."
RT Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047050; AAC03556.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 850 MW; 6AAANA8378637810 CRC64;

Query Match 30.6%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1:
Db 2 w 2

RESULT 10
P82065 PRELIMINARY; PRT; 7 AA.
ID P82065
AC P82065;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TRYPTOPHYLLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella". The skin peptide profile as a probe for the study
of evolutionary trends of amphibians."

RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KM Amphibian skin; Amidation; Neuropeptide.
FT MOD.RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT MOD.RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 983 MW: 74019D3676046B0 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 4 W 4

RESULT 11
ID 085406 PRELIMINARY; PRT: 8 AA.
AC 085406;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
OX NCBI_TaxId=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NINE MILE PHASE 1;
RA Willems H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
RT Coxiella burnetii.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA: 993 MW: 046B5AA453772727 CRC64;

Query Match 30.6%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 4 W 4

RESULT 12
ID 015888 PRELIMINARY; PRT: 8 AA.
AC 015888;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32069; AAA73878.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA: 993 MW: 046B5AA453772727 CRC64;

FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 1068 MW: 0315A37EAB5B0763 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 6 W 6

RESULT 13
ID 015890 PRELIMINARY; PRT: 8 AA.
AC 015890;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32083; AAA73880.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 975 MW: 605EAC65BEA5A2D3 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 1 W 1

RESULT 14
ID 015898 PRELIMINARY; PRT: 8 AA.
AC 015898;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP6A11B) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32078; AAA73888.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 938 MW: 34A415B0477B45BB CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4,7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 sy 6
 Db 2 sy 3

RESULT 15
 Q9VRD2 PRELIMINARY; PRT: 8 AA.

AC Q9VRD2; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 GN CG11666 PROTEIN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 NCBI_Taxid:7227;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BRKLEY;
 RX MEDLINE:20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandes P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Begoon K.Y., Bonos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Houtlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazolo M., Platan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein J., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03569; AAF50870.1; -;
 DR FLYBASE: FBgn0040648; CG11666;
 SO SEQUENCE 8 AA; 1062 MW; ED1185B044004376 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4,7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 30.6%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4,7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 w 1
 Db 2 w 2

RESULT 16
 P82685 PRELIMINARY; PRT: 8 AA.

AC P82685; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 GN KININ-1 (PEA-K-1).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 NCBI_Taxid:6978;
 [1]
 RN SEQUENCE, AND FUNCTION.
 RP TISSUE-CORPORA CARDIACA.
 RX MEDLINE:98010462; PubMed-9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, *Periplaneta
 americana*."
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 950 MW; 3263658449D5A774 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4,7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 w 1
 Db 7 w 7

RESULT 17
 P82686 PRELIMINARY; PRT: 8 AA.

AC P82686; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 GN KININ-2 (PEA-K-2).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattidae; Periplaneta.
 NCBI_Taxid:6978;
 [1]
 RN SEQUENCE, AND FUNCTION.
 RP TISSUE-CORPORA CARDIACA.
 RX MEDLINE:98010462; PubMed-9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, *Periplaneta
 americana*."
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

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Query Match          30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 18
P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match          30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 19
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

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CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match          30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 20
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 865 MW; C76365B449DCD775 CRC64;

Query Match          30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 21
002831 PRELIMINARY; PRT; 8 AA.
AC 002831;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
CC "Evidence for insufficient chondrocytic differentiation during repair

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RT of full-thickness defects of articular cartilage."
RL Matrix Biol. 15:39-47(1996).
DR EMBL: S83371; AAD1443.1; -
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 1028 MW: B859C7272EA77371 CRC64:

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 22

O9TRY3 PRELIMINARY; PRT; 8 AA.
ID O9TRY3
AC O9TRY3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Sulina; Suidae; Sus.
RX NCB1_TaxID=9826;
RN [1]
RP SEQUENCE.
RA MEDLINE=92049376; Pubmed=1719383;
RA Shimizu S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6."
RL Mol. Endocrinol. 5:938-948(1991).
SQ SEQUENCE 8 AA: 850 MW: 9FB2CEA37EA7687D CRC64:

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 5 w 5

RESULT 23

P82929 PRELIMINARY; PRT; 8 AA.
ID P82929
AC P82929;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE.
RA TISSUE=LIVER;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremull L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
RT of the full complement ribosomal proteins present."
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
DE -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 935 MW: 9639D1A72058637D CRC64:

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 24

O95213 PRELIMINARY; PRT; 8 AA.
ID O95213
AC O95213;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE GERM LINE DH (DF) GENE (FRAGMENT).
GN DF.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RX NCB1_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F-1/RGM;
RA Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
RL Mol. Immunol. 0:0-0(0).
DR EMBL: U62585; AAB18735.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 845 MW: 5CA861B5AB58677B CRC64:

Query Match 30.6%; Score 11; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
DB 1 ypg 3

RESULT 25

O34909 PRELIMINARY; PRT; 8 AA.
ID O34909
AC O34909;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE CYTOCHROME B (FRAGMENT).
OS Locusta migratoria (migratory locust).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
RX NCB1_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223478; Pubmed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene."
RL Curr. Genet. 11:625-630(1987).
DR EMBL: X05286; CAA28905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 1019 MW: F8E33723304B45B6 CRC64:

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 sy 6

db 2 sy 3

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:16 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1E
Perfect score: 36
Sequence: 1 wrxxyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: A_Geneseq_1101.*
2: /SID2/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SID2/gcgdata/geneseq/geneseq/AA1981.DAT:*
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6: /SID2/gcgdata/geneseq/geneseq/AA1984.DAT:*
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22: /SID2/gcgdata/geneseq/geneseq/AA2000.DAT:*
23: /SID2/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	88.9	8	21	AA06521
2	32	88.9	8	21	AA06574
3	31	86.1	8	21	AA06426
4	31	86.1	8	21	AA06512
5	28	77.8	8	21	AA06419
6	28	77.8	8	21	AA06479
7	28	77.8	8	21	AA06823
8	28	77.8	8	21	AA06876
9	28	77.8	8	21	AA06917
10	27	75.0	6	21	AA06519
11	27	75.0	6	21	AA06572

12	27	75.0	7	21	AA06520	Claudin-2 cell adh
13	27	75.0	7	21	AA06573	Claudin-2 cyclc c
14	27	75.0	8	21	AA06528	Claudin-2 cyclc c
15	27	75.0	8	21	AA06537	Claudin-2 cyclc c
16	27	75.0	8	21	AA06546	Claudin-2 cyclc c
17	27	75.0	8	21	AA06555	Claudin-2 cyclc c
18	27	75.0	8	21	AA06564	Claudin-2 cyclc c
19	25	69.4	6	21	AA06424	Claudin-1 cell adh
20	25	69.4	7	21	AA06510	Claudin-1 cyclc c
21	25	69.4	7	21	AA06425	Claudin-1 cell adh
22	25	69.4	7	21	AA06511	Claudin-1 cyclc c
23	25	69.4	8	21	AA06483	Claudin-1 cyclc c
24	25	69.4	8	21	AA06489	Claudin-1 cyclc c
25	25	69.4	8	21	AA06495	Claudin-1 cyclc c
26	25	69.4	8	21	AA06501	Claudin-1 cyclc c
27	25	69.4	8	21	AA06507	Claudin-1 cyclc c
28	24	66.7	8	21	AA06583	Claudin-3 cell adh
29	24	66.7	8	21	AA06636	Claudin-3 cyclc c
30	24	66.7	8	21	AA06645	Claudin-4 cell adh
31	24	66.7	8	21	AA06698	Claudin-4 cyclc c
32	22	61.1	6	21	AA06417	Claudin-1 cell adh
33	22	61.1	6	21	AA06477	Claudin-1 cyclc c
34	22	61.1	6	21	AA06821	Claudin-7 cell adh
35	22	61.1	6	21	AA06874	Claudin-7 cyclc c
36	22	61.1	7	21	AA06418	Claudin-1 cell adh
37	22	61.1	7	21	AA06478	Claudin-1 cyclc c
38	22	61.1	7	21	AA06822	Claudin-7 cell adh
39	22	61.1	7	21	AA06875	Claudin-7 cyclc c
40	22	61.1	8	21	AA06434	Claudin-1 cyclc c
41	22	61.1	8	21	AA06443	Claudin-1 cyclc c
42	22	61.1	8	21	AA06452	Claudin-1 cyclc c
43	22	61.1	8	21	AA06461	Claudin-1 cyclc c
44	22	61.1	8	21	AA06470	Claudin-1 cyclc c
45	22	61.1	8	21	AA06830	Claudin-7 cyclc c
46	22	61.1	8	21	AA06839	Claudin-7 cyclc c
47	22	61.1	8	21	AA06848	Claudin-7 cyclc c
48	22	61.1	8	21	AA06857	Claudin-7 cyclc c
49	22	61.1	8	21	AA06866	Claudin-7 cyclc c
50	21	58.3	7	21	AA06518	Claudin-2 cell adh

ALIGNMENTS

RESULT 1	
ID	AA06521 standard; peptide: 8 AA.
AC	AA06521;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX	
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OM, Symonds JM, Gour BJ;
XX	

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 8 AA;
SQ
Query Match 88.9%; Score 32; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsyxg 8
|| || |
Db 1 wrtssyvg 8
RESULT 2
AAB06574
ID AAB06574 standard; peptide; 8 AA.
AC AAB06574;
XX
XX 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
PS
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
SQ Sequence 8 AA;
Query Match 88.9%; Score 32; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsyxg 8
|| || |
Db 1 wrtssyvg 8
RESULT 3
AAB06426
ID AAB06426 standard; peptide; 8 AA.
AC AAB06426;
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
PS
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX Sequence 8 AA;
SQ
Query Match 86.1%; Score 31; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsyxg 8
|| || |
Db 1 wrtssyvg 8

```
RESULT 4
AAB06512
ID AAB06512 standard; peptide: 8 AA.
XX
AC AAB06512;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 86.1%; Score 31; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxsyxg 8
   1 1 1 1
DB 1 wrlysyag 8

RESULT 5
AAB06419
ID AAB06419 standard; peptide: 8 AA.
XX
AC AAB06419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
```

```
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908;
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxsyxg 8
   1 1 1 1
DB 1 wrlysyag 8

RESULT 6
AAB06479
ID AAB06479 standard; peptide: 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
```

CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site.
XX	
SQ	Sequence 8 AA;
QY	Query Match 77.8%; Score 28; DB 21; Length 8;
	Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches	4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Dd	1 wrxxsyxg 8
	:
	1 wqmsyag 8
RESULT	8
AAB06876	
ID	AAB06876 standard; peptide; 8 AA.
XX	
AC	AAB06876;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.
KW	Claudin-7 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW	graft rejection; cyclic.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WC-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Biaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 79; Page 105; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site. The present sequence has a cyclic
CC	conformation.
XX	
SD	Sequence 8 AA;
QY	Query Match 77.8%; Score 28; DB 21; Length 8;
	Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches	4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy	1 wrxxsyxg 8
	:
Dd	1 wqmsyag 8

	RESULT	9	
ID	AAB06917	standard; Protein:	8 AA.
XX			
AC	AAB06917;		
XX			
DJ	05-OCT-2000	(first entry)	
XX			
DE	Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.		
KW	Claudin-7 modulating agent; cell adhesion recognition sequence; car sequence; autoimmune disease; inflammatory disease; cancer; graft rejection.		
XZ	Synthetic.		
OS			
FH	Key	Location/Qualifiers	
FT	Modified-site	1	
FT	/note= "N-terminal acetyl"		
FT	Modified-site	8	
FT	/note= "C-terminal amide"		
XX			
PX	M0200026360-A1.		
PN			
PD	11-MAY-2000.		
PE	03-NOV-1999;	99WO-CAD01029.	
PR	03-NOV-1998;	98US-0185908.	
PR	30-MAR-1999;	99US-0282029.	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.		
PI	Biaschuck OW, Symonds JM, Gour BJ;		
DR	WPI: 2000-365610/31.		
PT	Antibody modulation of claudin-mediated cell adhesion for increasing vasopermeability, for delivering drugs to tumors and the nervous system and across the skin -		
PS	Claulin 77; Page 104; 121pp; English.		
CC	The present sequence is a peptide which can be used in a claudin-mediated cell adhesion modulator. The claudin group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and thus peptide can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, it can also be used to facilitate drug delivery to the desired target site.		
SQ	Sequence	8 AA;	
Query Match		77.8%; Score 28; DB 21; Length 8;	
Best Local Similarity		50.0%; Pred. No. 4.3e+05;	
Matches	4; Conservative	1; Mismatches	3; Indels
Gaps			0;
OY	1 wrxxyxg 8		
I :			
DB	1 wqmasayag 8		
Result		10	
AAB06519			
ID	AAB06519 standard; peptide;	6 AA.	
AC	AAB06519;		
DT	28-SEP-2000	(first entry)	

DE	Claudin-2 cell adhesion recognition sequence SEQ ID NO: 40.	
xx		
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;	
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW	graft rejection.	
xx		
OS	Mammalia.	
xx		
PN	WO200026360-A1.	
xx		
PD	11-MAY-2000.	
xx		
PF	03-NOV-1999; 99WO-CA01029.	
xx		
PR	03-NOV-1998; 98US-0185908.	
xx		
PR	30-MAR-1999; 99US-0282029.	
xx		
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
xx		
PI	Blaschuck OW, Symonds JM, Gour BU;	
xx		
DR	WPI: 2000-365610/31.	
xx		
PT	Antibody modulation of claudin-mediated cell adhesion for increasing	
xx	vasopermeability, for delivering drugs to tumors and the nervous system	
PT	and across the skin -	
xx		
PS	Claim 46; Page 97; 121pp: English.	
xx		
CC	The present invention relates to the use of peptides as claudin-mediated	
xx	cell adhesion modulators. The claudin-2 group of proteins are cadherins,	
CC	which are membrane glycoproteins involved in cell adhesion. In some	
xx	situations, cell adhesion occurs at abnormal levels, and these peptides	
CC	can be used to modulate these levels, and thus treat autoimmune diseases,	
xx	inflammatory diseases and cancer, and aid wound healing and implant	
CC	adhesion. In addition, they can also be used to facilitate drug delivery	
xx	to the desired target site.	
SQ	Sequence 6 AA;	
QY	1 wrxsy 6	75.0%; Score 27; DB 21; Length 6;
xx	11 11	Best Local Similarity 66.7%; Pred. NO. 4.3e+05;
DB	1 wrtsy 6	Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 11		
AAB06572		
ID	AAB06572 standard; peptide; 6 AA.	
xx		
AC	AAB06572;	
xx		
DT	28-SEP-2000 (first entry)	
xx		
DE	Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 161.	
xx		
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;	
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW	graft rejection; cyclic.	
xx		
OS	Mammalia.	
xx		
PN	WO200026360-A1.	
xx		
PD	11-MAY-2000.	
xx		
PF	03-NOV-1999; 99WO-CA01029.	
xx		
PR	03-NOV-1998; 98US-0185908.	
xx		

```

Query Match      75.0%; Score 27; DB 21; Length 6;
Best Local Similarity 66.7%; Pred No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 wrxxy 6
    | |
    | |
    | |
db 1 wrssy 6

```

	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site.
SQ	
XZ	Sequence 7 AA;
OY	
DB	
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Query Match 75.0%; Score 27; DB 21; Length 7;	
Best Local Similarity 66.7%;	
Pred. NO. 4.3e+05;	
Results:	
Seq ID No. AAB06573 standard; peptide; 7 AA.	
Amino Acid Sequence: WTSSSY	
Residue Position: 1	
Conservative Substitution: WTSYSY	
Mismatched Residues: S - Y	
Gapped Regions: None	
Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 162.	
Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cystic. Mammalia. WO200026360-AI. 11-MAY-2000. 03-NOV-1999; 99WO-CA01029. 03-NOV-1998; 98US-0185908. 30-MAR-1999; 99US-0282029. (ADHE-) ADHEREX TECHNOLOGIES INC. Blaschuck OW, Symonds JM, Gour BJ WPI: 2000-365610/31. Antibody modulation of claudin-mediated cell adhesion for increasing vascular permeability, for delivering drugs to tumors and the nervous system PT and across the skin - XX PS Claim 49; Page 98; 121pp; English. XX The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation. XX SQ Sequence 7 AA;	

75.0%; Score 27; DB 21; Length 7;

Query Match

Matches	4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	wrxxsy	6						
DB	1	wrtssy	6						
RESULT 14									
ID	AAB06528	standard;	peptide;	8	AA.				
XX									
AC	AAB06528;								
XX									
DT	28-SEP-2000	(first entry)							
XX									
DE	Claudin-2	cyclic cell adhesion recognition sequence SEQ ID NO: 117.							
XX									
KW	Claudin-2	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							
XX									
PR	03-NOV-1998;	98US-0185908.							
PR	30-MAR-1999;	99US-0282029.							
XX									
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.								
XX									
PI	Blaschuck OW, Symonds JM, Gour BJ;								
XX									
DR	WPI; 2000-365610/31.								
PT	Antibody modulation of claudin-mediated cell adhesion for increasing								
PT	vasopermeability, for delivering drugs to tumors and the nervous system								
PT	and across the skin -								
XX									
PS	Claim 49; Page 98; 121pp; English.								
XX									
CC	The present invention relates to the use of peptides as claudin-mediated								
CC	cell adhesion modulators. The claudin-2 group of proteins are cadherins,								
CC	which are membrane glycoproteins involved in cell adhesion. In some								
CC	situations, cell adhesion occurs at abnormal levels, and these peptides								
CC	can be used to modulate these levels, and thus treat autoimmune diseases,								
CC	inflammatory diseases and cancer, and aid wound healing and implant								
CC	adhesion. In addition, they can also be used to facilitate drug delivery								
CC	to the desired target site. The present sequence has a cyclic								
CC	conformation.								
XX									
SO	Sequence	8	AA;						
Query Match									
Best Local Similarity		75.0%;	Score 27;	DB 21;	Length 8;				
Matches		4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps
QY	1	wrxxsy	6						
DB	2	wrtssy	7						
RESULT 15									
ID	AAB06537	standard;	peptide;	8	AA.				
XX									
AC	AAB06537;								
XX									
DT	28-SEP-2000	(first entry)							

XX									
DE	Claudin-2	cyclic cell adhesion recognition sequence SEQ ID NO: 126.							
XX									
KW	Claudin-2	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							
XX									
PR	03-NOV-1998;	98US-0185908.							
PR	30-MAR-1999;	99US-0282029.							
XX									
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.								
XX									
PI	Blaschuck OW, Symonds JM, Gour BJ;								
XX									
DR	WPI; 2000-365610/31.								
XX									
PT	Antibody modulation of claudin-mediated cell adhesion for increasing								
PT	vasopermeability, for delivering drugs to tumors and the nervous system								
PT	and across the skin -								
XX									
PS	Claim 49; Page 98; 121pp; English.								
XX									
CC	The present invention relates to the use of peptides as claudin-mediated								
CC	cell adhesion modulators. The claudin-2 group of proteins are cadherins,								
CC	which are membrane glycoproteins involved in cell adhesion. In some								
CC	situations, cell adhesion occurs at abnormal levels, and these peptides								
CC	can be used to modulate these levels, and thus treat autoimmune diseases,								
CC	inflammatory diseases and cancer, and aid wound healing and implant								
CC	adhesion. In addition, they can also be used to facilitate drug delivery								
CC	to the desired target site. The present sequence has a cyclic								
CC	conformation.								
XX									
SO	Sequence	8	AA;						
Query Match									
Best Local Similarity		75.0%;	Score 27;	DB 21;	Length 8;				
Matches		4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps
QY	1	wrxxsy	6						
DB	2	wrtssy	7						
RESULT 16									
ID	AAB06546	standard;	peptide;	8	AA.				
XX									
AC	AAB06546;								
XX									
DT	28-SEP-2000	(first entry)							
XX									
DE	Claudin-2	cyclic cell adhesion recognition sequence SEQ ID NO: 135.							
XX									
KW	Claudin-2	modulating agent; cell adhesion recognition sequence;							
KM	CAR sequence;	autoimmune disease; inflammatory disease; cancer;							
KW	graft rejection;	cyclic.							
XX									
OS	Mammalia.								
XX									
PN	WO200026360-A1.								
XX									
PD	11-MAY-2000.								
XX									
PF	03-NOV-1999;	99WO-CA01029.							

XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsy 6
11 11
Db 2 wrtsysy 7

RESULT 17

AAB06555
ID AAB06555 standard; peptide: 8 AA.

XX AAB06555;

XX 28-SEP-2000 (first entry)

XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 144.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

PS Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsy 6
11 11
Db 2 wrtsysy 7

RESULT 18

AAB06564
ID AAB06564 standard; peptide: 8 AA.

XX AAB06564;

XX 28-SEP-2000 (first entry)

XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 153.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX

XX Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsy 6
1111
DB 2 wrtsys 7

RESULT 19

AAB06424
ID AAB06424 standard; peptide; 6 AA.

AC AAB06424;

DT 28-SEP-2000 (first entry)

DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 483.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 39; Page 96; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

XX Sequence 6 AA;

Query Match 69.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsy 6
1111
DB 1 wrtsys 6

RESULT 20

AAB06510
ID AAB06510 standard; peptide; 6 AA.

AC AAB06510;

XX 28-SEP-2000 (first entry)

DT Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 517.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 43; Page 97; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX Sequence 6 AA;

Query Match 69.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsy 6
1111
DB 1 wrtsys 6

RESULT 21

AAB06425
ID AAB06425 standard; peptide; 7 AA.

AC AAB06425;

DT 28-SEP-2000 (first entry)

DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 484.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site.
XX
XX Sequence 7 AA;

Query Match 69.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxsy 6
1111
Db 1 wrlysy 6

RESULT 22
AAB06511
ID AAB06511 standard; peptide; 7 AA.
XX
XX AAB06511;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 518.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -

XX Claim 43; Page 97; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.
XX
XX Sequence 7 AA;

Query Match 69.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxsy 6
1111
Db 1 wrlysy 6

RESULT 23
AAB06483
ID AAB06483 standard; peptide; 8 AA.
XX
XX AAB06483;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 490.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Claim 43; Page 96; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.
XX
XX Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxxy 6
| | | |
DB 2 wrlysy 7

RESULT 24
AAB06489
ID AAB06489 standard; peptide: 8 AA.
XX
AC AAB06489;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 496.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA:

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxxy 6
| | | |
DB 2 wrlysy 7

RESULT 25
AAB06495
ID AAB06495 standard; peptide: 8 AA.

XX AAB06495;
AC
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 502.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA:

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxxy 6
| | | |
DB 2 wrlysy 7

Search completed: January 14, 2002, 07:43:17
Job time: 428 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:36 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1e
Perfect score: 36
Sequence: 1 wrxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues 43125
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptcodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptcodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptcodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptcodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptcodata/2/1aa/PCMus.COMB.pep:*
6: /cgn2_6/ptcodata/2/1aa/backfile1e1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	58.3	8	2 US-08-350-260A-464	Sequence 464, App
2	20	55.6	6	4 US-09-196-934-16	Sequence 16, Appl
3	20	55.6	8	3 US-08-335-733D-23	Sequence 23, Appl
4	20	55.6	8	3 US-08-335-733D-24	Sequence 24, Appl
5	20	55.6	8	3 US-08-335-733D-25	Sequence 25, Appl
6	19	52.8	6	3 US-08-907-403A-8	Sequence 8, Appl
7	19	52.8	7	4 US-09-177-249-280	Sequence 280, App
8	19	52.8	7	4 US-09-326-718-6	Sequence 6, Appl
9	19	52.8	7	5 PCT-US95-11405-2	Sequence 2, Appl
10	18	50.0	6	2 US-09-127-574-17	Sequence 17, Appl
11	18	50.0	8	2 US-08-687-219B-36	Sequence 36, Appl
12	17	47.2	5	1 US-08-190-802A-263	Sequence 263, App
13	17	47.2	5	4 US-08-477-346-263	Sequence 263, App
14	17	47.2	6	1 US-08-338-890B-2	Sequence 2, Appl
15	17	47.2	6	1 US-08-338-890B-3	Sequence 3, Appl
16	17	47.2	6	2 US-08-340-208B-2	Sequence 2, Appl
17	17	47.2	6	2 US-08-340-208B-3	Sequence 3, Appl
18	17	47.2	6	3 US-08-997-263-2	Sequence 2, Appl
19	17	47.2	6	3 US-08-997-263-3	Sequence 3, Appl
20	17	47.2	8	2 US-08-687-219B-34	Sequence 34, Appl
21	17	47.2	8	2 US-08-687-219B-37	Sequence 37, Appl
22	17	47.2	8	4 US-08-444-818-325	Sequence 325, App
23	17	47.2	8	4 US-08-444-818-326	Sequence 326, App
24	17	47.2	8	4 US-08-444-818-327	Sequence 327, App
25	16	44.4	3	1 US-08-165-545-8	Sequence 8, Appl
26	16	44.4	3	1 US-08-305-768-27	Sequence 27, Appl
27	16	44.4	3	1 US-08-256-771-17	Sequence 17, Appl

28	16	44.4	3	1 US-08-381-984-17	Sequence 17, Appl
29	16	44.4	3	2 US-08-871-163-27	Sequence 27, Appl
30	16	44.4	3	3 US-08-767-903-27	Sequence 27, Appl
31	16	44.4	3	5 PCT-US95-11724-27	Sequence 27, Appl
32	16	44.4	4	1 US-08-165-545-7	Sequence 7, Appl
33	16	44.4	4	1 US-08-190-802A-265	Sequence 265, App
34	16	44.4	4	1 US-08-215-137-11	Sequence 11, Appl
35	16	44.4	4	1 US-08-256-771-16	Sequence 16, Appl
36	16	44.4	4	1 US-08-222-851-22	Sequence 22, Appl
37	16	44.4	4	1 US-08-381-984-16	Sequence 16, Appl
38	16	44.4	4	2 US-08-592-646A-62	Sequence 62, Appl
39	16	44.4	4	2 US-08-637-759B-108	Sequence 108, App
40	16	44.4	4	3 US-08-871-355A-108	Sequence 108, App
41	16	44.4	4	3 US-08-981-122-24	Sequence 24, Appl
42	16	44.4	4	3 US-08-981-122-28	Sequence 28, Appl
43	16	44.4	4	4 US-09-329-350-3	Sequence 3, Appl
44	16	44.4	4	4 US-08-591-632-40	Sequence 40, Appl
45	16	44.4	4	4 US-08-591-632-42	Sequence 42, Appl
46	16	44.4	4	4 US-08-477-346-265	Sequence 265, App
47	16	44.4	4	4 US-08-682-767-25	Sequence 25, App
48	16	44.4	5	1 US-07-851-941-1	Sequence 1, Appl
49	16	44.4	5	1 US-07-851-941-2	Sequence 2, Appl
50	16	44.4	5	1 US-07-851-941-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-350-260A-464
Sequence 464, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00083
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA: US 08/150,002
APPLICATION NUMBER: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 464:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-464

Query Match 58.3%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WXXXXY 6
1111
DB 3 WRVFDY 8

RESULT 2
US-09-196-934-16
Sequence 16, Application US/09196934
Patent No. 6191256
GENERAL INFORMATION:
APPLICANT: Chen, Li Ang
APPLICANT: Beutner, Joseph A.
APPLICANT: Carbonell, Ruben G.
TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides
FILE REFERENCE: MSB-7251
CURRENT APPLICATION NUMBER: US/09/196,934
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-196-934-16

Query Match 55.6%; Score 20; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WXXXXY 6
1111
DB 1 WRRHRY 6

RESULT 3
US-08-335-733D-23
Sequence 23, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Macleod, Janet M
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-335-733D-23

Query Match 55.6%; Score 20; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 WXXXXY 6
1111
DB 3 WRSELY 8

RESULT 4
US-08-335-733D-24
Sequence 24, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D

FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-335-733D-24

Query Match 55.6%; Score 20; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxy 6
111
Db 2 WRSELY 7

RESULT 5
US-08-335-733D-25
Sequence 25, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botsy, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M.
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-335-733D-25

Query Match 55.6%; Score 20; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxy 6
111
Db 1 WRSELY 6

RESULT 6
US-08-907-403A-8
Sequence 8, Application US/08907403A
Patent No. 6013633
GENERAL INFORMATION:
APPLICANT: Balasubramaniam, Ambikaipakan
TITLE OF INVENTION: Compounds For Control
TITLE OF INVENTION: Of Appetite, Blood Pressure, Cardiovascular
TITLE OF INVENTION: Response, Libido, And Circadian Rhythm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wood, Herron & Evans, L.L.P.
STREET: 441 Vine Street
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202-2917
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,403A
FILING DATE: 07-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,588
FILING DATE: 09-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Albainy-Jenel, Stephen R.
REGISTRATION NUMBER: 41,487
REFERENCE/DOCKET NUMBER: UOC-113A-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 241-2324
TELEFAX: (513) 421-7269
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-907-403A-8

Query Match 52.8%; Score 19; DB 3; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxy 6
1111
Db 1 WRWRY 6

RESULT 7

US-09-177-249-280
; Sequence 280, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramlin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-08612005
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 280
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-280

Query Match 52.8%; Score 19; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxy 6
1111
Db 2 WRWSW 7

RESULT 8

US-09-326-718-6
; Sequence 6, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deidre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-6

*Query Match 52.8%; Score 19; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxy 6
1111
Db 2 WGLASY 7

RESULT 9
PCT-US95-11405-2
; Sequence 2, Application PC/TUS9511405
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: PHOSPHOROUS-32 LABELING OF ANTIBODIES
; TITLE OF INVENTION: FOR CANCER THERAPY
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11405
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,103
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/599/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-11405-2

Query Match 52.8%; Score 19; DB 5; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxy 5
1111
Db 1 WRRAS 5

RESULT 10
US-09-127-574-17
; Sequence 17, Application US/09127574
; Patent No. 5985836
; GENERAL INFORMATION:

; APPLICANT: Basteck, Patrick
; APPLICANT: Lang, John M.
; APPLICANT: Baumbach, George A.
; APPLICANT: Carbonelli, Ruben G.
; TITLE OF INVENTION: Alpha-1 Protease Inhibitor Binding Peptides
; FILE REFERENCE: MSB-7248
; CURRENT APPLICATION NUMBER: US/09/127,574
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 17

*LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-127-574-17

Query Match 50.0%; Score 18; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WXXS 5
111
DB 2 WRRYS 6

RESULT 11
US-08-687-219B-36
; Sequence 36, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
; APPLICANT: JOLIVER-REYNAUD, Colette
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIVER & BERRIDGE, PLC
; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,219B
; FILING DATE: 25-JUL-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 95 09005
; FILING DATE: 25-JUL-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-2787
; TELEFAX: 703 836-6400
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal or C-terminal or Internal
US-08-687-219B-36

Query Match 50.0%; Score 18; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RXSXXS 8
111
DB 1 KASSYLG 7

RESULT 12
US-08-190-802A-263
; Sequence 263, Application US/08190802A

Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
; NAME: Fadian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTAA peptide
US-08-190-802A-263

Query Match 47.2%; Score 17; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WXXS 5
111
DB 1 WRTAA 5

RESULT 13
US-08-477-346-263
; Sequence 263, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-477-346-263

Query Match 47.2%; Score 17; DB 4; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WXXXS 5
11 :
DB 1 WRTAA 5

RESULT 14
US-08-338-890B-2
Sequence 2, Application US/08338890B
Patent No. 5700905
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at Line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /notes="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-338-890B-2

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 WXXXPY 6
11 :
DB 1 WXXFPY 6

RESULT 15
US-08-338-890B-3
Sequence 3, Application US/08338890B
Patent No. 5700905
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.**)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
NAME/KEY: Modified-site
LOCATION: 6, Xaa at Line 100

OTHER INFORMATION: /label-protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-338-890B-3

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxy 6
1 1 1
DB 1 WKXFPY 6

RESULT 16
US-08-340-208B-2
Sequence 2, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
TITLE OF INVENTION: Methods Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340.208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at line 72
OTHER INFORMATION: /label-protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-340-208B-2

Query Match 47.2%; Score 17; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxy 6
1 1 1
DB 1 WKXFPY 6

RESULT 17
US-08-340-208B-3
Sequence 3, Application US/08340208B
Patent No. 5965694
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Somatostatin Mimics And Synthetic
TITLE OF INVENTION: Methods Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5965694r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340.208B
FILING DATE: NOV. 16, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label-protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-340-208B-3

Query Match 47.2%; Score 17; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxy 6
1 1 1
DB 1 WKXFPY 6

RESULT 18
US-08-997-263-2
Sequence 2, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.*,*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997, 263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338, 890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at Line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /notes="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-997-263-2

Query Match 47.2%; Score 17; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxsy 6
1 1 1
1 WKXFPY 6

Db 1 WKXFPY 6

RESULT 19
US-08-997-263-3
Sequence 3, Application US/08997263
Patent No. 6001960
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz and No. 6001960ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS

SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(.*,*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997, 263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/338, 890
FILING DATE: NOV. 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1-3
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /note="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6, Xaa at Line 100
OTHER INFORMATION: /label=protecting2
OTHER INFORMATION: /note="a carboxyl protecting group can be
OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn
US-08-997-263-3

Query Match 47.2%; Score 17; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxsy 6
1 1 1
1 WKXFPY 6

Db 1 WKXFPY 6

RESULT 20
US-08-687-219B-34
Sequence 34, Application US/08687219B
Patent No. 5965541
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: OLIFF & BERRIDGE, PLC
STREET: 700 South Washington Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687, 219B
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 09005
FILING DATE: 25-JUL-1995


```
* ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal or C-terminal or Internal
US-08-687-219B-34

Query Match      47.2%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 rxssyxg 8
      : | | |
Db      1 KSSSYLG 7

RESULT  21
US-08-687-219B-37
; Sequence 37, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIVE & BERRIDGE, PLC
; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,219B
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 09005
; FILING DATE: 25-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal or C-terminal or Internal
US-08-687-219B-37

Query Match      47.2%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 rxssyxg 8
      : | | |
Db      1 KSSSYLG 7

RESULT  22
US-08-444-818-325
; Sequence 325, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Ailsa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 325:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-325

Query Match      47.2%; Score 17; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 wrssxy 6
      : | |
Db      3 WGPISY 8

RESULT  23
US-08-444-818-326
; Sequence 326, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
```

STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 326:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-326

Query Match 47.2%; Score 17; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsxy 6
| |
Db 2 WGPISY 7

RESULT 24
US-08-444-818-327
Sequence 327, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 327:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-327

Query Match 47.2%; Score 17; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsxy 6
| |
Db 1 WGPISY 6

RESULT 25
US-08-165-545-8
Sequence 8, Application US/08165545
Patent No. 5424396
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 44.4%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 wr 2
DB 2 wr 3

Search completed: January 14, 2002, 07:41:37
Job time: 458 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:22 ; Search time 43.28 Seconds
(Without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 36
Sequence: 1 wrxxxyxg 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	44.4	7	2	S33245 neuromodulatory pe
2	13	36.1	7	2	S33244 neuromodulatory pe
3	13	36.1	7	2	S33246 neuromodulatory pe
4	13	36.1	8	2	C61512 variant surface gl
5	12	33.3	5	2	B61445 Leu-enkephalin - b
6	12	33.3	5	2	A61445 Met-enkephalin - b
7	12	33.3	5	2	PT0278 1g heavy chain CRD
8	12	33.3	6	2	A41946 T-cell receptor ga
9	12	33.3	7	2	A60224 Met-enkephalin-Ary
10	12	33.3	8	2	PQ0012 cholecystokinin -
11	12	33.3	8	2	A43001 cholecystokinin -
12	12	33.3	8	2	S63493 dissimilatory sulf
13	12	33.3	8	2	A38887 T-cell receptor ga
14	11	30.6	3	2	F37196 bradykinin-potentl
15	11	30.6	4	2	A34626 RPCH-related neuro
16	11	30.6	4	2	PT0240 1g heavy chain CRD
17	11	30.6	4	2	B53284 T-cell receptor be
18	11	30.6	4	2	PT0661 T-cell receptor be
19	11	30.6	5	2	A32516 cholecystokinin-5
20	11	30.6	5	2	A60274 major protein anti
21	11	30.6	5	2	A60803 neuropeptide - sea
22	11	30.6	5	2	JH0253 gut pentapeptide -
23	11	30.6	5	2	G37196 bradykinin-potentl
24	11	30.6	5	2	PT0281 1g heavy chain CRD
25	11	30.6	5	2	PT0308 T-cell receptor be
26	11	30.6	5	2	PT0729 T-cell receptor be
27	11	30.6	5	2	PT0580 blood cell protein
28	11	30.6	5	2	S68326 alcohol dehydrogen
29	11	30.6	6	2	S66195

30	11	30.6	6	2	B34835 dnaA protein - pse
31	11	30.6	6	2	A31263 dihydrofolate redu
32	11	30.6	6	2	B31263 locustakinin - m19
33	11	30.6	6	2	A61068 cerebellar degener
34	11	30.6	6	2	B35640 T-cell receptor be
35	11	30.6	6	2	PT0629 T-cell receptor be
36	11	30.6	6	2	PT0532 T-cell receptor be
37	11	30.6	6	2	PT0519 T-cell receptor be
38	11	30.6	6	2	PT0637 T-cell receptor be
39	11	30.6	6	2	PT0641 T-cell receptor be
40	11	30.6	6	2	PT0726 T-cell receptor be
41	11	30.6	6	2	F41946 T-cell receptor ga
42	11	30.6	6	2	PD0028 T-cell receptor ga
43	11	30.6	6	4	I79564 hypotheical TCR3
44	11	30.6	7	2	S21230 demorphin (Trp-4,
45	11	30.6	7	2	A58512 venom heptapeptide
46	11	30.6	7	2	A61081 trypsinylilin, bas
47	11	30.6	7	2	S57274 tricyclyglycerol 11
48	11	30.6	7	2	S09652 hypochetical prote
49	11	30.6	7	2	PM0649 alpha-dextrin endo
50	11	30.6	7	2	PQ0727 H2 class I protein

ALIGNMENTS

RESULT 1
S33245 neuromodulatory peptide Wmamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 44.4% Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 1 wr 2

RESULT 2
S33244 neuromodulatory peptide Wmamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 36.1% Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 wr 2
I:

Db 1 WK 2

RESULT 3
S33246

neuromodulatory peptide Wmamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33246

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 36.1%; Score 13; DB 2; Length 7;
Best local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wrxa 5
1 WK 2

RESULT 4
C61512

variant surface glycoprotein M19at 1.4 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei

C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999

C:Accession: C61512

R:Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A:Title: Glycoproteins from variant surface glycoproteins of Trypanosoma brucei. C-term

A:Reference number: A61512; MUID:81172836

A:Accession: C61512

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Keywords: glycoprotein

Query Match 36.1%; Score 13; DB 2; Length 8;
Best local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxa 5
1 WKNA 5

RESULT 5
B61445

Leu-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: B61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A:Reference number: A61445; MUID:84144823

A:Accession: B61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1 yfg 3

RESULT 6
A61445

Met-enkephalin - blue mussel

C:Species: Mytilus edulis (blue mussel)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C:Accession: A61445

R:Leung, M.K.; Stefano, G.B.

Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984

A:Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul

A:Reference number: A61445; MUID:84144823

A:Accession: A61445

A:Molecule type: protein

A:Residues: 1-5 <LEU>

A:Experimental source: pedal ganglia

C:Keywords: neuropeptide; opioid peptide

Query Match 33.3%; Score 12; DB 2; Length 5;
Best local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1 yfg 3

RESULT 7
PT0278

Ig heavy chain CRD3 region (clone 4-88) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0278

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Royera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0278

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 12; DB 2; Length 5;
Best local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
1 yfg 3

RESULT 8
A41946

T-cell receptor gamma chain (1L22) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A41946

R:Whitsett, M.; Mosley, R.L.; Whitsett, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma

A:Reference number: A41946; MUID:92049316

A:Accession: A41946

A:Molecule type: DNA

A:Residues: 1-6 <YME>

Query Match 33.3%; Score 12; DB 2; Length 5;
Best local Similarity 66.7%; Pred. No. 2.2e+05;

C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 1 YRG 3

RESULT 9

A60224
Met-enkephalin-Arg-Phe - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C:Accession: A60224
R:Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Maki, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A:Title: Isolation and characterization of opiod peptides from rabbit cerebellum.
A:Reference number: A60224; MUID:91225680
A:Accession: A60224

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MAD>
C:Superfamily: proenkephalin
C:Keywords: neuropeptide; opiod peptide

Query Match 33.3%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 1 YRG 3

RESULT 10

PQ0012
cholecystokinin - southeastern quoll
N:Alternate names: CCK
C:Species: Dasyurus viverrinus (southeastern quoll)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C:Accession: PQ0012
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: PQ0012
A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 2 YMG 4

RESULT 11

A43001
cholecystokinin - tammar wallaby
N:Alternate names: CCK
C:Species: Macropus eugenii (tammar wallaby)

C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C:Accession: A43001; PQ0012
R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A:Reference number: PQ0012; MUID:88234141
A:Accession: A43001

A:Molecule type: protein
A:Residues: 1-8 <FAN>
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F:2/Binding site: sulfate (Tyr) (covalent) #status predicted
F:8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 2 YMG 4

RESULT 12

S63493
disimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio
C:Species: Desulfovibrio desulfuricans
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63493; S63494
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152
A:Accession: S63493

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <STE>
A:Accession: S63494
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <ST2>

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 5 YKG 7

RESULT 13

A38887
T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316
A:Accession: A38887

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHF>
C:Keywords: T-cell receptor

Query Match 33.3%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 wrxxy 6
|
Db 3 WDSSGF 8

RESULT 14

F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C>Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196
R:Cintre, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557
A:Accession: F37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 15

A34626
RPCH-related neuropeptide - ferruginous spindle
C:Species: Fustinus ferrugineus (ferruginous spindle)
C>Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:9019762
A:Accession: A34626
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 4 w 4

RESULT 16

PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Iamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
| |
Db 1 yfg 3

RESULT 17

B53284
T-cell receptor beta 2 chain D region, dpeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity an
A:Reference number: A53284; MUID:91342695
A:Accession: B53284
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:q233916; PIDN:AB19518.1; PID:q233918
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60738)
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 2 w 2

RESULT 18

PT0661
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0661
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0661
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 30.6%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 19

A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest
A:Reference number: A32516; MUID:87155871
A:Accession: A32516

A:Molecule type: protein
A:Residues: 1-5 <SH1>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystic
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 20
E60274

major protein antigen MPF63 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274

R:Nagui, S.; Wilker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991

A:Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; MUID:91099989
A:Accession: E60274

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 30.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
DB 1 Ay 2

RESULT 21
A60803

neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803

R:Griff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988

A:Title: Isolation of <Glu-Ser-Iu-Arg-Trp-NH₂> a novel neuropeptide from sea anemones.
A:Reference number: A60803; MUID:88222764
A:Accession: A60803

A:Molecule type: protein
A:Residues: 1-5 <GRN>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 22
JH0253

gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253

R:Usaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991

A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113
A:Accession: JH0253

A:Molecule type: protein
A:Residues: 1-5 <UES>

A:Experimental source: gut
C:Comment: This peptide increased basal tone of the circular muscle of the esophagoga

, and of the circular muscle of the gastro-intestinal junction.

Query Match 30.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 23
G37196

bradykinin-potentiating peptide 7 - Island Jararaca
C:Species: Bothrops insularis (Island Jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196

R:Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptide
A:Reference number: A37196; MUID:90351557
A:Accession: G37196

A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-5 <CIN>
C:Keywords: pyroglutamic acid

F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 3 W 3

RESULT 24
PT0281

Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108357
A:Accession: PT0281

A:Molecule type: DNA
A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 |
 Db 4 w 4

RESULT 25

PT0308
 Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0308
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 595-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337
 A:Accession: PT0308
 A:Molecule type: DNA
 A:Residues: 1-5 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 30.6%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 |
 Db 2 w 2

Search completed: January 14, 2002, 07:44:22
 Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds
(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 36
Sequence: 1 wrxxxxyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	16	44.4	7 1 MNPL_LEPDE	P42984 lepliotars
2	16	44.4	7 1 MNAL_ACHFU	P35919 echatina fu
3	13	36.1	7 1 WMA2_ACHFU	P35920 echatina fu
4	13	36.1	7 1 WMA3_ACHFU	P35921 echatina fu
5	12	33.3	8 1 CCKN_WACEU	P30365 mecirops eu
6	11	30.6	5 1 BP77_BOTIN	P30425 botcirops in
7	11	30.6	5 1 UF01_MOUSE	P38639 mus musculu
8	11	30.6	6 1 LOK1_LOCMT	P41491 locusta mlg
9	11	30.6	6 1 OVM_LEPDE	P42985 lepliotars
10	11	30.6	7 1 ALI2_CARMA	P81805 carclnus ma
11	11	30.6	7 1 FAR3_HNECO	P81298 haemochlus
12	11	30.6	7 1 FAR3_PANRE	P41874 panagrellus
13	11	30.6	8 1 ACI_THUUL	P18691 thunnus alb
14	11	30.6	8 1 AKHG_GRAYBI	P14086 gryllus bim
15	11	30.6	8 1 AKH_LIRAU	P25418 libellula a
16	11	30.6	8 1 AKH_MEIUL	P25423 melolontha
17	11	30.6	8 1 AKH_TABAT	P14595 tabanus atr
18	11	30.6	8 1 HTF1_PERAM	P04548 periplaneta
19	11	30.6	8 1 HTF2_PERAM	P04549 periplaneta
20	11	30.6	8 1 HTF_TENMO	P25419 tenebrio mo
21	11	30.6	8 1 LCK1_LEUMA	P21140 leucophaea
22	11	30.6	8 1 LCK2_LEUMA	P21141 leucophaea
23	11	30.6	8 1 LCK3_LEUMA	P21142 leucophaea
24	11	30.6	8 1 LCK4_LEUMA	P21143 leucophaea
25	11	30.6	8 1 LCK5_LEUMA	P19987 leucophaea
26	11	30.6	8 1 LCK6_LEUMA	P19988 leucophaea
27	11	30.6	8 1 LCK7_LEUMA	P19989 leucophaea
28	11	30.6	8 1 LCK8_LEUMA	P19990 leucophaea
29	11	30.6	8 1 PLP_BRANA	P81707 brassica na
30	11	30.6	8 1 RPCH_PANBO	P08933 panastica bo
31	11	30.6	8 1 UF06_MOUSE	P38644 mus musculu
32	11	30.6	8 1 UPAA_HUMAN	P30096 homo sapien
33	8	22.2	5 1 TPIS_CANFA	P47714 canis famli

34	8	22.2	7 1 HY7_PIG	P01153 sus scrofa
35	8	22.2	8 1 ALI6_CARMA	P81819 carclnus ma
36	8	22.2	8 1 CLP_THICU	P80488 thlobacillu
37	8	22.2	8 1 GLUR_HUMAN	P02729 homo sapien
38	7	19.4	4 1 FAR3_HIRME	P42562 hirudo medl
39	7	19.4	4 1 FAR4_HIRME	P42563 hirudo medl
40	7	19.4	5 1 ALI4_CARMA	P81817 carclnus ma
41	7	19.4	5 1 FARP_ARTTR	P41853 arlioposchl
42	7	19.4	5 1 PRCT_PERAM	P01373 periplaneta
43	7	19.4	5 1 PSK_DAUCA	P58261 daucus caro
44	7	19.4	6 1 ASP2_LACSN	P82655 lactobacill
45	7	19.4	7 1 ALL3_CARMA	P81806 carclnus ma
46	7	19.4	7 1 ALL4_CARMA	P81807 carclnus ma
47	7	19.4	7 1 ALL5_CARMA	P81808 carclnus ma
48	7	19.4	7 1 ALL7_CYPPO	P82158 cydia pomon
49	7	19.4	7 1 FAR2_ASCSU	P31890 ascaris suu
50	7	19.4	7 1 FAR5_HIRME	P42564 hirudo medl

ALIGNMENTS

RESULT 1				
ID MNPL_LEPDE	STANDARD:	PRT:	7 AA.	
AC P42984;				
DT 01-NOV-1995 (Rel. 32, Created)				
DT 01-NOV-1995 (Rel. 32, Last sequence update)				
DT 01-NOV-1995 (Rel. 32, Last annotation update)				
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-I).				
OS Lepitnotarsa decemlineata (Colorado potato beetle).				
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;				
OC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;				
OC Chrysomelinae; Lepitnotarsa.				
OX NCBI_TaxID=7539;				
RN [1]				
RC SEQUENCE, AND SYNTHESIS.				
RP TISSUE-Head;				
RX MEDLINE=95380343; PubMed=7651886;				
RA Spilltaels K., Vankeerberghen A., Schoofs L., Torrekens S.,				
RA Grauwels L., van Leuven F., de Loof A.;				
RT "Identification, characterization, and immunological localization of				
RT a novel myotropic neuropeptide in the Colorado potato beetle,				
RT Lepitnotarsa decemlineata.";				
RL Peptides 16:365-374(1995).				
CC -I- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE				
CC OVIDUCT.				
KW Neuropeptide; Amidation.				
FT MOD_RES 7 AA;				
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;				

Query Match 44.4%; Score 16; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1e+05; 1; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1;

QY 5 ayyx 8	
DB 1 AYN 4	
RESULT 2	
ID MNAL_ACHFU	STANDARD;
AC P35919;	PRT: 7 AA.
DT 01-JUN-1994 (Rel. 29, Created)	
DT 01-JUN-1994 (Rel. 29, Last sequence update)	
DT 01-OCT-1994 (Rel. 30, Last annotation update)	
DE WMAWIDE-1.	
OS Achatina fulica (Giant African snail).	
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;	
OC Achatinacea; Achatinidae; Achatina.	

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OX NCB1_TaxID=6530;
RN SEQUENCE.
RP TISSUE=Ganglion;
RC MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
  ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DE WMAWIDE-3.
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
  SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR Neuropeptide; Amidation.
KM MOD_RES 7 AA; 993 MW; 7362D5B69B041310 CRC64;
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 44.4%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
   11
Db 1 WR 2

RESULT 3
WMA2_ACHFU STANDARD; PRT; 7 AA.
ID WMA2_ACHFU
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
CC Achatinacea; Achatinidae; Achatina.
OX NCB1_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
  ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DE Neuropeptide; Amidation.
KM MOD_RES 7 AA; 964 MW; 7362D5B686D32310 CRC64;
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 36.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY .1 wr 2
   11
Db 1 WK 2

RESULT 4
WMA3_ACHFU STANDARD; PRT; 7 AA.
ID WMA3_ACHFU
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMAWIDE-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
CC Achatinacea; Achatinidae; Achatina.
OX NCB1_TaxID=6530;
RN [1]

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RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
  ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DE PIR: S33244; S33244.
KM Neuropeptide; Amidation.
FT MOD_RES 7 AA; 965 MW; 7362D5B69B132310 CRC64;
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 36.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
   11
Db 1 WK 2

RESULT 5
CCKN_MACEU STANDARD; PRT; 8 AA.
ID CCKN_MACEU
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLECYSTOKININ (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
  Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Metatheria; Diprodontia; Macropodidae; Macropus.
OX NCB1_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
  marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
  AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
  IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN. 1.
KM Amidation; Sulfation; Hormone.
FT MOD_RES 2
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 33.3%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
   11
Db 2 YMG 4

RESULT 6
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Quelmada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
NCBI_TaxId=8723;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintrera A.C.O., Vieira C.A., Giglio J.R.;
RT Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
KW Hypotensive agent; Venom.
DR PIR: G37196; G37196.
FT MOD_RES 1
SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 W 1
DB 3 W 3

RESULT 7
ID UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC TISSUE-Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Michler L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON_TER 5
SQ SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 W 1
DB 1 W 1

RESULT 8
ID LOK1_LOCM1 STANDARD; PRT; 6 AA.
SQ SEQUENCE 6 AA: 629 MW: 776DC37326B00000 CRC64;

AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
NCBI_TaxId=7004;
RN [1]
RP SEQUENCE.
RC TISSUE-Corpus cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
RT Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
TUBULES.
DR PIR: A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA: 654 MW: 686365A5B9CDB000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 W 1
DB 5 W 5

RESULT 9
ID OVM_LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phyllophaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
NCBI_TaxId=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Sptlebens K., Schoofs L., Grauwels L., Smet H., van Damme J.,
Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
stimulating head peptide in the Colorado potato beetle, Leptinotarsa
deceimlineata."
RL Peptides 12:31-36(1991).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA: 720 MW: 6B07632B5DD03000 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ay 6

Db 2 AY 3

RESULT 10
ALL2_CARMA STANDARD; PRT; 7 AA.
ID ALL2_CARMA
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINOSTATIN 2.
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Fortuinidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN (1)
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
RA Dube H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpé A.,
"Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 770 MW; 672879CDBC85DB870 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 2 AY 3

RESULT 11
FAR3_HAECO STANDARD; PRT; 7 AA.
ID FAR3_HAECO
AC P81298;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMR-AMIDE).
OS Haemochus contortus.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
OX NCBI_TaxID=6289;
RN (1)
RP SEQUENCE.
RX TISSUE=Neuron;
RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Geary T.G.,
Thompson D.P., Shaw C.;
Submitted (MAY-1998) to the SWISS-PROT data bank.
CC -I- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6

Db 3 AY 4

RESULT 12
FAR3_PANRE STANDARD; PRT; 7 AA.
ID FAR3_PANRE
AC P41874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE PF3 (KSAYMR-AMIDE).
OS Panagrellus redivivus.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN (1)
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94235053; PubMed=8179635;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
Geary T.G., Thim L.;
"KSAYMRamide: a novel FMRFamide-related heptapeptide from the free-
living nematode, Panagrellus redivivus, which is myoactive in the
parasitic nematode, Ascaris suum.";
RL Biochem. Biophys. Res. Commun. 200:973-980(1994).
CC -I- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
MUSCLE TENSION INCREASE.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
KW Family.
DR PIR; PC2132; PC2132.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
Db 3 AY 4

RESULT 13
ACT_THUAL STANDARD; PRT; 8 AA.
ID ACT_THUAL
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE ANGIOTENSIN-CONVERTING ENZYME INHIBITOR.
OS Thunnus albacares (Yellowfin tuna) (Neochunnus macropterus).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN (1)
RP SEQUENCE.
RX TISSUE=Muscle;
MEDLINE=88326322; PubMed=2415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
"Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR; A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 W 1
DB      6 W 6

RESULT 14
AKHG_GRYBI STANDARD: PRT: 8 AA.
AC PI4086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus.
FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 8 AA: 938 MW: 867661B5B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 W 1
DB      8 W 8

RESULT 15
AKH_LIBAU STANDARD: PRT: 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 8 AA: 938 MW: 867661B5B9C452D6 CRC64;
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RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetin/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S10596; S10595.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 8 AMIDATION.
SQ SEQUENCE 8 AA: 978 MW: 8665A771A9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 W 1
DB      8 W 8

RESULT 16
AKH_MEMLL STANDARD: PRT: 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=Melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetin
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21663; S21663.
DR InterPro: IPR002047; AKH.
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DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD.RES 8 8 AMIDATION
SO SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 8 w 8

RESULT 17
AKH_TABAT STANDARD; PRT; 8 AA.
ID AKH_TABAT
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
OX NCBI_TaxId=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DILYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DILYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD.RES 8 8 AMIDATION.
SO SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 8 w 8

RESULT 18
HTF1_PERAM STANDARD; PRT; 8 AA.
ID HTF1_PERAM
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-I)
DE (PEA-CAH-1) (LED-CC-1) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach),

OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxId=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;

RA "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;

RA "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;

RA "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.

RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;

RT "Primary structures of hypertrehalosemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae, and
Griphodornina portentosa, Blatteia germanica and Blatta orientalis
and of the stick insect Exaltosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).

CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.

DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD.RES 8 8 AMIDATION.
SO SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 8 w 8

RESULT 19
HTF2_PERAM STANDARD; PRT; 8 AA.
ID HTF2_PERAM
AC P04549;

DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
 DE (PER-CAH-II) (LED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
 OS Periplaneta americana (American cockroach),
 OS Lepidoptera doemelinaea (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxId=6978, 7539, 6976;
 OX [1]
 RP SEQUENCE.
 RC SPECIES-P. americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Blochm. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-L. decemlineata; TISSUE-Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Rinehart R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES-B. orientalis; TISSUE-Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryllodromia porteri, Blattella germanica and Blattella orientalis
 RT and of the stick insect Exaltosoma latatum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 DB 8 w 8

RESULT 20
 HTF_TEMMO STANDARD: PRT: 8 AA.
 ID HTF_TEMMO
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR (HOTN) (HYPERTREHALOSAEMIC NEUROPEPTIDE).
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxId=7067, 7075;
 OX [1]
 RP SEQUENCE.
 RC TISSUE-Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosaemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990)
 CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
 DB 8 w 8

RESULT 21
 LCK1_LEUMA STANDARD: PRT: 8 AA.
 ID LCK1_LEUMA
 AC P21140;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE LEUCOKININ I (L-I).
 OS Leucophaea maderae (Madeira cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxId=6988;
 OX [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.W., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotopins.";
 RL Comp. Biochem. Physiol. 84C:205-211(1986).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SO SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 22

LCK2_LEUMA STANDARD; PRT; 8 AA.
ID LCK2_LEUMA
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotrotopins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
KW MOD.RES 8
FT SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 23

LCK3_LEUMA STANDARD; PRT; 8 AA.
ID LCK3_LEUMA
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotrotopins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 24

LCK4_LEUMA STANDARD; PRT; 8 AA.
ID LCK4_LEUMA
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotrotopins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
KW MOD.RES 8
FT SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD8A CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 25

LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; Pubmed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).

CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 784 MW: 736365A5B9C865B8 CRC64;

Query Match 30.6%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
Db 7 w 7

Search completed: January 14, 2002, 07:52:04
Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:46 : Search time 80.15 Seconds
(without alignments)
14,600 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 36
Sequence: 1 wrxayxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	44.4	8	11 062721	062721 ratius norv
2	15	8	2 009258	009258 synchococc
3	41.7	8	2 095945	095945 saccharomyc
4	13	7	8 09TWH6	09Twh6 perinereis
5	12	8	11 P70243	P70243 mus musculu
6	33.3	8	11 09QVND3	09Qvnd3 rattus sp.
7	12	6	13 P82096	P82096 rattus sp.
8	11	7	10 049223	049223 glycinine max
9	11	7	13 P82065	P82065 ilitoria rub
10	11	8	2 095443	095443 pseudomonas
11	11	8	2 085406	085406 coxiella bu
12	11	8	4 015888	015888 homo sapien
13	11	8	4 015890	015890 homo sapien
14	11	8	5 09VRD2	09VRd2 drosophila
15	11	8	5 P82685	P82685 periplaneta
16	11	8	5 P82686	P82686 periplaneta
17	11	8	5 P82687	P82687 periplaneta
18	11	8	5 P82688	P82688 periplaneta
19	11	8	5 P82689	P82689 periplaneta

20	11	30.6	8	6 002831	002831 oryctolagus
21	11	30.6	8	6 09TRV3	09Trv3 sus sp. ins
22	11	30.6	8	6 P82929	P82929 bos taurus
23	11	30.6	8	7 095213	095213 oryctolagus
24	11	30.6	8	8 09TD02	09TD02 terranacos
25	11	30.6	8	8 09TAY2	09TAY2 asterina pe
26	11	30.6	8	10 095824	095824 spinacia ol
27	11	30.6	8	10 P82324	P82324 pisum sativ
28	11	30.6	8	11 035835	035835 rattus norv
29	11	30.6	8	11 P82598	P82598 rattus norv
30	11	30.6	8	11 09ERT8	09ERT8 mus spreus
31	11	30.6	8	11 09ERT7	09ERT7 mus caroll
32	11	30.6	8	11 09ERT6	09ERT6 mesocricetu
33	11	30.6	8	11 099AM0	099AM0 mus musculu
34	11	30.6	8	13 P79940	P79940 xenopus lae
35	11	30.6	8	13 098TU5	098Tus xenopus lae
36	10	27.8	7	12 09YVE3	09Yve3 human adeno
37	10	27.8	7	12 09YIR0	09YIr0 human adeno
38	10	27.8	7	12 09YIO9	09YIq9 human adeno
39	9	25.0	7	2 050556	050556 actinobacill
40	8	22.2	8	4 015898	015898 homo sapien
41	8	22.2	8	8 034909	034909 locusta mig
42	7	19.4	7	4 015903	015903 homo sapien
43	7	19.4	7	8 099182	099182 gnatholebia
44	7	19.4	7	12 09YQ10	09Yq10 porcine tra
45	7	19.4	7	13 P82101	P82101 ilitoria rub
46	7	19.4	8	2 052062	052062 bacillus me
47	7	19.4	8	2 P72221	P72221 pseudomonas
48	7	19.4	8	2 09RO57	09Rq57 buchnera ap
49	7	19.4	8	2 09R049	09Rq49 buchnera ap
50	7	19.4	8	2 09R9C2	09R9c2 borrelia bu

ALIGNMENTS

RESULT 1
Q62721
ID 062721
AC 062721;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.T., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT Prohibitin-encoding genes.";
RL Gene 158:291-294 (1995).
DR EMBL; U17178; AAA86692.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 44.4%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wr 2
Db 2 wr 3
RESULT 2

009258 ID 009258 PRELIMINARY; PRT; 8 AA.
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE N1TH (FRAGMENT).
 GN N1TH.
 OS Synechococcus sp. (strain PCC 8801 / Rf-1) (Cyanothecae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rf-1;
 RA Chen H.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF001780; AAC33369.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 41.7%; Score 15; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 4.7e+05;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 rxxayxg 8
 1 1 1
 2 RQIAFYG 8

RESULT 3
 Q95945 ID Q95945 PRELIMINARY; PRT; 7 AA.
 AC Q95945;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INSIDE INTRON 5 (FRAGMENT).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system. Structure and
 RT nucleotide sequence of the gene coding for subunit 1 of yeast
 RT cytochrome oxidase.";
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL: V00694; CAA24066.1; -.
 KM Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 36.1%; Score 13; DB 8; Length 7;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 1 1
 4 WK 5

RESULT 4
 Q9TWH6 ID Q9TWH6 PRELIMINARY; PRT; 8 AA.
 AC Q9TWH6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE BIOACTIVE PEPTIDE P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
 OS Perinereis vancaurica.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Acioulata;
 OC Phyllodoctida; Nereididae; Perinereis.
 NCBI_TaxID=6355;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95323338; PubMed=7599979;
 RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
 RA Fujita T., Minakata H., Nomoto K.;
 RT "Isolation and characterization of four novel bioactive peptides from
 RT a polychaete annelid, Perinereis vancaurica.";
 RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-304(1995).
 SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 33.3%; Score 12; DB 5; Length 8;
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 yxg 8
 1 1
 2 YEG 4

RESULT 5
 P70243 ID P70243 PRELIMINARY; PRT; 8 AA.
 AC P70243;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Ophoff R.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X98325; CAA66969.1; -.
 KW Calcium channel.
 FT NON_TER
 SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 1 1
 7 WQ 8

RESULT 6
 Q9QVD3 ID Q9QVD3 PRELIMINARY; PRT; 8 AA.
 AC Q9QVD3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92202192; PubMed:1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
R Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA: 1047 MW; D7415BB06C37041 CRC64;

Query Match 33.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 2
1;
DB 3 WQ 4

RESULT 7
P82096 PRELIMINARY; PRT; 6 AA.

ID P82096;
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
NCBI_TaxID=104895;
RN [1]
RX SEQUENCE.
RP TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RT Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA: 792 MW; 6683704772C9A000 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1;
DB 5 W 5

RESULT 8
O49223 PRELIMINARY; PRT; 7 AA.

ID O49223;
AC O49223;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA MEDLINE=91367679; PubMed:1891369;
RL Lau T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
with HMG-box proteins.";

RL Nucleic Acids Res. 19:4769-4769(1991).

RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF047050; AAC03556.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA: 850 MW; 6AAAAAB378637810 CRC64;

Query Match 30.6%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1;
DB 2 W 2

RESULT 9
P82065 PRELIMINARY; PRT; 7 AA.

ID P82065;
AC P82065;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TRYPTOPHYLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
NCBI_TaxID=104895;
RN [1]
RX SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RT Aust. J. Chem. 49:955-963(1996).
CC -I- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTAXMITTER.
CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -I- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1
SQ SEQUENCE 7 AA: 983 MW; 7401E9D3676046B0 CRC64;

Query Match 30.6%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1;
DB 4 W 4

RESULT 10
O85406 PRELIMINARY; PRT; 8 AA.

ID O85406;
AC O85406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OC Coxiella burnetii.
CC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE 1;
 RA Williams H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 RT *Coxiella burnetii*.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF064963; AAD09947.1; -
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match 30.6%; Score 11; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 4 w 4

RESULT 11
 ID 09S443 PRELIMINARY; PRT; 8 AA.
 AC 09S443;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE BETA-LACTAMASE (FRAGMENT).
 GN PSE2.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=R545;
 RA Roy D., Coulombe M., Perron K., Roy P.H.;
 RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase
 RT gene aac(6')-IIc from the integron of a Chinese Pseudomonas aeruginosa
 RT clinical isolate.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162771; AAD46628.1; -
 FT NON_TER
 SQ SEQUENCE 8 AA; 930 MW; EBD85DDDD9D1A336 CRC64;

Query Match 30.6%; Score 11; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ay 6
 DB 6 ay 7

RESULT 12
 ID 015888 PRELIMINARY; PRT; 8 AA.
 AC 015888;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
 DE (CLONE XP15H84) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,

RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32069; AAA73878.1; -
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 6 w 6

RESULT 13
 ID 015890 PRELIMINARY; PRT; 8 AA.
 AC 015890;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
 DE (CLONE XP19G12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32083; AAA73880.1; -
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 30.6%; Score 11; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 1 w 1

RESULT 14
 ID 09VRD2 PRELIMINARY; PRT; 8 AA.
 AC 09VRD2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE CG11666 PROTEIN.
 GN CG11666.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abdl J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A.P., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertl S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris W.,
RA Hostin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mokulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.H., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RT Science 287:2185-2195(2000). DR
EMBL: AE003569; AAF50870.1; -.
DR FLYbase: FBgn0040648; CG11666.
SQ SEQUENCE 8 AA; 1062 MW; ED11B5B044004376 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
2 w 2

RESULT 15
P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RC MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta
americana*.";
RT Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 16
P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RC MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta
americana*.";
RT Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1
7 w 7

RESULT 17
P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RN SEQUENCE, AND FUNCTION.
RP TISSUE-CORPORA CARDIACA;
RC MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, *Periplaneta*

```

RT americana."
RC Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 909 MW: DC6365B449D5A76A CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 18
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
CC Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 839 MW: 736365A5B9D6DD8 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 19
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;

RN [1]
RP SEQUENCE, AND FUNCTION.

```

```

RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
CC Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA: 865 MW: C76365B449CDC775 CRC64;

Query Match 30.6%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 20
002831 PRELIMINARY; PRT; 8 AA.
AC 002831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC NCBI_TaxID=9986;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage."
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA: 1028 MW: B859C7272EA77371 CRC64;

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 21
09TRY3 PRELIMINARY; PRT; 8 AA.
ID 09TRY3
AC 09TRY3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
OS Sus sp.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC NCBI_TaxID=9826;

RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;

```

RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
SQ SEQUENCE 8 AA: 850 MW: 9FB2CEA37EA7687D CRC64:

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
|
Db 5 w 5

RESULT 22
ID P82929 PRELIMINARY; PRT; 8 AA.
AC P82929;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
RT "Small subunit of the mammalian mitochondrial ribosome. Identification
of the full complement ribosomal proteins present.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 935 MW: 9639D1A72058637D CRC64:

Query Match 30.6%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
|
Db 2 w 2

RESULT 23
ID 095213 PRELIMINARY; PRT; 8 AA.
AC 095213;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE GERM LINE DH (DF) GENE (FRAGMENT).
CN DP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F-1/RGM;
RA Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
RL Mol. Immunol. 0:0-0(0).
DR EMBL: U62585; AAB18735.1; -.
KW MHC.
FT NON_TER 1 1

FT NON_TER 8 8
SQ SEQUENCE 8 AA: 845 MW: 5CA861B5AB58677B CRC64:

Query Match 30.6%; Score 11; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 yxg 8
|
Db 1 ypg 3

RESULT 24
ID Q9TD02 PRELIMINARY; PRT; 8 AA.
AC Q9TD02;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Terranatos dolichopterus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorphia; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxID=61836;
RN [1]
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
(Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AAF03041.1; -.
KW Mitochondrion.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 1084 MW: F0C9D3640DD44056 CRC64:

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
|
Db 6 w 6

RESULT 25
ID Q9T4Y2 PRELIMINARY; PRT; 8 AA.
AC Q9T4Y2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Asterina pectinifera (Starfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatocoea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89354669; PubMed=2766382;
RA Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL Curr. Genet. 15:193-206(1989).
DR EMBL: X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 1114 MW: F0C9D36415B736D6 CRC64:

Query Match 30.6%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
Db 6 W 6

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:17 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 36
Sequence: 1 wrxxxyxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
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2: /SIDS2/gcgdata/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/AA1982.DAT:*
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5: /SIDS2/gcgdata/geneseq/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/AA1986.DAT:*
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20: /SIDS2/gcgdata/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/AA2001.DAT:*

Prct. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	80.6	8	21	AA06521
2	29	80.6	8	21	AA06574
3	28	77.8	8	21	AA06426
4	28	77.8	8	21	AA06512
5	27	75.0	8	21	AA06583
6	27	75.0	8	21	AA06636
7	27	75.0	8	21	AA06645
8	27	75.0	8	21	AA06698
9	25	69.4	8	21	AA06419
10	25	69.4	8	21	AA06479
11	25	69.4	8	21	AA06823

12	25	69.4	8	21	AA06876	Claudin-7 cyclic c
13	25	69.4	8	21	AA06917	Claudin-7 cell adh
14	24	66.7	6	21	AA06519	Claudin-2 cell adh
15	24	66.7	6	21	AA06572	Claudin-2 cyclic c
16	24	66.7	7	21	AA06520	Claudin-2 cell adh
17	24	66.7	7	21	AA06573	Claudin-2 cyclic c
18	24	66.7	8	21	AA06528	Claudin-2 cyclic c
19	24	66.7	8	21	AA06537	Claudin-2 cyclic c
20	24	66.7	8	21	AA06546	Claudin-2 cyclic c
21	24	66.7	8	21	AA06555	Claudin-2 cyclic c
22	24	66.7	8	21	AA06564	Claudin-2 cyclic c
23	24	66.7	8	21	AA06764	Claudin-6/9 cell a
24	24	66.7	8	21	AA06814	Claudin-6/9 cyclic
25	24	66.7	8	21	AA06916	Claudin cell adhes
26	22	61.1	6	4	AA030170	Sequence of a cycl
27	22	61.1	6	21	AA06424	Claudin-1 cell adh
28	22	61.1	6	21	AA06510	Claudin-1 cyclic c
29	22	61.1	6	21	AA06581	Claudin-3 cell adh
30	22	61.1	6	21	AA06634	Claudin-3 cyclic c
31	22	61.1	6	21	AA06643	Claudin-4 cell adh
32	22	61.1	6	21	AA06696	Claudin-4 cyclic c
33	22	61.1	7	21	AA06425	Claudin-1 cell adh
34	22	61.1	7	21	AA06511	Claudin-1 cyclic c
35	22	61.1	7	21	AA06582	Claudin-3 cell adh
36	22	61.1	7	21	AA06635	Claudin-3 cyclic c
37	22	61.1	7	21	AA06644	Claudin-4 cell adh
38	22	61.1	7	21	AA06697	Claudin-4 cyclic c
39	22	61.1	8	21	AA06483	Claudin-1 cyclic c
40	22	61.1	8	21	AA06489	Claudin-1 cyclic c
41	22	61.1	8	21	AA06495	Claudin-1 cyclic c
42	22	61.1	8	21	AA06501	Claudin-1 cyclic c
43	22	61.1	8	21	AA06507	Claudin-1 cyclic c
44	22	61.1	8	21	AA06590	Claudin-3 cyclic c
45	22	61.1	8	21	AA06599	Claudin-3 cyclic c
46	22	61.1	8	21	AA06608	Claudin-3 cyclic c
47	22	61.1	8	21	AA06617	Claudin-3 cyclic c
48	22	61.1	8	21	AA06626	Claudin-3 cyclic c
49	22	61.1	8	21	AA06652	Claudin-4 cyclic c
50	22	61.1	8	21	AA06661	Claudin-4 cyclic c

ALIGNMENTS

RESULT .1
ID AAB06521 standard; peptide: 8 AA.
XX
AC AAB06521:
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX
OS Mammalia.
PN W0200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 80.6%; Score 29; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxayxg 8
||:| |
Db 1 wrtsyvg 8

RESULT 2
AAB06574
ID AAB06574 standard; peptide; 8 AA.
XX
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
SQ Sequence 8 AA;

Query Match 80.6%; Score 29; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxayxg 8
||:| |
Db 1 wrtsyvg 8

RESULT 3
AAB06426
ID AAB06426 standard; peptide; 8 AA.
XX
AC AAB06426;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxayxg 8
||:| |
Db 1 wrtsyvg 8

RESULT 1
ID AAB06512 standard; peptide: 8 AA.
XX
AC AAB06512;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
OS Mammalia.
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA:

Query Match 77.8%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
II : I I
DB 1 wrlysyag 8

RESULT 5
ID AAB06583 standard; peptide: 8 AA.
XX
AC AAB06583;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.

OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 52; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA:

Query Match 75.0%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
II : I I
DB 1 wrvsafig 8

RESULT 6
ID AAB06636 standard; peptide: 8 AA.
XX
AC AAB06636;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
OS Mammalia.
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;


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RESULT 9
AAB06419
ID AAB06419 standard; peptide; 8 AA.
XX
AC AAB06419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
I: | | |
Db 1 wklysyag 8

RESULT 10
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
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OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
I: | | |
Db 1 wklysyag 8

RESULT 11
AAB06823
ID AAB06823 standard; peptide; 8 AA.
XX
AC AAB06823;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-7 cell adhesion recognition sequence SEQ ID NO: 394.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
```

XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 76; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxayxg 8
| : | |
Db 1 wqmsyag 8

RESULT 12
AAB06876
ID AAB06876 standard; peptide; 8 AA.
XX
AC AAB06876;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 79; Page 105; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-7 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxayxg 8
| : | |
Db 1 wqmsyag 8

RESULT 13
AAB06917
ID AAB06917 standard; Protein; 8 AA.
XX
AC AAB06917;
XX
DT 05-OCT-2000 (first entry)
XX
DE Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
KW Claudin-7 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 8 /note= "C-terminal amide"
FT FT
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 77; Page 104; 121pp; English.
XX
CC The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 69.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
1 : : 1 1
Db 1 wqmsyag 8

RESULT 14

AAB06519 standard; peptide; 6 AA.

AAB06519;

28-SEP-2000 (first entry)

Claudin-2 cell adhesion recognition sequence SEQ ID NO: 40.

Claudin-2 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection.

Mammalia.

WO200026360-A1.

11-MAY-2000.

03-NOV-1999; 99WO-CA01029.

03-NOV-1998; 98US-0185908.

30-MAR-1999; 99US-0282029.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Biaschuck OW, Symonds JM, Gour BJ;

WPI; 2000-365610/31.

Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

Claim 46; Page 97; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-2 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site.

Sequence 6 AA;

Query Match 66.7%; Score 24; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 1 wrtssy 6

RESULT 15

AAB06572 standard; peptide; 6 AA.

AAB06572;

28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 161.

Claudin-2 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection; cyclic.

Mammalia.

WO200026360-A1.

11-MAY-2000.

03-NOV-1999; 99WO-CA01029.

03-NOV-1998; 98US-0185908.

30-MAR-1999; 99US-0282029.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Biaschuck OW, Symonds JM, Gour BJ;

WPI; 2000-365610/31.

Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

Claim 49; Page 98; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-2 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site. The present sequence has a cyclic
conformation.

Sequence 6 AA;

Query Match 66.7%; Score 24; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 1 wrtssy 6

RESULT 16

AAB06520 standard; peptide; 7 AA.

AAB06520;

28-SEP-2000 (first entry)

Claudin-2 cell adhesion recognition sequence SEQ ID NO: 41.

Claudin-2 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection.

Mammalia.

WO200026360-A1.

11-MAY-2000.

03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 46; Page 97; 121pp; English.
XX
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
XX Sequence 7 AA;

Query Match 66.7%; Score 24; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 wrxxay 6
11 :1
Db 1 wrtssy 6

RESULT 17
AAB06573
ID AAB06573 standard; peptide; 7 AA.
XX
XX AAB06573;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 162.
DE
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection; cyclic.
XX
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
FN
XX
XX 11-MAY-2000.
PD
XX
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
DR
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 49; Page 98; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
XX Sequence 7 AA;

Query Match 66.7%; Score 24; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 wrxxay 6
11 :1
Db 1 wrtssy 6

RESULT 18
AAB06528
ID AAB06528 standard; peptide; 8 AA.
XX
XX AAB06528;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 117.
DE
XX
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
KM graft rejection; cyclic.
XX
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX
XX 03-NOV-1999; 99WO-CA01029.
PF
XX
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI; 2000-365610/31.
DR
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX
XX Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;

Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 2 wrtsay 7

RESULT 19
AAB06537

ID AAB06537 standard; peptide: 8 AA.

AC AAB06537;

DT 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 126.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KM graft rejection; cyclic.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 2 wrtsay 7

RESULT 20
AAB06546

ID AAB06546 standard; peptide: 8 AA.

AC AAB06546;

XX

DT 28-SEP-2000 (first entry)

XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 135.

DE Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KM graft rejection; cyclic.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 2 wrtsay 7

RESULT 21
AAB06555

ID AAB06555 standard; peptide: 8 AA.

AC AAB06555;

DT 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 144.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KM graft rejection; cyclic.

XX Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

XX

PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI; 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 2 wrtssy 7

RESULT 22

AAB06564 ID AAB06564 standard; peptide; 8 AA.

XX AAB06564;

XX 28-SEP-2000 (first entry)

XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 153.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 : 1
Db 2 wrtssy 7

RESULT 23

AAB06764 ID AAB06764 standard; peptide; 8 AA.

XX AAB06764;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.

XX Claudin-6 modulating agent; claudin-9 modulating agent;

KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;

XX inflammatory disease; cancer; graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 70; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site.

SQ Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 wrxxayxg 8
1 : 1 : 1
DB 1 wkvtatfg 8

RESULT 24

AAB06814
ID AAB06814 strand: peptide: 8 AA.

AC AAB06814;

DT 28-SEP-2000 (first entry)

DE Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 385.

KM Claudin-6 modulating agent; claudin-9 modulating agent;
cell adhesion recognition sequence; CAR sequence; autoimmune disease;
inflammatory disease; cancer; graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

PS Claim 73; Page 104; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
are cadherins, which are membrane glycoproteins involved in cell
adhesion. In some situations, cell adhesion occurs at abnormal levels,
and these peptides can be used to modulate these levels, and thus treat
autoimmune diseases, inflammatory diseases and cancer, and aid wound
healing and implant adhesion. In addition, they can also be used to
facilitate drug delivery to the desired target site. The present
sequence has a cyclic conformation.

SO Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
1 : 1 : 1
DB 1 wkvtatfg 8

RESULT 25

AAB06916
ID AAB06916 strand: protein: 8 AA.

AC AAB06916;
XX 05-OCT-2000 (first entry)
DT
XX
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX
KM Claudin modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 8 /note= "C-terminal amide"

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

PS Claim 71; Page 103; 121pp; English.

CC The present sequence is a peptide which can be used in a claudin-mediated
cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.

SO Sequence 8 AA;

Query Match 66.7%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxayxg 8
1 : 1 : 1
DB 1 wkvtatfg 8

Search completed: January 14, 2002, 07:43:17
Job time: 428 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:37 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1f
Perfect score: 36
Sequence: 1 wrxxayxg 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	58.3	8	3	US-08-335-733D-23 Sequence 23, Appl
2	21	58.3	8	3	US-08-335-733D-24 Sequence 24, Appl
3	21	58.3	8	3	US-08-335-733D-25 Sequence 25, Appl
4	20	55.6	5	1	US-08-190-802A-263 Sequence 263, App
5	20	55.6	5	4	US-08-477-346-263 Sequence 263, App
6	20	55.6	6	4	US-09-196-934-16 Sequence 16, Appl
7	19	52.8	6	1	US-08-089-994A-12 Sequence 12, Appl
8	19	52.8	6	3	US-08-907-403A-8 Sequence 8, Appl
9	19	52.8	6	3	PCT-US94-07605-12 Sequence 12, Appl
10	19	52.8	7	2	US-08-463-230A-4 Sequence 4, Appl
11	19	52.8	7	2	US-08-463-230A-5 Sequence 5, Appl
12	19	52.8	8	1	US-08-633-760-3 Sequence 3, Appl
13	19	52.8	8	2	US-08-350-260A-464 Sequence 44, App
14	18	50.0	5	4	US-09-020-880-44 Sequence 44, Appl
15	18	50.0	7	4	US-09-139-802-65 Sequence 65, Appl
16	17	47.2	6	1	US-08-428-488-79 Sequence 29, Appl
17	17	47.2	6	1	US-08-428-488-79 Sequence 29, Appl
18	17	47.2	6	1	US-08-428-488-80 Sequence 80, Appl
19	17	47.2	6	1	US-08-428-488-81 Sequence 81, Appl
20	17	47.2	6	1	US-08-428-488-87 Sequence 87, Appl
21	17	47.2	6	1	US-08-428-488-89 Sequence 89, Appl
22	17	47.2	6	1	US-08-428-488-90 Sequence 90, Appl
23	17	47.2	6	1	US-08-428-488-91 Sequence 91, Appl
24	17	47.2	6	1	US-08-338-890B-2 Sequence 2, Appl
25	17	47.2	6	1	US-08-338-890B-3 Sequence 3, Appl
26	17	47.2	6	1	US-08-340-208B-2 Sequence 2, Appl
27	17	47.2	6	2	US-08-340-208B-3 Sequence 3, Appl

28	17	47.2	6	3	US-08-997-263-2	Sequence 2, Appl
29	17	47.2	6	3	US-08-997-263-3	Sequence 3, Appl
30	17	47.2	7	1	US-08-428-488-83	Sequence 83, Appl
31	17	47.2	7	1	US-08-428-488-84	Sequence 84, Appl
32	17	47.2	7	1	US-08-428-488-85	Sequence 85, Appl
33	17	47.2	7	1	US-08-428-488-86	Sequence 86, Appl
34	17	47.2	7	1	US-08-428-488-88	Sequence 88, Appl
35	17	47.2	7	1	US-08-428-488-104	Sequence 104, Appl
36	17	47.2	7	1	US-08-428-488-105	Sequence 105, App
37	17	47.2	7	1	US-08-428-488-106	Sequence 106, App
38	17	47.2	7	1	US-08-428-488-107	Sequence 107, App
39	16	44.4	3	1	US-08-165-545-8	Sequence 8, Appl
40	16	44.4	3	1	US-08-305-768-27	Sequence 27, Appl
41	16	44.4	3	1	US-08-256-771-17	Sequence 17, Appl
42	16	44.4	3	1	US-08-381-984-17	Sequence 17, Appl
43	16	44.4	3	2	US-08-871-163-27	Sequence 27, Appl
44	16	44.4	3	3	US-08-767-903-27	Sequence 27, Appl
45	16	44.4	3	5	PCT-US95-11724-27	Sequence 27, Appl
46	16	44.4	4	1	US-08-165-545-7	Sequence 7, Appl
47	16	44.4	4	1	US-08-190-802A-265	Sequence 265, Appl
48	16	44.4	4	1	US-08-215-137-11	Sequence 11, Appl
49	16	44.4	4	1	US-08-256-771-16	Sequence 16, Appl
50	16	44.4	4	1	US-08-222-851-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-335-733D-23
; Sequence 23, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO

FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-335-733D-23

Query Match 58.3%; Score 21; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 1
Db 3 WRSELY 8

RESULT 2
US-08-335-733D-24
Sequence 24, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Macleod, Janet M
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-335-733D-24

Query Match 58.3%; Score 21; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 1
Db 2 WRSELY 7
1

RESULT 3
US-08-335-733D-25
Sequence 25, Application US/08335733D
Patent No. 6042831
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES
TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,733D
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Macleod, Janet M
REGISTRATION NUMBER: 35,263
REFERENCE/DOCKET NUMBER: A29928-PCT-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-335-733D-25

Query Match 58.3%; Score 21; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 1
Db 1 WRSELY 6

RESULT 4
US-08-190-802A-263
Sequence 263, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto

Query Match 58.3%; Score 21; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxay 6
11 1
Db 2 WRSELY 7
1

STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-190-802A-263

Query Match 55.6%; Score 20; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrrxa 5
||
1
Db 1 WRTAA 5

RESULT 5
US-08-477-346-263
Sequence 263, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-477-346-263

Query Match 55.6%; Score 20; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrrxa 5
||
1
Db 1 WRTAA 5

RESULT 6
US-09-196-934-16
Sequence 16, Application US/09196934
Patent No. 6191256
GENERAL INFORMATION:
APPLICANT: Chen, Li Ang
APPLICANT: Beutner, Joseph A.
APPLICANT: Carbone, Ruben G.
TITLE OF INVENTION: Recombinant Factor VII Binding Peptides
FILE REFERENCE: MSB-7251
CURRENT APPLICATION NUMBER: US/09/196,934
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-196-934-16

Query Match 55.6%; Score 20; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrrxy 6
||
1
Db 1 WRRHY 6

RESULT 7
US-08-089-994A-12
Sequence 12, Application US/08089994A
Patent No. 5380668
GENERAL INFORMATION:
APPLICANT: Herion, James N.
TITLE OF INVENTION: Compounds Having the Antigenicity of
TITLE OF INVENTION: hCG
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Utah Technology
ADDRESS: Transfer Office
STREET: 421 Wakara Way, Suite 170

CITY: Salt Lake City
STATE: UT
COUNTRY: USA
ZIP: 84108
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 144mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,994A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2224
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-089-994A-12

Query Match 52.8%; Score 19; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wrxxa 5
111
Db 2 WREAA 6

RESULT 8
US-08-907-403A-8
Sequence 8, Application US/08907403A
Patent No. 6013633
GENERAL INFORMATION:
APPLICANT: Balasubramaniam, Ambikaipakan
APPLICANT: Chance, William T.
TITLE OF INVENTION: Compounds For Control
TITLE OF INVENTION: Of Appetite, Blood Pressure, Cardiovascular
TITLE OF INVENTION: Response, Libido, And Circadian Rhythm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wood, Herron & Evans, L.L.P.
STREET: 441 Vine Street
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202-2917
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,403A
FILING DATE: 07-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,588
FILING DATE: 09-AUG-1996
ATTORNEY/AGENT INFORMATION:

NAME: Albalay-Jenei, Stephen R.
REGISTRATION NUMBER: 41,487
REFERENCE/DOCKET NUMBER: UOC-113A-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 241-2324
TELEFAX: (513) 421-7269
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-907-403A-8

Query Match 52.8%; Score 19; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxay 6
111
Db 1 WRXYWR 6

RESULT 9
PCT-US94-07605-12
Sequence 12, Application PC/TUS9407605
GENERAL INFORMATION:
APPLICANT: Herron, James N.
TITLE OF INVENTION: Compounds Having the Antigenicity of
TITLE OF INVENTION: hCG
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Utah Technology
ADDRESSEE: Transfer Office
STREET: 421 Wakara Way, Suite 170
CITY: Salt Lake City
STATE: UT
COUNTRY: USA
ZIP: 84108
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07605
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/089,994
FILING DATE: 6 Jul 1993
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2224
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07605-12

Query Match 52.8%; Score 19; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;

Matches * 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxa 5
111
Db 2 WREA 6

RESULT 10
US-08-463-230A-4
Sequence 4, Application US/08463230A
Patent No. 5827498
GENERAL INFORMATION:
APPLICANT: SEKI, Ikuya
APPLICANT: ITAYA, Yoshitoshi
APPLICANT: SHIRAKUMI, Yoshifumi
APPLICANT: WASHINO, Komei
TITLE OF INVENTION: TUMOR AFFINITY PEPTIDE, AND RADIOACTIVE
TITLE OF INVENTION: DIAGNOSTIC AGENT AND RADIOACTIVE THERAPEUTIC AGENT
TITLE OF INVENTION: CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,230A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 148655/94
FILING DATE: 07-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, Charles S.
REGISTRATION NUMBER: 39,013
REFERENCE/DOCKET NUMBER: 5803/0B212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7663
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-463-230A-4

Query Match 52.8%; Score 19; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 rxxyxg 8
1111
Db 1 RTNAYWG 7

RESULT 11
US-08-463-230A-5
Sequence 5, Application US/08463230A
Patent No. 5827498
GENERAL INFORMATION:
APPLICANT: SEKI, Ikuya
APPLICANT: ITAYA, Yoshitoshi

APPLICANT: SHIRAKUMI, Yoshifumi
APPLICANT: WASHINO, Komei
TITLE OF INVENTION: TUMOR AFFINITY PEPTIDE, AND RADIOACTIVE
TITLE OF INVENTION: DIAGNOSTIC AGENT AND RADIOACTIVE THERAPEUTIC AGENT
TITLE OF INVENTION: CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,230A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 148655/94
FILING DATE: 07-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, Charles S.
REGISTRATION NUMBER: 39,013
REFERENCE/DOCKET NUMBER: 5803/0B212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7663
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-463-230A-5

Query Match 52.8%; Score 19; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 rxxyxg 8
1111
Db 1 RTNAYWG 7

RESULT 12
US-08-633-760-3
Sequence 3, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
APPLICANT: NIWA, MINRO
APPLICANT: SATO, YOSHIMASA
APPLICANT: FUJIMURA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: NOGUCHI, YUJI
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OHION, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-760-3

Query Match 52.8%; Score 19; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
111
Db 2 WRALA 6

RESULT 13
US-08-350-260A-464
Sequence 464, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Missim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 464:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-464

Query Match 52.8%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxay 6
111
Db 3 WRVFDY 8

RESULT 14
US-09-020-880-44
Sequence 44, Application US/09020880A
Patent No. 6136558
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Wells, James A.
TITLE OF INVENTION: HERGULIN VARIANTS
FILE REFERENCE: 14918-720CON1
CURRENT APPLICATION NUMBER: US/09/020,880A
CURRENT FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: US 60/037,581
EARLIER FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 5
TYPE: PPT
ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-44

Query Match 50.0%; Score 18; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
111
Db 1 WRLVA 5

```
RESULT 15
US-09-139-802-65
; Sequence 65, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; FILE REFERENCE: Same
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-139-802-65

Query Match      50.0%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 wrxx 5
        1111
Db      1 WRVLA 5

RESULT 16
US-08-428-488-29
; Sequence 29, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-428-488-29

Query Match      47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      5 ayxx 8
        1111
Db      1 AYAG 4

RESULT 17
US-08-428-488-79
; Sequence 79, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = Nicotiny] -Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = D-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Position 6 = D-Leu-Cholesteryl ester."
US-08-428-488-79

Query Match      47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
```

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 aayxg 8
111
Db 1 AYAG 4

RESULT 18

US-08-428-488-80
; Sequence 80, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = trigonellyl-Ala
; OTHER INFORMATION: methylsulfate."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = D-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Position 6 = D-Leu-Cholesteryl ester."
US-08-428-488-80

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aayxg 8
111
Db 1 AYAG 4

RESULT 19
US-08-428-488-81

; Sequence 81, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = 1,4-Dihydrotrigonellyl-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Position 3 = D-Ala."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Position 6 = D-Leu-Cholesteryl ester."
US-08-428-488-81

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 aayxg 8
111
Db 1 AYAG 4

RESULT 20
US-08-428-488-87
; Sequence 87, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404


```

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = Trigonellyl-Ala
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Position 3 = D-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Position 6 = D-Leu-OH."
US-08-428-488-87

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 aysxg 8
Db 1 AYAG 4

RESULT 21
US-08-428-488-89
Sequence 89, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

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```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = Trigonellyl-Ala
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Position 3 = D-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Position 6 = D-Leu-ethyl ester."
US-08-428-488-89

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 aysxg 8
Db 1 AYAG 4

RESULT 22
US-08-428-488-90
Sequence 90, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
NUMBER OF SEQUENCES: 107
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = 1,4-dihydrotrigonellyl-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Position 3 = D-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Position 6 = D-Leu-ethyl ester."
US-08-428-488-90

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ayxg 8
1 1 1
Db 1 AYAG 4

RESULT 23

US-08-428-488-91
Sequence 91, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = 1,4-dihydrotrigonellyl-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Position 3 = D-Ala."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "Position 6 = D-Leu-OH."
US-08-428-488-91

Query Match 47.2%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ayxg 8
1 1 1
Db 1 AYAG 4

RESULT 24

US-08-338-890B-2
Sequence 2, Application US/08338890B
Patent No. 5700905
GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph
APPLICANT: Spanewello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905tris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPN-2040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)568-3100
TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2-3, Xaa at Line 72
OTHER INFORMATION: /label=protecting1
OTHER INFORMATION: /notes="an amine protecting group or a solid
OTHER INFORMATION: support can be present or absent on the primary
OTHER INFORMATION: amino group", Xaa=Orn
US-08-338-890B-2

Query Match 47.2%; Score 17; DB 1; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
1:1
Db 1 WKXFPY 6

RESULT 25

US-08-338-890B-3
Sequence 3, Application US/08338890B

Patent No. 5700905

GENERAL INFORMATION:
APPLICANT: Hirschmann, Ralph

APPLICANT: Spanevello, Rolando

APPLICANT: Nutt, Ruth

TITLE OF INVENTION: Synthetic Somatostatin Mimics

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905rls

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS/WINDOWS

SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)

CURRENT APPLICATION DATA: US/08/338,890B

APPLICATION NUMBER: US/08/338,890B

FILING DATE: NOV. 14, 1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Malinoski, Lynn

REGISTRATION NUMBER: 38,788

REFERENCE/DOCKET NUMBER: UPN-2040

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215)568-3100

TELEFAX: (215)568-3439

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 6

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1-3

OTHER INFORMATION: /label=protecting1

OTHER INFORMATION: /note="an amine protecting group or a solid

OTHER INFORMATION: support can be present or absent on the primary

OTHER INFORMATION: amino group", Xaa="Orn

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6, Xaa at line 100

OTHER INFORMATION: /label=protecting2

OTHER INFORMATION: /note="a carboxyl protecting group can be

OTHER INFORMATION: present or absent on the hydroxyl group", Xaa=Orn

US-08-338-890B-3

Query Match 47.2%; Score 17; DB 1; Length 6;

Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxay 6
1:1
Db 1 WKXFPY 6

Search completed: January 14, 2002, 07:41:37
Job time: 458 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:22 ; Search time 43.28 Seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 35
Sequence: 1 wrxxsfxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	51.4	7	2 S33245	neuromodulatory pe
2	15	42.9	7	2 S33244	neuromodulatory pe
3	15	42.9	7	2 S33246	neuromodulatory pe
4	15	42.9	8	2 A42057	fibroblast growth
5	15	42.9	8	2 A38887	T-cell receptor ga
6	13	37.1	8	2 S13661	polygalacturonase
7	12	34.3	6	2 A41946	T-cell receptor ga
8	12	34.3	8	2 D47393	neuromodulatory pe
9	11	31.4	3	2 F37196	bradykinin-potentl
10	11	31.4	4	2 A34626	RPC4-related neuro
11	11	31.4	4	2 B53284	T-cell receptor be
12	11	31.4	4	2 PT0661	T-cell receptor be
13	11	31.4	5	2 A32516	cholecystokinin-5
14	11	31.4	5	2 A60803	neuropeptide - sea
15	11	31.4	5	2 JH0253	gut pentapeptide -
16	11	31.4	5	2 G37196	bradykinin-potentl
17	11	31.4	5	2 PT0281	Ig heavy chain CRD
18	11	31.4	5	2 PT0308	Ig heavy chain CRD
19	11	31.4	5	2 PT0729	T-cell receptor be
20	11	31.4	5	2 PT0580	T-cell receptor be
21	11	31.4	6	2 S66195	alcohol dehydrogen
22	11	31.4	6	2 B34835	dna protein - pse
23	11	31.4	6	2 A31263	dihydrofolate redu
24	11	31.4	6	2 B31263	dihydrofolate redu
25	11	31.4	6	2 A61068	locustakinin - mlg
26	11	31.4	6	2 B35640	cerebellar degener
27	11	31.4	6	2 PT0629	T-cell receptor be
28	11	31.4	6	2 PT0532	T-cell receptor be
29	11	31.4	6	2 PT0519	T-cell receptor be

30	11	31.4	6	2 PT0637	T-cell receptor be
31	11	31.4	6	2 PT0641	T-cell receptor be
32	11	31.4	6	2 PT0726	T-cell receptor be
33	11	31.4	6	2 F41946	T-cell receptor ga
34	11	31.4	6	2 PD0028	pev-kinin 2 - pena
35	11	31.4	6	4 I79564	hypothetical TGL3
36	11	31.4	7	2 S21230	dermorphin (Trp-4,
37	11	31.4	7	2 A58512	venom heptapeptide
38	11	31.4	7	2 A61081	tryptophyllin, bas
39	11	31.4	7	2 S57274	triacetyl glycerol 11
40	11	31.4	7	2 S09652	hypothetical prote
41	11	31.4	7	2 PNO649	alpha-dextrin endo
42	11	31.4	7	2 P00727	H2 class I protein
43	11	31.4	7	2 H33098	180k exoantigen -
44	11	31.4	7	2 S33567	tubulin beta-3 cha
45	11	31.4	7	2 E48394	glycoprotein compo
46	11	31.4	7	2 PH1602	Ig H chain V-D-J r
47	11	31.4	7	2 E33932	Ig mu chain D regl
48	11	31.4	7	2 PT0526	T-cell receptor be
49	11	31.4	7	2 PT0628	T-cell receptor be
50	11	31.4	7	2 PT0642	T-cell receptor be

ALIGNMENTS

RESULT 1
S33245
neuromodulatory peptide Wamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 51.4%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxs 5
DB 1 WREMS 5

RESULT 2
S33244
neuromodulatory peptide Wamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 42.9%; Score 15; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxs 5
I: I

DB 1 WKEMS 5

RESULT 3

S33246

neuromodulatory peptide Wwamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A:Reference number: S33244; MUID:93265912

A:Accession: S33246

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 42.9%; Score 15; DB 2; Length 7;

Best Local Similarity 40.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxs 5

I: |

DB 1 WKQMS 5

RESULT 4

A42057

fibroblast growth factor receptor 1, secreted - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999

C:Accession: A42057

R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.

Mol. Cell. Biol. 12, 82-88, 1992

A:Title: Differential splicing in the extracellular region of fibroblast growth factor r

A:Reference number: A42057; MUID:92107200

A:Accession: A42057

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <WER>

A:Cross-references: GB:M80363

C:Keywords: growth factor receptor

Query Match 42.9%; Score 15; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 sfxg 8

I: |

DB 5 SFLG 8

RESULT 5

A38887

T-cell receptor gamma chain (5t.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A38887

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge

A:Reference number: A41946; MUID:92049316

A:Accession: A38887

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-8 <WHE>

C:Keywords: T-cell receptor

Query Match 42.9%; Score 15; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 wrxxsf 6

I: |

DB 3 WDSGCF 8

RESULT 6

S13661

polygalacturonase (EC 3.2.1.15) isoform PG2 - fungus (Sclerotinia sclerotiorum) (frag

N:Alternate names: endopolygalacturonase; pectin depolymerase; pectinase

C:Species: Sclerotinia sclerotiorum

C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C:Accession: S13661

R:Waksman, G.; Keon, J.P.R.; Turner, G.

Biochim. Biophys. Acta 1073, 43-48, 1991

A:Title: Purification and characterization of two endopolygalacturonases from Sclerot

A:Reference number: S13661; MUID:91120822

A:Accession: S13661

A:Molecule type: protein

A:Residues: 1-8 <WAK>

C:Function: A:Description: involved in pectin degradation

C:Keywords: glycosidase; hydrolase

Query Match 37.1%; Score 13; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 sfxg 8

I: |

DB 5 TFSG 8

RESULT 7

A41946

T-cell receptor gamma chain (1t.22) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A41946

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma

A:Reference number: A41946; MUID:92049316

A:Accession: A41946

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <WHE>

C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 6;

Best Local Similarity 33.3%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxsf 6

I: |

DB 1 YRSGSF 6

RESULT 8

D47393

neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria

C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C:Accession: D47393

R:Duve, H.; Johnson, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with seq

A:Reference number: A47393; MUID:93211980

A:Accession: D47393

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Experimental source: thoracic ganglia
A:Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 34.4%; Score 12; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 rxsf 6
DB 2 RPYSF 6

RESULT 9
F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (Island Jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196
R:Cluere, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557
A:Accession: F37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 3 W 3

RESULT 10
A34626
RCH-related neuropeptide - ferruginous spindie
C:Species: Fustinus ferrugineus (ferruginous spindie)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626
R:Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A:Reference number: A34626; MUID:90179762
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 4 W 4

RESULT 11
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity an
A:Reference number: A53284; MUID:91342695

A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 2 W 2

RESULT 12
PT0661
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0661
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEF>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
DB 3 W 3

RESULT 13
A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 257, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A:Reference number: A32516; MUID:87153871
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SHI>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 w 1
|
Db 2 w 2

RESULT 14
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803

R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Tyr-NH-2, a novel neuropeptide from sea anemones.
A:Reference number: A60803; MUID:86222764

A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GRA>

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 5 w 5

RESULT 15

JH0253
gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253

R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A:Reference number: JH0253; MUID:92062113

A:Accession: JH0253

A:Molecule type: protein

A:Residues: 1-5 <UES>

A:Experimental source: gut

C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric and of the circular muscle of the gastro-intestinal junction.

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 3 w 3

RESULT 16

G37196
bradykinin-potentiating peptide 7 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196

R:Cintria, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A37196; MUID:90351557

A:Accession: G37196

A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-5 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 3 w 3

RESULT 17

PT0281
Ig heavy chain CRD3 region (clone 4-91c) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281

R:Ramada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0281

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 4 w 4

RESULT 18

PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0308

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0308

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
|
Db 2 w 2

RESULT 19

PT0729
T-cell receptor beta chain V-D-J region (120-15) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0640; PT0685; PT0729

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0640
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE3>
A:Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
DB 5 W 5

RESULT 20
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0580

A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
DB 4 W 4

RESULT 21
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)

C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195

R:Hjeltny, L.; Hackelt, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett. 367, 237-240, 1995

A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. N
zyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195

A:Molecule type: protein
A:Residues: 1-6 <HE>

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
DB 5 W 5

RESULT 22
B34835

dnaA protein - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa

C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835

R:Yee, T.W.; Smith, D.W.

Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990

A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from
A:Reference number: A34835; MUID:90160310
A:Accession: B34835

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <YEE>

A:Cross-references: GB:M30125; NID:9151419; PIDN:AAA25916.1; PID:9151421
C:Keywords: DNA binding

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
DB 6 W 6

RESULT 23
A31263

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu

C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263

R:Peterson, D.S.; Walliker, D.; Wellens, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886
A:Accession: A31263

A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>

C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 W 1
|
DB 3 W 3

RESULT 24
B31263

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodiu

C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263

R:Peterson, D.S.; Walliker, D.; Wellens, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886
A:Accession: B31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PRT>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1
DB 3 W 3

RESULT 25

A61068

Locustakinin - migratory locust

C:Species: Locusta migratoria (migratory locust)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995

C:Accession: A61068

R:Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992

A:Title: Locustakinin, a novel myotropic peptide from locusta migratoria, isolation, pr

A:Reference number: A61068; MUID:92262851

A:Accession: A61068

A:Molecule type: protein

A:Residues: 1-6 <SCH>

C:Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide

F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
1
DB 5 W 5

Search completed: January 14, 2002, 07:44:22
Job time: 408 sec


```
RC TISSUE-Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1", -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RI FEBS Lett. 323:104-108(1993).
RW Neuuropeptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA: 964 MW: 7362D5B686D32310 CRC64;

Query Match
Best Local Similarity 42.9%; Score 15; DB 1; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxs 5
DB 1 WKOMS 5

RESULT 3
WMA3_ACHFU STANDARD; PRT; 7 AA.
ID WMA3_ACHFU
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE-Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1", -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RI FEBS Lett. 323:104-108(1993).
RW Neuuropeptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA: 965 MW: 7362D5B69B132310 CRC64;

Query Match
Best Local Similarity 42.9%; Score 15; DB 1; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 wxxs 5
DB 1 WKOMS 5

RESULT 4
ALL3_CYPDPO STANDARD; PRT; 8 AA.
ID ALL3_CYPDPO
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASSTATIN 3.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE-Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
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RA Davey M., East P.D., Thorpe A.;
RT "pepidopteran peptides of the allatostatatin superfamily.";
RI Peptides 18:1301-1309(1997).
RW Neuuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 926 MW: C82879D5AB477415 CRC64;

Query Match
Best Local Similarity 34.3%; Score 12; DB 1; Length 8;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 rxxsf 6
DB 2 RPYSF 6

RESULT 5
ALL4_CALVO STANDARD; PRT; 8 AA.
ID ALL4_CALVO
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CALATOSTATIN 4 (Leu-CALATOSTATIN 4).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestrolida; Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Toke S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatins.";
RI Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RW Neuuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA: 954 MW: D32879D5AB47740A CRC64;

Query Match
Best Local Similarity 34.3%; Score 12; DB 1; Length 8;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 rxxsf 6
DB 2 RPYSF 6

RESULT 6
```

ALL4_CYPDPO
ID ALL4_CYPDPO STANDARD; PRT: 8 AA.
AC P82155;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATIN 4.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RN SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A., Scott A.G., Winstanley D.,
RA "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8
FT SEQUENCE 8 AA; 910 MW; 922879D5AB47740D CRC64;

Query Match 34.3%; Score 12; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 rxssf 6
1 1
Db 2 RPYSF 6

RESULT 7
ID BPP7_BOTIN STANDARD; PRT: 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE 55.2 (3A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island Jararaca) (Quelana Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cincta A.C.O., Vieira C.A., Giglio J.R.;
RA "Primary structure and biological activity of bradykinin potentiating
RA peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASAS THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KM Hypotensive agent; Venom.
FT MOD.RES 1
FT SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 w 1
1

Db 3 w 3
RESULT 8
ID TPIS_CANFA STANDARD; PRT: 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN TPIS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RN SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RA "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE -> DIHYDROXY-
CC ACETONE PHOSPHATE.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro: IPR000652; Trioseph_isomrse.
DR PROSITE: PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 fxg 8
1 1
Db 1 FVG 3

RESULT 9
ID UF01_MOUSE STANDARD; PRT: 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6. ITS MW IS: 19 KDA.
FT NON_TER 5
FT SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 |
 Db 1 w 1

RESULT 10

LOC1_LOCM1 STANDARD; PRT; 6 AA.
 AC P41491;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE LOCUSTAKININ I.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 OX NCBI_TaxId=7004;
 RN [1]

SEQUENCE.
 RP TISSUE=Corpora cardiaca;
 RX MEDLINE=92262851; PubMed=1585017;
 RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
 de Loof A.;
 "Locustakinin, a novel myotropic peptide from Locusta migratoria,
 isolation, primary structure and synthesis.";
 RL Regul. Pept. 37:49-57(1992).
 CC -I- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
 OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
 TUBULES.
 CC

DR PIR: A61068; A61068.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6
 SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 |
 Db 5 w 5

RESULT 11

ACI_THUAI STANDARD; PRT; 8 AA.
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE ANGIOTENSIN-CONVERTING ENZYME INHIBITOR.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxId=8236;
 RN [1]

SEQUENCE.
 RP TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 "Isolation of angiotensin-converting enzyme inhibitor from tuna
 muscle.";
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DT PIR: A31570; A31570.

SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 |
 Db 6 w 6

RESULT 12

AKHG_GRYBI STANDARD; PRT; 8 AA.
 ID AKHG_GRYBI
 AC P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE ADIPOKINETIC HORMONE G (AKH-G) (RO II).
 OS Gryllus bimaculatus (Two-spotted cricket), and
 OS Romalea microptera (Lubber grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
 OC Gryllinae; Gryllus.
 OX NCBI_TaxId=6999, 7007;
 RN [1]

SEQUENCE.
 RP SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
 RX MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L., Jr.;
 "Primary sequence analysis by fast atom bombardment mass spectrometry
 of a peptide with adipokinetic activity from the corpora cardiaca of
 the cricket Gryllus bimaculatus";
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 RN [2]

SEQUENCE.
 RP SPECIES=R.microptera; TISSUE=Corpora cardiaca;
 RX MEDLINE=89145002; PubMed=3226948;
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L., Jr.;
 "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
 the lubber grasshopper, Romalea microptera.";
 RL Peptides 9:681-688(1988).
 CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC

-I- SIMILARITY: BELONGS TO THE AKH / RPCH FAMILY.
 DR PIR: A28004; A28004.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH, 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT MOD_RES 1 1
 SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 |
 Db 8 w 8

RESULT 13

AKH_LTBV STANDARD; PRT; 8 AA.
 ID AKH_LTBV
 AC P25418;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DT PIR: A31570; A31570.

DE ADIPOKINETIC HORMONE (AKH).
CC Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
CC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxId=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 14
AKH_MELML
ID AKH_MELML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer), and
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxId=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=w.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=p.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF

CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21663; S21663.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 15
AKH_TABAT
ID AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR I) (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
OX NCBI_TaxId=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 16
CCKN_MACEU
ID CCKN_MACEU STANDARD; PRT; 8 AA.
AC P30369;

DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLECYSTOKININ (CCK).
OS Macropus eugenii (Tammam wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxId=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
marsupials."
RL Peptides 9:429-431(1988).
CC -I- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -I- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR PIR: P00012; P00012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCA68378768B5A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 w 1
1
Db 5 w 5

RESULT 17
HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-I)
DE (PEA-CAH-II) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattidae; Periplaneta.
OX NCBI_TaxId=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Janteson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with

RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
and of the stick insect Exaltosoma tlaxiatum assigned by tandem fast
atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: A05169; A05169.
DR PIR: S08995; S08995.
DR PIR: A49823; A49823.
DR PIR: A44960; A44960.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
1
Db 8 w 8
RESULT 18
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
DE (PEA-CAH-II) (LED-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattidae; Periplaneta.
OX NCBI_TaxId=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]

RP SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.W., Jamieson G.C., Kolish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardiacacceleratory and hyperglycemic activity from the corpora
cardiaca of *Periplaneta americana*.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Poplides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Griemphadorfina portenosae, *Blattella germanica* and *Blattia orientalis*
and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [1]
RP FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
DR PIR: A05170; A05170.
DR PIR: S08996; S08996.
DR PIR: B44960; B44960.
DR PIR: B49823; B49823.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 8
SO SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 19
HTF_TEMNO STANDARD; PRT; 8 AA.
AC P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
OS Tenebrio molitor (yellow mealworm), and Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebriono.
OX NCBI_Taxid=7067, 7075;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; PubMed=2381871;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrehalosemic neuropeptide from
Tenebrio beetle: a novel member of the AKH/RPCH family.";

RL Peptides 11:455-459(1990).
CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / RHTH / RPCH FAMILY.
DR PIR: A43876; A43976.
DR PIR: B43976; B43976.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 8
SO SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 20
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE LKUCOKININ I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_Taxid=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
from *Leucophaea maderae*: members of a new family of
Cephalomyotroplins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODERM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LKUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT MOD_RES 8
SO SEQUENCE 8 AA; 893 MW; DC6365B449CDCT6A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 21
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LKUCOKININ II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
from Leucophaea maderae: members of a new family of
Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 7 w 7

RESULT 22

LCK3_LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RM SEQUENCE, AND SYNTHESIS.
RP TISSUE=Head;
RC Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
from Leucophaea maderae: members of a new family of
Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 7 w 7

RESULT 23

LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).

OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
from Leucophaea maderae: members of a new family of
Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 7 w 7

RESULT 24

LCK5_LEUMA STANDARD; PRT; 8 AA.
AC P19367;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RM SEQUENCE.
RP TISSUE=Head;
RC MEDLINE=87052651; Pubmed-2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 7 w 7

RESULT 25

LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE LEUCOKININ VI (L-VI).
 OS Leucophaea maderae (Madagira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaea.
 OX NCHI_TaxID=6988;
 RN (1)
 RP SEQUENCE.
 RC TISSUE-Head;
 RX MEDLINE=87052651; PubMed=2877794;
 RA HOLMAN G.M., COOK B.J., NACHMAN R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
 CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
 DR PIR: JS0316; JS0316.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION
 SO SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
 |
 Db 7 W 7

Search completed: January 14, 2002, 07:52:04
 Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:46 ; Search time 80.15 Seconds
(Without alignments) 14.600 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 35
Sequence: 1 wrxxsfmg 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP-REMBL_17: *
2: sp_archaea: *
3: sp_bacteria: *
4: sp_fungi: *
5: sp_human: *
6: sp_invertebrate: *
7: sp_mammal: *
8: sp_mhc: *
9: sp_organelle: *
10: sp_phage: *
11: sp_plant: *
12: sp_rodent: *
13: sp_virus: *
14: sp_vertebrate: *
14: sp_unclassified: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	8	11	062721
2	15	42.9	8	2	009258
3	14	40.0	8	6	P82929
4	13	37.1	7	8	P82929
5	12	34.3	8	11	P70243
6	12	34.3	8	11	P70243
7	11	31.4	6	13	P82096
8	11	31.4	7	10	O49223
9	11	31.4	7	13	P82065
10	11	31.4	8	2	O85406
11	11	31.4	8	4	O15888
12	11	31.4	8	4	O15890
13	11	31.4	8	5	O9VWD2
14	11	31.4	8	5	P82685
15	11	31.4	8	5	P82686
16	11	31.4	8	5	P82687
17	11	31.4	8	5	P82688
18	11	31.4	8	5	P82689
19	11	31.4	8	6	O02831

20	11	31.4	8	6	O9TRY3	sus sp. ins
21	11	31.4	8	8	O9TD02	terranatos
22	11	31.4	8	8	O9TAY2	asterlina pe
23	11	31.4	8	11	O35835	rattus norv
24	11	31.4	8	11	P82598	rattus norv
25	11	31.4	8	11	O9ET18	mus spreus
26	11	31.4	8	11	O9ET17	mus caroll
27	11	31.4	8	11	O9ET16	mesocricetu
28	11	31.4	8	11	O99MNO	mus musculu
29	11	31.4	8	13	P79940	xenopus lae
30	11	31.4	8	13	O98TU5	xenopus lae
31	10	28.6	7	2	O07354	synechococc
32	10	28.6	8	3	P87225	saccharomyc
33	10	28.6	8	4	O9HC00	homo sapien
34	10	28.6	8	10	O9S824	homo sapien
35	9	25.7	8	8	O9GD00	mascula mad
36	9	25.7	8	11	O9QVFP4	rattus sp.
37	8	22.9	8	5	O9TMH5	perlinereis
38	7	20.0	7	4	O15903	homo sapien
39	7	20.0	7	8	O98866	spinnacia ol
40	7	20.0	8	2	O52062	baclillus me
41	7	20.0	8	2	O45889	streplococc
42	7	20.0	8	2	O45889	clostridium
43	7	20.0	8	2	O9S6D5	eschericchia
44	7	20.0	8	2	O9S443	pseudomonas
45	7	20.0	8	2	O9R9C2	borrelia bu
46	7	20.0	8	2	O9R5R0	shigella dy
47	7	20.0	8	2	O9R5L7	clostridium
48	7	20.0	8	4	O15898	homo sapien
49	7	20.0	8	7	O95213	oryctolagus
50	7	20.0	8	8	O34909	locusta mlg

ALIGNMENTS

RESULT 1
ID 062721 PRELIMINARY: PRT: 8 AA.
AC 062721;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE PROHIBITIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT Prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17178; AAA86692.1; -;
FT NON_TER
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 45.78; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 2 wr 3
RESULT 2

009258
 ID 009258 PRELIMINARY; PRT; 8 AA.
 AC 009258;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE NIFH (FRAGMENT).
 GN NIFH.
 OS *Synechococcus* sp. (strain PCC 8801 / RF-1) (Cyanophyceae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RF-1;
 RA Chen H.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF001780; AAC33369.1; -.
 FT NON_TER 6 8
 SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 42.9%; Score 15; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 4.7e+05;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 rxsfxf 8
 Db 2 RQIAFYG 8

RESULT 3
 ID P82929 PRELIMINARY; PRT; 8 AA.
 AC P82929;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
 OS *Bos taurus* (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LIVER;
 RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "Small subunit of the mammalian mitochondrial ribosome. Identification
 of the full complement ribosomal proteins present.";
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 935 MW; 9639DIA72058637D CRC64;

Query Match 40.0%; Score 14; DB 6; Length 8;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxsxf 6
 Db 2 WGIILTF 7

RESULT 4
 ID Q95945 PRELIMINARY; PRT; 7 AA.
 AC Q95945;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE INSIDE INTRON 5 (FRAGMENT).
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system. Structure and
 nucleotide sequence of the gene coding for subunit 1 of yeast
 cytochrome oxidase.";
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL: V00694; CAA24066.1; -.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362C0C460 CRC64;

Query Match 37.1%; Score 13; DB 8; Length 7;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 Db 4 WK 5

RESULT 5
 ID P70243 PRELIMINARY; PRT; 8 AA.
 AC P70243;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Ophoff R.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X98325; CAA66969.1; -.
 KW Calcium channel.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 Db 7 WQ 8

RESULT 6
 ID Q9QVD3 PRELIMINARY; PRT; 8 AA.
 AC Q9QVD3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE INOSTOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
 OS *Rattus* sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;
 RP [1]
 RT SEQUENCE
 RA MEDLINE:92202192; PubMed:1313009;
 RX Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
 RT Iwanaga S., Hirata M.;
 RT "Putative Inositol 1,4,5-trisphosphate binding proteins in rat brain
 cytosol."
 RL J. Biol. Chem. 267:6518-6525(1992).
 SQ SEQUENCE 8 AA: 1047 MW: D72415BB06C37041 CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 2
 1:
 Db 3 w 4

RESULT 7
 ID P82096 PRELIMINARY; PRT; 6 AA.
 AC P82096;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ELECTRIN 1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella."
 RL Aust. J. Chem. 52:0-0(1999).
 RT Amphibian skin; Amidation.
 FT MOD.RES 6
 SQ SEQUENCE 6 AA: 792 MW: 6683704772C9A000 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 1:
 Db 5 w 5

RESULT 8
 ID 049223 PRELIMINARY; PRT; 7 AA.
 AC 049223;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE HMG-1-LIKE PROTEIN (FRAGMENT).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
 RT STRAIN=CV. ESSEX; TISSUE=ROOTS;
 RX MEDLINE=91367679; PubMed=1091369;

RA Laux T., Goldberg R.B.;
 RT "A plant DNA binding protein shares highly conserved sequence motifs
 with HMG-box proteins."
 RL Nucleic Acids Res. 19:4769-4769(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
 RA Mahalingam R., Knap H.T.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF047050; AAC03556.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA: 850 MW: 6AAAAAB378637810 CRC64;

Query Match 31.4%; Score 11; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 1:
 Db 2 w 2

RESULT 9
 ID P82065 PRELIMINARY; PRT; 7 AA.
 AC P82065;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE TRIPTOPHYLIN 5.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steindorner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RT Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella'. The skin peptide profile as a probe for the study
 of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB.
 KW Amphibian skin; Amidation; Neuropeptide.
 FT MOD.RES 7
 SQ SEQUENCE 7 AA: 983 MW: 7401E9D367604680 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 7;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 1:
 Db 4 w 4

RESULT 10
 ID 085406 PRELIMINARY; PRT; 8 AA.
 AC 085406;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
 OS Coxiella burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;

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OC Coxiella group; Coxiella.
OX NCBI_TaxID=777;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NINE MILE PHASE 1;
RA Willems H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
RT Coxiella burnetii."
RT EMBL; AF064963; AAD09947.1; -.
DR EMBL; AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 2; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 4 w 4

RESULT 11
ID 015888 PRELIMINARY; PRT; 8 AA.
AC 015888;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RA Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32069; AAA73878.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 12
ID 015890 PRELIMINARY; PRT; 8 AA.
AC 015890;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
```

```
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RA Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 975 MW; 605FA6C5BEA5A2D3 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 4; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 1 w 1

RESULT 13
ID 09VRD2 PRELIMINARY; PRT; 8 AA.
AC 09VRD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paule J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
```


RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003569; AAF50870.1; -.
DR FlyBase: FBgn0040648; CG11666.
SQ SEQUENCE 8 AA; 1062 MW; ED11B5D044004376 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 2 w 2

RESULT 14
P82685 ID PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 15
P82686 ID PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BD4 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 16
P82687 ID PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_Taxid=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; Pubmed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD.RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 17
P82688 ID PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_Taxid=6978;

RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE-CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 retrocerebral complex of the American cockroach, Periplaneta
 americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KM Neuropeptide; Amidation.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 7 w 7

RESULT 18
 ID P82689 PRELIMINARY; PRT; 8 AA.
 AC P82689;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE KININ-5 (PEA-K-5).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE-CORPORA CARDIACA;
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of eight kinins from the
 retrocerebral complex of the American cockroach, Periplaneta
 americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
 KM Neuropeptide; Amidation.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 865 MW; C76365B449CDC775 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 7 w 7

RESULT 19
 ID 002831 PRELIMINARY; PRT; 8 AA.
 AC 002831;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE PRO ALPRA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96377339; PubMed=8783186;
 RA Metsaranata M., Kujala U.M., Pellinleml L., Osterman H., Aho H.,
 RA Vuorio E.;
 RT "Evidence for insufficient chondrocytic differentiation during repair
 of full-thickness defects of articular cartilage.";
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL; S83371; AAD14433.1; -;
 FT NON TER 1
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 2 w 2

RESULT 20
 ID Q9TRY3 PRELIMINARY; PRT; 8 AA.
 AC Q9TRY3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
 OS Sus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9826;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92049376; PubMed=1719383;
 RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
 RT "Isolation and molecular cloning of insulin-like growth factor-binding
 protein-6.";
 RL Mol. Endocrinol. 5:938-948(1991).
 SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
 DB 5 w 5

RESULT 21
 ID Q9TD02 PRELIMINARY; PRT; 8 AA.
 AC Q9TD02;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
 OS Terranatos dolichopterus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
 OX NCBI_TaxID=61836;
 RN [1]

RP SEQUENCE FROM N.A.
RA Hreke T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
RM EMBL; AF092421; AAF03041.1; -.
KW Mitochondrion.
SQ SEQUENCE 8 AA: 1084 MW: F0C9D3640DD44056 CRC64;
FT NON_TER

Query Match 31.4%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 22
O9TAY2 PRELIMINARY; PRT; 8 AA.
AC O9TAY2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COI GENE PRODUCT (FRAGMENT).
OS Asterina pectinifera (Starfish).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID:7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:89354669; PubMed-2766382;
RA Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL Curr. Genet. 15:193-206(1989).
DR EMBL; X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER

Query Match 31.4%; Score 11; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 23
O35835 PRELIMINARY; PRT; 8 AA.
AC O35835;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORF1 PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE:98008057; PubMed-9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of

RT NR2 convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA: 886 MW: EA7EA1BIADC5A5B6 CRC64;
FT NON_TER

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 24
P82598 PRELIMINARY; PRT; 8 AA.
AC P82598;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 38KDA NON-ARGINASE GROWTH INHIBITORY FACTOR (NAGIF)(FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE:20198203; PubMed-10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -I- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
CC -I- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON_TER

Query Match 31.4%; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 25
O9ET18 PRELIMINARY; PRT; 8 AA.
AC O9ET18;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RT (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286200; AAC01474.1; -.

FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 31.48; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:17 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1G
Perfect score: 35
Sequence: 1 wxsxfxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

_A_Geneseq_1101.*
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5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT:*
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22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	80.0	8	21	AA06521	Claudin-2 cell adh
2	28	80.0	8	21	AA06574	Claudin-2 cyclic c
3	27	77.1	8	21	AA06426	Claudin-1 cell adh
4	27	77.1	8	21	AA06512	Claudin-1 cyclic c
5	27	77.1	8	21	AA06583	Claudin-3 cell adh
6	27	77.1	8	21	AA06636	Claudin-3 cyclic c
7	27	77.1	8	21	AA06645	Claudin-4 cell adh
8	27	77.1	8	21	AA06698	Claudin-4 cyclic c
9	24	68.6	8	21	AA06419	Claudin-1 cell adh
10	24	68.6	8	21	AA06479	Claudin-1 cyclic c
11	24	68.6	8	21	AA06764	Claudin-6/9 cell a

12	24	68.6	8	21	AA06814	Claudin-6/9 cyclic c
13	24	68.6	8	21	AA06823	Claudin-7 cell adh
14	24	68.6	8	21	AA06876	Claudin-7 cyclic c
15	24	68.6	8	21	AA06916	Claudin cell adhes
16	24	68.6	8	21	AA06917	Claudin-7 cell adh
17	23	65.7	6	21	AA06519	Claudin-2 cell adh
18	23	65.7	6	21	AA06572	Claudin-2 cyclic c
19	23	65.7	7	21	AA06520	Claudin-2 cell adh
20	23	65.7	7	21	AA06573	Claudin-2 cyclic c
21	23	65.7	8	21	AA06528	Claudin-2 cyclic c
22	23	65.7	8	21	AA06537	Claudin-2 cyclic c
23	23	65.7	8	21	AA06546	Claudin-2 cyclic c
24	23	65.7	8	21	AA06535	Claudin-2 cyclic c
25	23	65.7	8	21	AA06564	Claudin-3 cyclic c
26	22	62.9	6	21	AA06581	Claudin-3 cell adh
27	22	62.9	6	21	AA06634	Claudin-3 cyclic c
28	22	62.9	6	21	AA06643	Claudin-4 cell adh
29	22	62.9	6	21	AA06696	Claudin-4 cyclic c
30	22	62.9	7	21	AA06582	Claudin-3 cell adh
31	22	62.9	7	21	AA06635	Claudin-3 cyclic c
32	22	62.9	7	21	AA06644	Claudin-4 cell adh
33	22	62.9	7	21	AA06697	Claudin-4 cyclic c
34	22	62.9	8	21	AA06590	Claudin-3 cyclic c
35	22	62.9	8	21	AA06539	Claudin-3 cyclic c
36	22	62.9	8	21	AA06608	Claudin-3 cyclic c
37	22	62.9	8	21	AA06617	Claudin-3 cyclic c
38	22	62.9	8	21	AA06626	Claudin-3 cyclic c
39	22	62.9	8	21	AA06652	Claudin-4 cyclic c
40	22	62.9	8	21	AA06661	Claudin-4 cyclic c
41	22	62.9	8	21	AA06670	Claudin-4 cyclic c
42	22	62.9	8	21	AA06679	Claudin-4 cyclic c
43	22	62.9	8	21	AA06688	Claudin-4 cyclic c
44	22	62.9	8	21	AA06879	Claudin-8 cell adh
45	22	62.9	8	21	AA06897	Claudin-8 cyclic c
46	22	62.9	8	21	AA06918	Claudin-8 cell adh
47	21	60.0	6	21	AA06424	Claudin-1 cell adh
48	21	60.0	6	21	AA06510	Claudin-1 cyclic c
49	21	60.0	7	21	AA06425	Claudin-1 cell adh
50	21	60.0	7	21	AA06511	Claudin-1 cyclic c

ALIGNMENTS

RESULT 1	
ID	AA06521 standard; peptide: 8 AA.
AC	AA06521;
XX	
DT	28-SEP-2000 (first entry)
DE	
XX	Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.
XX	
KW	Claudin-2 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection.
XX	
OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
XX	Blaschuck OM, Symonds JM, Gour BJ;
PI	
XX	

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 80.0%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsfxxg 8
11111111
Db 1 wrtsyyvg 8

RESULT 2
AAB06574
ID AAB06574 standard; peptide; 8 AA.
XX
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 80.0%; Score 28; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsfxxg 8
11111111
Db 1 wrtsyyvg 8

RESULT 3
AAB06426
ID AAB06426 standard; peptide; 8 AA.
XX
AC AAB06426;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PD
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxsfxxg 8
11111111
Db 1 wrtsyyvg 8

RESULT	4
AAB06512	standard; peptide: 8 AA.
ID	AAB06512 standard; peptide: 8 AA.
XX	
AC	AAB06512;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX	
KW	Claudin-1 modulating agent; cell adhesion recognition sequence;
KM	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection; cyclic.
OS	Mammalia.
PN	WO200026360-A1.
PD	11-MAY-2000.
PF	03-NOV-1999; 99MO-CA01029.
PR	03-NOV-1998; 98US-0185908.
PA	30-MAR-1999; 99US-0282029.
PI	(ADHE-) ADHEREX TECHNOLOGIES INC.
PT	Biaschuck OM, Symonds JM, Gour BJ;
PS	WPI; 2000-365610/31.
PP	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	virosopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
XX	Claim 43; page 97; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC	which are membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, they can also be used to facilitate drug delivery
CC	to the desired target site. The present sequence has a cyclic
CC	conformation.
SO	Sequence 8 AA:
Query Match	77.1%; Score 27; DB 21; Length 8;
Best Local Similarity	50.0%; Pred. No. 4.3e+05;
Matches	4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY	1 wrxxsfyg 8
DB	1 wrlysyag 8
RESULT	5
AAB06583	
ID	AAB06583 standard; peptide: 8 AA.
XX	
AC	AAB06583;
XX	
DT	28-SEP-2000 (first entry)
XX	
DE	Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.
XX	
KW	Claudin-3 modulating agent; cell adhesion recognition sequence;
KM	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection.

OS	Mammalia
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PA	30-MAR-1999; 99US-0282029.
XX	
PI	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
XX	
PT	vasopermeability, for delivering drugs to tumors and the nervous system
XX	
PS	and across the skin -
XX	
PS	Claim 52; Page 99; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
XX	
CC	cell adhesion modulators. The claudin-3 group of proteins are cadherins,
XX	
CC	which are membrane glycoproteins involved in cell adhesion. In some
XX	
CC	situations, cell adhesion occurs at abnormal levels, and these peptides
XX	
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
XX	
CC	inflammatory diseases and cancer, and aid wound healing and implant
XX	
CC	adhesion. In addition, they can also be used to facilitate drug delivery
XX	
SQ	to the desired target site.
SQ	Sequence 8 AA:
OY	Query Match 77.1%; Score 27; DB 21; Length 8;
	Best Local Similarity 50.0%; Pred. No. 4.3e+03;
	Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Db	1 wrxxsfkg 8
	:
	1 wrvsafg 8
RESULT 6	
AAB06636	
ID AAB06636 standard; peptide: 8 AA.	
XX	
AC AAB06636:	
XX	
DT 28-SEP-2000 (first entry)	
XX	
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.	
XX	
DE Claudin-3 modulating agent; cell adhesion recognition sequence;	
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;	
KW graft rejection; cyclic.	
XX	
OS Mammalia.	
OS	
PN WO200026360-A1.	
XX	
PD 11-MAY-2000.	
XX	
PF 03-NOV-1999; 99WO-CA01029.	
XX	
PR 03-NOV-1998; 98US-0185908.	
XX	
PA 30-MAR-1999; 99US-0282029.	
XX	
PA (ADHE-) ADHEREX TECHNOLOGIES INC.	
XX	
PI Blaschuck OW, Symonds JM, Gour BJ;	
XX	
PI Blaschuck OW, Symonds JM, Gour BJ;	

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsfxg 8
11 : 11
1 wrvsafg 8
Db

RESULT 7
AAB06645
ID AAB06645 standard; peptide; 8 AA.
XX
AC AAB06645;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; Inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 58; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsfxg 8
11 : 11
1 wrvatfg 8
Db

RESULT 8
AAB06698
ID AAB06698 standard; peptide; 8 AA.
XX
AC AAB06698;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 216.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; Inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
PD 11-MAY-2000.
XX
PF Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsfxg 8
11 : 11
1 wrvatfg 8
Db


```
RESULT 9
AAB06419
XX AAB06419 standard; peptide: 8 AA.
AC
XX AAB06419:
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SO Sequence 8 AA:

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsfxg 8
I: I: I
Db 1 wklysyag 8

RESULT 10
AAB06479
XX AAB06479 standard; peptide: 8 AA.
AC
XX AAB06479:
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
```

```
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SO Sequence 8 AA:

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxsfxg 8
I: I: I
Db 1 wklysyag 8

RESULT 11
AAB06764
XX AAB06764 standard; peptide: 8 AA.
AC
XX AAB06764:
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335.
XX
KW Claudin-6 modulating agent; claudin-9 modulating agent;
KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KW inflammatory disease; cancer; graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
```


	RESULT_14	
ID	AAB06876	standard; peptide; 8 AA.
AC	AAB06876;	
DT	28-SEP-2000	(first entry)
DE	Claudin-7 cyclic cell adhesion recognition sequence SEQ ID NO: 447.	
KW	Claudin-7 modulating agent; cell adhesion recognition sequence; CMR sequence; autoimmune disease; inflammatory disease; cancer; KW graft rejection; cyclic.	
OS	Mammalia.	
PN	WO200026360-A1.	
PD	11-MAY-2000.	
PF	03-NOV-1999;	99MO-CA01029.
PR	03-NOV-1998;	98US-0185908.
XX	30-MAR-1999;	99US-0282029.
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.	
PI	Biaschuck OW, Symonds JM, Gour BJ:	
DR	WPI; 2000-365610/31.	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing vulnerability, for delivering drugs to tumors and the nervous system and across the skin -	
PS	Claim 79; Page 105; 121pp; English.	
CC	The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-7 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation.	
SQ	Sequence	8 AA;
Query Match	68.6%;	Score 24; DB 21; Length 8;
Best Local Similarity	37.5%;	Pred. No. 4.3e+05;
Matches	3; Conservative	2; Mismatches 3; Indels 0; Gaps 0
OY	1 wrxxsfxyg 8	
I:	: :	
Db	1 wgmssyayg 8	
RESULT_15		
ID	AAB06916	standard; Protein; 8 AA.
AC	AAB06916;	
DT	05-OCT-2000	(first entry)
DE	Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.	
KW	Claudin modulating agent; cell adhesion recognition sequence; CMR sequence; autoimmune disease; inflammatory disease; cancer; KW graft rejection.	

XX	Synthetic.
OS	
XX	Key
FH	Modified-site
FT	1
FT	/note= "N-terminal acetyl"
FT	8
FT	/note= "C-terminal amide"
XX	
XX	WO200026360-A1.
PN	
PD	11-MAY-2000.
XX	
PE	03-NOV-1999;
XX	99WO-CA01029.
PR	03-NOV-1998;
PR	98US-0185908.
XX	30-MAR-1999;
PA	99US-0282029.
(ADHE-)	ADHEREX TECHNOLOGIES INC.
PI	
PI	Blaschuck OW, Symonds JM, Gour BJ;
XX	
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 71; Page 103; 121pp; English.
XX	
CC	The present sequence is a peptide which can be used in a claudin-mediated
CC	cell adhesion modulator. The claudin group of proteins are cadherins,
CC	situations where membrane glycoproteins involved in cell adhesion. In some
CC	situations, cell adhesion occurs at abnormal levels, and this peptide
CC	can be used to modulate these levels, and thus treat autoimmune diseases,
CC	inflammatory diseases and cancer, and aid wound healing and implant
CC	adhesion. In addition, it can also be used to facilitate drug delivery
CC	to the desired target site.
XX	
SO	Sequence 8 AA;
OY	1 wrxsfxg 8
I:	: :
Db	1 wkvtafig 8
RESULT 16	
AAB06917	
ID AAB06917	standard; Protein: 8 AA.
XX	
AC	AAB06917;
XX	
DT	05-OCT-2000 (first entry)
XX	
DE	Claudin-7 cell adhesion recognition modulating sequence SEQ ID NO: 50.
XX	
KW	Claudin-7 modulating agent; cell adhesion recognition sequence;
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX	graft rejection.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site
FT	1
FT	/note= "N-terminal acetyl"
FT	8
FT	/note= "C-terminal amide"
XX	

PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
PS Claim 77; Page 104; 121pp; English.
XX
CC The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 68.6%; Score 24; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxsfxxg 8
1 : 1 : 1
Db 1 wqmsasyag 8

RESULT 17
AAB06519
ID AAB06519 standard; peptide; 6 AA.
XX
AC AAB06519;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 40.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; Inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 6 AA;

Query Match 65.7%; Score 23; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
1 : 1 :
Db 1 wrtssy 6

RESULT 18
AAB06572
ID AAB06572 standard; peptide; 6 AA.
XX
AC AAB06572;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 161.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; Inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
PS Claim 49; Page 98; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX Sequence 6 AA;

Query Match 65.7%; Score 23; DB 21; Length 6;
Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 1 wrtsxy 6

RESULT 19
AAB06520
ID AAB06520 standard; peptide: 7 AA.

AC AAB06520;
XX
XX 28-SEP-2000 (first entry)

DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 41.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 46; Page 97; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

XX Sequence 7 AA;

Query Match 65.7%; Score 23; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 1 wrtsxy 6

RESULT 20
AAB06573

ID AAB06573 standard; peptide: 7 AA.

XX AAB06573;

XX 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 162.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.

XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX Sequence 7 AA;

Query Match 65.7%; Score 23; DB 21; Length 7;
Best Local Similarity 50.0%; Pred. NO. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 1 wrtsxy 6

RESULT 21
AAB06528
ID AAB06528 standard; peptide: 8 AA.

XX AAB06528;

XX 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 117.

XX Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX

PN WO200026360-A1.
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 8 AA;
XX

Query Match 65.7%; Score 23; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wrxxsf 6
|| 1;
Db 2 wrtssy 7

RESULT 22
AAB06537
ID AAB06537 standard; peptide; 8 AA.
XX
XX AAB06537;
XX AC
XX 28-SEP-2000 (first entry)
XX DT
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 126.
DE
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX PN
XX 11-MAY-2000.
XX PD
XX 03-NOV-1999; 99WO-CA01029.
XX PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2600-365610/31.
XX DR

XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 8 AA;
XX

Query Match 65.7%; Score 23; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 wrxxsf 6
|| 1;
Db 2 wrtssy 7

RESULT 23
AAB06546
ID AAB06546 standard; peptide; 8 AA.
XX
XX AAB06546;
XX AC
XX 28-SEP-2000 (first entry)
XX DT
XX
XX Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 135.
DE
XX Claudin-2 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX PN
XX 11-MAY-2000.
XX PD
XX 03-NOV-1999; 99WO-CA01029.
XX PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX WPI: 2000-365610/31.
XX DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 49; Page 98; 121pp; English.
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
XX conformation.
SQ Sequence 8 AA;

Query Match 65.7%; Score 23; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 2 wrtsy 7

RESULT 24
AAB06555
ID AAB06555 standard; peptide; 8 AA.
XX
AC AAB06555;

DT 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 144.

XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
XX PT vasopermeability, for delivering drugs to tumors and the nervous system
XX PT and across the skin -

XX PS Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX SQ Sequence 8 AA;

Query Match 65.7%; Score 23; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 2 wrtsy 7

RESULT 25
AAB06564
ID AAB06564 standard; peptide; 8 AA.
XX
AC AAB06564;

DT 28-SEP-2000 (first entry)

DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 153.

XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuck OW, Symonds JM, Gour BJ;

XX WPI: 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
XX PT vasopermeability, for delivering drugs to tumors and the nervous system
XX PT and across the skin -

XX PS Claim 49; Page 98; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX SQ Sequence 8 AA;

Query Match 65.7%; Score 23; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxsf 6
111:
Db 2 wrtsy 7

Search completed: January 14, 2002, 07:43:17
Job time: 428 sec

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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:37 ; Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1g
Perfect score: 35
Sequence: 1 wrxxsfxx 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues 43125

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 8
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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2: /cgcn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgcn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgcn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgcn2_6/prodata/2/1aa/PCBUS.COMB.pep.*
6: /cgcn2_6/prodata/2/1aa/backfile1a1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	54.3	7	5 PCT-US95-11405-2	Sequence 17, Appl
2	18	51.4	6	2 US-09-127-574-17	Sequence 12, Appl
3	18	51.4	7	4 US-09-177-249-280	Sequence 280, App
4	17	48.6	5	1 US-08-190-802A-263	Sequence 263, App
5	17	48.6	5	4 US-08-477-346-263	Sequence 263, App
6	17	48.6	6	4 US-09-189-060B-58	Sequence 58, Appl
7	17	48.6	8	2 US-08-350-260A-464	Sequence 464, App
8	16	45.7	3	1 US-08-165-545-8	Sequence 8, Appl
9	16	45.7	3	1 US-08-305-768-27	Sequence 27, Appl
10	16	45.7	3	1 US-08-256-771-17	Sequence 17, Appl
11	16	45.7	3	1 US-08-381-984-17	Sequence 17, Appl
12	16	45.7	3	2 US-08-871-163-27	Sequence 27, Appl
13	16	45.7	3	3 US-08-767-903-27	Sequence 27, Appl
14	16	45.7	3	5 PCT-US95-11724-27	Sequence 27, Appl
15	16	45.7	4	1 US-08-165-545-7	Sequence 7, Appl
16	16	45.7	4	1 US-08-190-802A-265	Sequence 265, App
17	16	45.7	4	1 US-08-215-137-11	Sequence 11, Appl
18	16	45.7	4	1 US-08-256-771-16	Sequence 16, Appl
19	16	45.7	4	1 US-08-222-851-22	Sequence 22, Appl
20	16	45.7	4	1 US-08-381-984-16	Sequence 16, Appl
21	16	45.7	4	2 US-08-592-646A-62	Sequence 62, Appl
22	16	45.7	4	2 US-08-637-759B-108	Sequence 108, App
23	16	45.7	4	3 US-08-871-355A-108	Sequence 108, App
24	16	45.7	4	3 US-08-981-122-24	Sequence 24, Appl
25	16	45.7	4	3 US-08-981-122-28	Sequence 28, Appl
26	16	45.7	4	4 US-09-329-350-3	Sequence 3, Appl
27	16	45.7	4	4 US-08-591-632-40	Sequence 40, Appl

28	16	45.7	4	4 US-08-591-632-42	Sequence 42, Appl
29	16	45.7	4	4 US-08-477-346-265	Sequence 265, App
30	16	45.7	4	4 US-08-682-767-25	Sequence 25, Appl
31	16	45.7	5	1 US-07-851-941-1	Sequence 1, Appl
32	16	45.7	5	1 US-07-851-941-2	Sequence 2, Appl
33	16	45.7	5	1 US-07-851-941-3	Sequence 3, Appl
34	16	45.7	5	1 US-08-190-802A-264	Sequence 264, App
35	16	45.7	5	3 US-08-907-403A-7	Sequence 7, Appl
36	16	45.7	5	3 US-08-984-173-34	Sequence 34, Appl
37	16	45.7	5	3 US-08-981-122-12	Sequence 12, Appl
38	16	45.7	5	3 US-08-981-122-16	Sequence 16, Appl
39	16	45.7	5	3 US-08-981-122-19	Sequence 19, Appl
40	16	45.7	5	3 US-08-981-122-20	Sequence 20, Appl
41	16	45.7	5	3 US-08-981-122-26	Sequence 26, Appl
42	16	45.7	5	3 US-08-981-122-33	Sequence 33, Appl
43	16	45.7	5	3 US-08-981-122-35	Sequence 35, Appl
44	16	45.7	5	3 US-08-981-122-89	Sequence 89, Appl
45	16	45.7	5	4 US-09-020-880-39	Sequence 39, Appl
46	16	45.7	5	4 US-09-020-880-44	Sequence 44, Appl
47	16	45.7	5	4 US-08-672-850-27	Sequence 27, Appl
48	16	45.7	5	4 US-09-398-193-34	Sequence 34, Appl
49	16	45.7	5	4 US-08-477-346-264	Sequence 264, App
50	16	45.7	5	4 US-09-461-697-279	Sequence 279, App

ALIGNMENTS

RESULT 1
PCT-US95-11405-2
Sequence 2, Application PC/TUS9511405
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PHOSPHOROUS-32 LABELLING OF ANTIBODIES
TITLE OF INVENTION: FOR CANCER THERAPY
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11405
FILING DATE: 18-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,103
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/599/IMIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-11405-2

Query Match 54.3% Score 19; DB 5; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wrxs 5
111
Db 1 WRRAS 5

RESULT 2
US-09-127-574-17
; Sequence 17, Application US/09127574
; Patent No. 5985836
; GENERAL INFORMATION:
; APPLICANT: Basteck, Patrick
; APPLICANT: Lang, John M.
; APPLICANT: Baumbach, George A.
; APPLICANT: Carbonell, Ruben G.
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides
; FILE REFERENCE: MSB-7248
; CURRENT APPLICATION NUMBER: US/09/127,574
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-127-574-17

Query Match 51.4%; Score 18; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 wrxs 5
111
Db 2 WRRKS 6

RESULT 3
US-09-177-249-280
; Sequence 280, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nit
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramlin
; APPLICANT: Margosian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-280

Query Match 51.4%; Score 18; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxsf 6
111
Db 2 WRHWSW 7

RESULT 4
US-08-190-802A-263
; Sequence 263, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theoreof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTAA peptide
US-08-190-802A-263

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxs 5
111
Db 1 WRTAA 5

RESULT 5
US-08-477-346-263
; Sequence 263, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theoreof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
US-08-477-346-263

STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTAA peptide
US-08-477-346-263

Query Match 48.6%; Score 17; DB 4; Length 5;
Best Local Similarly 40.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXSF 5
11:
DB 1 WRTAA 5

RESULT 6
US-09-189-060B-58
Sequence 58, Application US/09189060B
Patent No. 6270968
GENERAL INFORMATION:
APPLICANT: Dablog, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Kauppinen, Markus
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method Of Providing No. 6270968el DNA sequences
FILE REFERENCE: 4772-204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 58
LENGTH: 6
TYPE: PRT
ORGANISM: Prokaryotic
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)...(6)
OTHER INFORMATION: Xaa u Phe or Tyr
US-09-189-060B-58

Query Match 48.6%; Score 17; DB 4; Length 6;
Best Local Similarly 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXSF 6
1111:
DB 1 WRXDMF 6

RESULT 7
US-08-350-260A-464
Sequence 464, Application US/08350260A
Patent No. 596225
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 464:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-464

Query Match 48.6%; Score 17; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wxxxsf 6
11
Db 3 WRVFDY 8

RESULT 8

US-08-165-545-8
; Sequence 8, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,545
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,981
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 2 wr 3

RESULT 9

US-08-305-768-27
; Sequence 27, Application US/08305768
; Patent No. 5602097
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,768
; FILING DATE: 12-SEPT-1994
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
Db 1 wr 2

RESULT 10
US-08-256-771-17
; Sequence 17, Application US/08256771

Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 Inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-17

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 11
US-08-381-984-17
Sequence 17, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note="the specified peptide as well as
peptides including the specified peptide as a fragment the
US-08-381-984-17

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 12
US-08-871-163-27
Sequence 27, Application US/08871163
Patent No. 5885782
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (PRO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,163
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-871-163-27

Query Match 45.7%; Score 16; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 1 wr 2

RESULT 13
US-08-767-903-27
; Sequence 27, Application US/08767903
; Patent No. 6020312
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,903
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-767-903-27

Query Match 45.7%; Score 16; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 1 wr 2

RESULT 14
PCT-US95-11724-27
; Sequence 27, Application PC/TUS9511724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11724
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-11724-27

Query Match 45.7%; Score 16; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
DB 1 wr 2

RESULT 15
US-08-165-545-7
; Sequence 7, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Displaywrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,545
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/871,981
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:

VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wr 2
11
DB 3 wr 4

RESULT 16
US-08-190-802A-265
Sequence 265, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: WRTA peptide
US-08-190-802A-265

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wr 2
11

DB 1 wr 2

RESULT 17
US-08-215-137-11
Sequence 11, Application US/08215137
Patent No. 5614370
GENERAL INFORMATION:
APPLICANT: Konteatis, Zenon
APPLICANT: Siciliano, Salvatore J
APPLICANT: Springer, Martin S
TITLE OF INVENTION: ASSAY TO IDENTIFY HUMAN C5A ANTAGONISTS
TITLE OF INVENTION: AND AGONISTS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,137
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bencon, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Tlc
OTHER INFORMATION: /note= "tetrahydroisoguanoline carboxyllic acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /label= dcha
OTHER INFORMATION: /note= "D-cyclohexylalanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= darg
OTHER INFORMATION: /note= "D-arginine"
US-08-215-137-11

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 wr 2
11
DB 3 wr 4

RESULT 18
US-08-256-771-16
Sequence 16, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-16

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 WR 4

RESULT 19
US-08-222-851-22
Sequence 22, Application US/08222851
Patent No. 5723128
GENERAL INFORMATION:
APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: KRENSKY, ALAN M.
APPLICANT: PARHAM, PETER
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,851
FILING DATE: 05-Apr-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28600-20200.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 494-0792
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-851-22

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 WR 4

RESULT 20
US-08-381-984-16
Sequence 16, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-16

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 3 WR 4

RESULT 21
US-08-592-646A-62
Sequence 62, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592.646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-62

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 3 WR 4

RESULT 22
US-08-637-759B-108
Sequence 108, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637.759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-108

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
DB 1 WR 2

RESULT 23
US-08-871-355A-108
Sequence 108, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871.355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPLS 101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ. ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-108

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wr 2
11
DB 1 wr 2
11
RESULT 24
US-08-981-122-24
Sequence 24, Application US/08981122B
Patent No. 6127339
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
APPLICANT: Aritomi, Masaharu
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981.122B
CURRENT FILING DATE: 1997-12-18
PRIORITY APPLICATION NUMBER: JP 7-176904
PRIORITY FILING DATE: 1995-06-21
PRIORITY APPLICATION NUMBER: PCT/JP96/01734
PRIORITY FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of a peptide synthesized in Example 4 from L-form
Patent No. 6127339
OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetptide
OTHER INFORMATION: synthesizing system (Ramps)
US-08-981-122-24

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 wr 4

RESULT 25
US-08-981-122-28
Sequence 28, Application US/08981122B
Patent No. 6127339
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
APPLICANT: Aritomi, Masaharu
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981.122B
CURRENT FILING DATE: 1997-12-18
PRIORITY APPLICATION NUMBER: JP 7-176904
PRIORITY FILING DATE: 1995-06-21
PRIORITY APPLICATION NUMBER: PCT/JP96/01734
PRIORITY FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of a peptide synthesized in Example 5 from L-form
Patent No. 6127339
OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetptide
OTHER INFORMATION: synthesizing system (Ramps)
US-08-981-122-28

Query Match 45.7%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 wr 2
11
DB 3 wr 4

Search completed: January 14, 2002, 07:41:37
Job time: 458 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:44:22 ; Search time 43.28 Seconds
(without alignments)
14.080 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 35
Sequence: 1 wrxxafxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	7	2 S33245	neuromodulatory pe
2	15	42.9	8	2 A38887	T-cell receptor ga
3	14	40.0	8	2 A46306	spasmogenic toxin
4	13	37.1	7	2 S33244	neuromodulatory pe
5	13	37.1	7	2 S33246	neuromodulatory pe
6	13	37.1	8	2 C61512	variant surface gl
7	12	34.3	6	2 A41946	T-cell receptor ga
8	12	34.3	8	2 S13661	polygalacturonase
9	12	34.3	8	2 A42057	fibroblast growth
10	11	31.4	3	2 F37196	bradykinin-potent
11	11	31.4	4	2 A34526	RGH-related neuro
12	11	31.4	4	2 B53284	T-cell receptor be
13	11	31.4	4	2 PT0661	T-cell receptor be
14	11	31.4	5	2 A32516	cholecystokinin-5
15	11	31.4	5	2 A60803	neuropeptide - sea
16	11	31.4	5	2 JH0253	gut pentapeptide -
17	11	31.4	5	2 G37196	bradykinin-potent
18	11	31.4	5	2 PT0281	Ig heavy chain CRD
19	11	31.4	5	2 PT0308	Ig heavy chain CRD
20	11	31.4	5	2 PT0729	T-cell receptor be
21	11	31.4	5	2 PT0580	T-cell receptor be
22	11	31.4	6	2 S66195	alcohol dehydrogen
23	11	31.4	6	2 B34835	dnaa protein - pse
24	11	31.4	6	2 A31263	dihydrofolate redu
25	11	31.4	6	2 B31263	dihydrofolate redu
26	11	31.4	6	2 A61068	locustakinin - mig
27	11	31.4	6	2 B35640	cerebellar degener
28	11	31.4	6	2 PT0629	T-cell receptor be
29	11	31.4	6	2 PT0532	T-cell receptor be

30	11	31.4	6	2 PT0519	T-cell receptor be
31	11	31.4	6	2 PT0637	T-cell receptor be
32	11	31.4	6	2 PT0641	T-cell receptor be
33	11	31.4	6	2 PT0726	T-cell receptor be
34	11	31.4	6	2 F41946	T-cell receptor ga
35	11	31.4	6	2 PD0028	pev-kinin 2 - pena
36	11	31.4	6	4 I79564	hypothetical TGL3
37	11	31.4	7	2 S21230	dermorphin (Trp-4,
38	11	31.4	7	2 A58512	venom heptapeptide
39	11	31.4	7	2 A61081	tryptophyllin, bas
40	11	31.4	7	2 S57274	triacylglycerol 11
41	11	31.4	7	2 S09652	hypothetical prote
42	11	31.4	7	2 PM0649	alpha-dextrin endo
43	11	31.4	7	2 PQ0727	H2 class I protein
44	11	31.4	7	2 H33098	180K exoantigen -
45	11	31.4	7	2 S33567	tubulin beta-3 cha
46	11	31.4	7	2 E48394	glycoprotein compo
47	11	31.4	7	2 PH1602	Ig H chain V-D-J r
48	11	31.4	7	2 E33932	Ig mu chain D reg1
49	11	31.4	7	2 PT0526	T-cell receptor be
50	11	31.4	7	2 PT0628	T-cell receptor be

ALIGNMENTS

RESULT 1
S33245 neuromodulatory peptide Wmamide-2 - giant African snail
C:Species: Achatina fulica (giant African snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33245
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: Wmamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A:Reference number: S33244; MUID:99265912
A:Accession: S33245
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 45.7% Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 wr 2
Db 1 WR 2

RESULT 2
A38887 T-cell receptor gamma chain (5t.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A38887
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A11946; MUID:92049316
A:Accession: A38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <WHE>
C:Keywords: T-cell receptor

Query Match 42.9% Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 wrxxaf 6

Db 3 WDSSGF 8

RESULT 3
A:Accession: A46306
spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A46306
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicol 31, 377-384, 1993
A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A:Reference number: A46306; MUID:93276438
A:Accession: A46306
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match 40.0%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 atxg 8
1 1
1 1
Db 2 AFGG 5

RESULT 4
S33244
neuromodulatory peptide WMemide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: WMemide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A:Reference number: S33244; MUID:93265912
A:Accession: S33244
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 37.1%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
1 1
Db 1 WK 2

RESULT 5
S33246
neuromodulatory peptide WMemide-3 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33246
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A:Title: WMemide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A:Reference number: S33244; MUID:93265912
A:Accession: S33246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match 37.1%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
1 1
Db 1 WK 2

RESULT 6
C61512
variant surface glycoprotein MITRat 1.4 - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C:Accession: C61512
R:Holder, A.A.; Cross, G.A.M.
Mol. Biochem. Parasitol. 2, 135-150, 1981
A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te
A:Reference number: A61512; MUID:81172836
A:Accession: C61512
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Keywords: glycoprotein

Query Match 37.1%; Score 13; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxa 5
1 1
Db 1 WENNA 5

RESULT 7
A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316
A:Accession: A41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
C:Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 wrxxaf 6
1 1
1 1
Db 1 YRSGSF 6

RESULT 8
S13661
polygalacturonase (EC 3.2.1.15) isoform PG2 - fungus (Sclerotinia sclerotiorum) (frag
N:Alternate names: endopolygalacturonase; pectin depolymerase; pectinase
C:Species: Sclerotinia sclerotiorum
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S13661
R:Waksman, G.; Keon, J.P.R.; Turner, G.
Biochim. Biophys. Acta 1073, 43-48, 1991
A:Title: Purification and characterization of two endopolygalacturonases from Sclerot
A:Reference number: S13661; MUID:91120822
A:Accession: S13661
A:Molecule type: protein
A:Residues: 1-8 <WAK>
C:Function:

A:Description: involved in pectin degradation
C:Keywords: glycosidase; hydrolase

Query Match 34.3%: Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 fxx 8
| |
Db 6 FSG 8

RESULT 9
A42057 fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057

R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992

A:Title: Differential splicing in the extracellular region of fibroblast growth factor 1
A:Reference number: A42057; MUID:92107200

A:Accession: A42057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <MER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match 34.3%: Score 12; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 afxx 8
| |
Db 5 SFLG 8

RESULT 10
F37196 bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: F37196

R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides 6
A:Reference number: A37196; MUID:90351557

A:Accession: F37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>

C:Keywords: pyroglutamic acid
F:1/Modified site: pyroglutidone carboxylic acid (Gln) #status experimental

Query Match 31.4%: Score 11; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 11
A34626 RPKH-related neuropeptide - ferruginous spindle
C:Species: Fusinus ferrugineus (ferruginous spindle)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C:Accession: A34626

R:Kuraki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake,
Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A:Title: A molluscan neuropeptide related to the crustacean hormone, RPKH.
A:Reference number: A34626; MUID:90179762

A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KUR>
C:Keywords: neuropeptide

Query Match 31.4%: Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 4 w 4

RESULT 12
B53284 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity an
A:Reference number: A53284; MUID:91342695

A:Accession: B53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <HAR>
A:Cross-references: GB:S60737; NID:q233916; PIDN:AB19518.1; PID:q233918
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60738)
C:Keywords: T-cell receptor

Query Match 31.4%: Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 2 w 2

RESULT 13
PT0661 T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0661

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0661; MUID:91277601

A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEF>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%: Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 3 w 3

RESULT 14
A32516
cholecystokinin-5 - dog
N:Alternate names: CCK-5
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C:Accession: A32516
R:Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A:Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestines
A:Reference number: A32516; MUID:87153871
A:Accession: A32516
A:Molecule type: protein
A:Residues: 1-5 <SH1>
C:Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide
F:5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 2 W 2

RESULT 15
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Tyr-NH-2, a novel neuropeptide from sea anemones.
A:Reference number: A60803; MUID:88222764
A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GRA>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 5 W 5

RESULT 16
JH0253
gut pentapeptide - Japanese eel
C:Species: Anguilla japonica (Japanese eel)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C:Accession: JH0253
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A:Reference number: JH0253; MUID:92062113
A:Accession: JH0253
A:Molecule type: protein
A:Residues: 1-5 <DES>
A:Experimental source: gut
C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric

, and of the circular muscle of the gastro-intestinal junction.

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 3 W 3

RESULT 17
G37196
bradykinin-potentiating peptide 7 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196
R:Cintura, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptide
A:Reference number: A37196; MUID:90351557
A:Accession: G37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <GIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 3 W 3

RESULT 18
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yanada, M.; Wassefman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0281
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 4 W 4

RESULT 19
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yanada, M.; Wassefman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A:Title: preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108357
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 2 W 2

RESULT 20

PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0640; PT0685; PT0729
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0640
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-5 <FEF>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0640
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-5 <FE3>
A:Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 5 W 5

RESULT 21
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0580
A:Status: translation not shown

A:Molecule type: mRNA
A:Residues: 1-5 <FEF>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 5 W 5

RESULT 22
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fra
S66195
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltnes, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases
nzyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HJE>
C:superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 31.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 4 W 4

RESULT 22

S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fra
S66195
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjeltnes, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases
nzyme.
A:Reference number: S66191; MUID:95331382
A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HJE>
C:superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 5 W 5

RESULT 23
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990

A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from
A:Reference number: A34835; MUID:90160310
A:Accession: B34835
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <YEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C:Keywords: DNA binding

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 6 W 6

RESULT 24
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodi
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 6 W 6

RESULT 24
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodi
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
|
Db 6 W 6

RESULT 24
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodi
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate syntha
A:Reference number: A94217; MUID:89057886

Query Match 31.4%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:52:04 ; Search time 29.66 Seconds

(without alignments)
9.889 Million cell updates/sec

Title: 09-185908-1h

Perfect score: 35

Sequence: 1 wrxxafxg 8

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	7	1	WMAL_ACHFU
2	13	37.1	7	1	WMAL_ACHFU
3	13	37.1	7	1	WMAL_ACHFU
4	12	34.3	7	1	WMAL_ACHFU
5	11	31.4	5	1	BPB7_BOTIN
6	11	31.4	5	1	TPIS_CANFA
7	11	31.4	5	1	UF01_MOUSE
8	11	31.4	6	1	LOK1_LOCM1
9	11	31.4	8	1	ACT_THOAL
10	11	31.4	8	1	AKH_GRYBI
11	11	31.4	8	1	AKH_LIBAU
12	11	31.4	8	1	AKH_MEML
13	11	31.4	8	1	AKH_TABAT
14	11	31.4	8	1	CCKN_MACEU
15	11	31.4	8	1	HTF1_PERAM
16	11	31.4	8	1	HTF2_PERAM
17	11	31.4	8	1	HTF_TENMO
18	11	31.4	8	1	LCK1_LEUMA
19	11	31.4	8	1	LCK2_LEUMA
20	11	31.4	8	1	LCK3_LEUMA
21	11	31.4	8	1	LCK4_LEUMA
22	11	31.4	8	1	LCK5_LEUMA
23	11	31.4	8	1	LCK6_LEUMA
24	11	31.4	8	1	LCK7_LEUMA
25	11	31.4	8	1	LCK8_LEUMA
26	11	31.4	8	1	PLP_BRANA
27	11	31.4	8	1	RPH_PANBO
28	11	28.6	7	1	AL12_CARMA
29	10	28.6	7	1	AL13_CARMA
30	10	28.6	7	1	AL14_CARMA
31	10	28.6	7	1	AL15_CARMA
32	10	28.6	8	1	AL17_CARMA
33	10	28.6	8	1	AL17_CARMA

ALIGNMENTS

RESULT	1	STANDARD	PRT	7 AA.
WMAL_ACHFU				
AC	P35919;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1994 (Rel. 30, Last annotation update)			
DE	WMAMIDE-1.			
OS	Achatina fulica (Giant African snail).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;			
OC	Achatinacea; Achatinidae; Achatina.			
OX	NCBI_TaxID=6530;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=ganglion;			
RA	MEDLINE=93265912; PubMed=8495720;			
RM	Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;			
RT	"Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from			
RT	ganglia of the African giant snail, Achatina fulica.";			
RL	FEBS Lett. 323:104-108(1993)			
CC	-1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS			
CC	CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.			
DR	PIR: S33245; S33245.			
KW	Neuropeptide; Amidation.			
FT	MOD. RES			
FT	SEQUENCE 7 AA: 993 MW: 7362DSB69B041310 CRC64:			
QY	1 wr 2	45.7%; Score 16; DB 1; Length 7;		
QY	11	Best local similarity 100.0%; Pred. No. 1e+05;		
Db	1 wr 2	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT	2			
WMAL_ACHFU				
ID	WMAL_ACHFU	STANDARD;	PRT;	7 AA.
AC	P35920;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1994 (Rel. 30, Last annotation update)			
DE	WMAMIDE-2.			
OS	Achatina fulica (Giant African snail).			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;			
OC	Achatinacea; Achatinidae; Achatina.			
OX	NCBI_TaxID=6530;			
RN	[1]			
RP	SEQUENCE.			

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RC TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mwamide-1, -2 and -3, novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108(1993).
RW Neuropetptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. NO. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
1:
Db 1 WK 2

RESULT 3
MMW3_ACHFU STANDARD; PRT; 7 AA.
ID MMW3_ACHFU
AC P35921.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE MMWAMIDE-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Mwamide-1, -2 and -3, novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica."
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
DR PIR: S33244; S33244.
KW Neuropetptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. NO. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
1:
Db 1 WK 2

RESULT 4
MNP1_LEPDE STANDARD; PRT; 7 AA.
ID MNP1_LEPDE
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiforma; Phytophaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;

```

```

RA Splitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:365-374(1995).
CC -I- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropetptide; Amidation.
FT MOD.RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. NO. 1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 afxg 8
1:
Db 1 AYNQ 4

RESULT 5
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Quelimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -I- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD.RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
1:
Db 3 W 3

RESULT 6
TPIS_CANFA STANDARD; PRT; 5 AA.
ID TPIS_CANFA
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN TP11.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE: Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE -- DIHYDROXY-
CC ACETONE PHOSPHATE.
CC -I- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro: IPR000652; Trioseph_1somrse.
DR PROSITE: PS00171; TIM; PARTIAL.
RW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT SEQUENCE 5 AA: 550 MW: 64444862C9A00000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 fxg 8
|
Db 1 FVG 3

RESULT 7
ID UP01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT NON_TER 5 5
FT SEQUENCE 5 AA: 717 MW: 7364087043100000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 1 w 1

RESULT 8
LOK1_LOCM1 STANDARD; PRT; 6 AA.
ID LOK1_LOCM1

AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LOCUSTAKININ I.
OS Locusta migratoria (Migratory Locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
"Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis."
RL Regul. Pept. 37:49-57(1992).
CC -I- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
CC OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
CC TUBULES.
DR PIR: A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6
FT SEQUENCE 6 AA: 654 MW: 686365A5B9CDB000 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 5 w 5

RESULT 9
ID ACI_THUAI STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE ANGIOENSIN-CONVERTING ENZYME INHIBITOR.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciliiformes; Scombroidei;
OX Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
"Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle."
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
FT SEQUENCE 8 AA: 953 MW: 6AA863733051F1B7 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 6 w 6

RESULT 10

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AKHG_GRYBI          STANDARD;          PRT;          8 AA.
ID AKHG_GRYBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE G (AKH-G) (NO 11).
CC Gryllus bimaculatus (Two-spotted cricket), and
OC Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
OC Gryllinae; Gryllus.
CX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RX SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
RN [3]
RP SEQUENCE.
RX SPECIES=THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
RX CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
RX DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
RX MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRH / RPCH FAMILY.
CC PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
RX PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 8 w 8

RESULT 11
AKH_LIBAU          STANDARD;          PRT;          8 AA.
ID AKH_LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
CC Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
CX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";

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RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRH / RPCH FAMILY.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
RX PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match          31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
   1
Db 8 w 8

RESULT 12
AKH_MELML          STANDARD;          PRT;          8 AA.
ID AKH_MELML
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
CC Melolontha melonchus (Cockchafer),
CC Geotrupes stercorosus (Dor beetle), and
CC Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RX SPECIES=M.melonchus, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RX SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;
RA Gaede G., Iopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-seyler 373:133-142(1992).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRH / RPCH FAMILY.
DR PIR: S15422; S15422.
DR PIR: S21653; S21653.
DR InterPro: IPR002047; AKH.
RX PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

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Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

RESULT 13
AKH_TABAT
ID AKH_TABAT STANDARD: PRT: 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH) (DIPTERAN CORPORA CARDIACA FACTOR 1)
DE (DCC 1).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
OC Tabanidae; Tabanus.
OX NCBI_TaxID=7207;

RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Ralna A.K., Riley C.T., Fraser B.A., Nechman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RA "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGESTERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGESTERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HHTH / RPCH FAMILY.
DR PIR: A33995; A33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Neuropeptide; Amidation; Flight.
KW MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

RESULT 14
CCKN_MACEU
ID CCKN_MACEU STANDARD: PRT: 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLECYSTOKININ (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;

RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
IN THE BRAIN IS NOT CLEAR.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
CC PIR: A43001; A43001.
DR PIR: P00012; P00012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN: 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 15
HTFL_PERAM
ID HTFL_PERAM STANDARD: PRT: 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HYPERTREHALOSAEMIC FACTOR I (NEUROPEPTIDE M-I) (PERIPLANETIN CC-1)
DE (PEA-CAH-I) (LED-CC-I) (HYPERTREHALOSAEMIC NEUROPEPTIDE I).
DE Periplaneta americana (American cockroach).
OS Lepidoptera decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffner M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L., Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RT Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller G.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.

RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RA MEDLINE=90253659; PubMed=2340112;
 RX Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A05169; A05169.
 DR PIR: S08995; S08995.
 DR PIR: A49823; A49823.
 DR PIR: A44960; A44960.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 8
 FT MOD_RES 1 8
 SO SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 Db 8 w 8

RESULT 16
 HTF2_PERAM STANDARD; PRT; 8 AA.
 ID HTF2_PERAM
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR II (NEUROPEPTIDE M-II) (PERIPLANETIN CC-2)
 DE (PERA-CAH-II) (LEB-CC-II) (HYPERTREHALOSAEMIC NEUROPEPTIDE II).
 OS Periplaneta americana (American cockroach),
 Lepidoptera decemlineata (Colorado potato beetle), and
 Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.V., Schaffer W.H., O'Shea M., Cook J.C., Hemling M.E.,
 Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P. americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 cardiotaceleratory and hyperglycemic activity from the corpora
 cardiaca of *Periplaneta americana*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;

RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.

RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RA MEDLINE=90253659; PubMed=2340112;
 RX Gaede G., Rinehart K.L., Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 SO SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 w 1
 Db 8 w 8

RESULT 17
 HTF2_TENMO STANDARD; PRT; 8 AA.
 ID HTF2_TENMO
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOSAEMIC FACTOR (HOTN) (HYPERTREHALOSAEMIC NEUROPEPTIDE).
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tenebrio.
 NCBI_TaxID=7067, 7075;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990).
 CC -I- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 SO SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
DB 8 w 8

RESULT 18
LCK1_LEUMA
ID LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ I (L-I).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RT Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
DB 7 w 7

RESULT 19
LCK2_LEUMA
ID LCK2_LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ II (L-II).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RT Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
DB 7 w 7

RESULT 20
LCK3_LEUMA
ID LCK3_LEUMA STANDARD; PRT; 8 AA.
AC P21142;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ III (L-III).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RT Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -I- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -I- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
DB 7 w 7

RESULT 21
LCK4_LEUMA
ID LCK4_LEUMA STANDARD; PRT; 8 AA.
AC P21143;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEUCOKININ IV (L-IV).
OS Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RT Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).

```
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
FT MOD.RES 8 AA; 906 MW; DC6365B1E9D5BD4 CRC64;
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 22
LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ V (L-V).
OS Leucophaea maderae (Madeira cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blaberoidea; Blaberidae; Leucophaea.
OX NCB|TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
CC PIR; JS0315; JS0315.
DR Neuropeptide; Amidation.
KW MOD.RES 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
FT MOD.RES 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 23
LCK6_LEUMA STANDARD; PRT; 8 AA.
ID LCK6_LEUMA
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE LEUCOKININ VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blaberoidea; Blaberidae; Leucophaea.
OX NCB|TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
```

```
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation.
FT MOD.RES 1 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 24
LCK7_LEUMA STANDARD; PRT; 8 AA.
ID LCK7_LEUMA
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blaberoidea; Blaberidae; Leucophaea.
OX NCB|TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
CC PIR; JS0317; JS0317.
DR Neuropeptide; Amidation.
KW MOD.RES 8 AA; 866 MW; DC6365A5B9C865A6 CRC64;
FT MOD.RES 8 AA; 866 MW; DC6365A5B9C865A6 CRC64;
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9C865A6 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 7 W 7

RESULT 25
LCK8_LEUMA STANDARD; PRT; 8 AA.
ID LCK8_LEUMA
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LEUCOKININ VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
```

OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN (1)
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTOPEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DC PIR: JS0318; JS0318.
DR Neuropeptide; Amidation.
KW MOD.RES 8
FT SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
SQ

Query Match 31.4%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
|
Db 7 w 7

Search completed: January 14, 2002, 07:52:04
Job time: 679 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:53:46 ; Search time 80.15 Seconds
(without alignments)
14,600 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 35
Sequence: 1 wrxxafxy 8

Scoring table: BIOSUM62
Gapox 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 50 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vortebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	51.4	8	2	009258	009258 synechococ
2	16	45.7	8	11	062721	062721 rattus norv
3	13	37.1	7	8	095945	095945 saccharomyc
4	13	37.1	8	6	P82929	P82929 bos taurus
5	12	34.3	8	11	P70243	P70243 mus musculu
6	12	34.3	8	11	Q90VD3	Q90VD3 rattus sp.
7	11	31.4	6	13	P82096	P82096 litorea rub
8	11	31.4	7	10	049223	049223 glycine max
9	11	31.4	7	13	P82065	P82065 litorea rub
10	11	31.4	8	2	085406	085406 coxiella bu
11	11	31.4	8	4	Q15888	Q15888 homo sapien
12	11	31.4	8	4	Q15890	Q15890 homo sapien
13	11	31.4	8	5	Q9VRD2	Q9VRD2 drosophila
14	11	31.4	8	5	P82685	P82685 periplaneta
15	11	31.4	8	5	P82686	P82686 periplaneta
16	11	31.4	8	5	P82687	P82687 periplaneta
17	11	31.4	8	5	P82688	P82688 periplaneta
18	11	31.4	8	5	P82689	P82689 periplaneta
19	11	31.4	8	6	002831	002831 cryctolagus

20	11	31.4	8	6	Q9TRY3	Q9TRY3 sus sp. ins
21	11	31.4	8	8	Q9TD02	Q9TD02 terranatos
22	11	31.4	8	8	Q9T4Y2	Q9T4Y2 asterina pe
23	11	31.4	8	11	Q35835	Q35835 rattus norv
24	11	31.4	8	11	P82598	P82598 rattus norv
25	11	31.4	8	11	Q9ETI8	Q9ETI8 mus spretus
26	11	31.4	8	11	Q9ETI7	Q9ETI7 mus caroli
27	11	31.4	8	11	Q9ETI6	Q9ETI6 mesocricetu
28	11	31.4	8	11	Q9WMN0	Q9WMN0 mus musculu
29	11	31.4	8	13	P79940	P79940 xenopus lae
30	11	31.4	8	13	Q98T05	Q98T05 xenopus lae
31	10	28.6	7	4	Q15903	Q15903 homo sapien
32	10	28.6	8	11	Q9JLD7	Q9JLD7 mesocricetu
33	10	28.6	8	12	Q98YK9	Q98YK9 human immun
34	8	22.9	8	5	Q9TWH6	Q9TWH6 periteneis
35	7	20.0	7	2	007354	007354 synechococc
36	7	20.0	8	2	052062	052062 bacillus me
37	7	20.0	8	2	056759	056759 xanthobacte
38	7	20.0	8	2	Q9S443	Q9S443 pseudomonas
39	7	20.0	8	2	Q9R9C2	Q9R9C2 borrelia bu
40	7	20.0	8	3	P87225	P87225 saccharomyc
41	7	20.0	8	4	Q9HCQ0	Q9HCQ0 homo sapien
42	7	20.0	8	7	Q95213	Q95213 oryctolagus
43	7	20.0	8	8	Q9GDA7	Q9GDA7 hydriastele
44	7	20.0	8	8	Q9GDP0	Q9GDP0 masoia mad
45	7	20.0	8	8	Q9GCZ4	Q9GCZ4 nenga pumil
46	7	20.0	8	10	Q9S8Z4	Q9S8Z4 spinacia ol
47	7	20.0	8	10	P82324	P82324 pisum sativ
48	7	20.0	8	11	Q99MH2	Q99MH2 mus musculu
49	7	20.0	8	12	Q83977	Q83977 influenza a
50	6	17.1	5	13	P82070	P82070 litorea rub

ALIGNMENTS

RESULT 1
ID 009258 PRELIMINARY: PRT: 8 AA.
AC 009258;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NTFH (FRAGMENT).
GN NTFH.
OS Synechococcus sp. (Strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_Taxid=41431.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RF-1;
RA Chen H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF001780; AAC33369.1; -.
FT NON TER
SQ SEQUENCE 8 AA: 985 MW: F16B59CDD046C406 CRC64;
--

Query Match 51.4%; Score 18; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.7e+05;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 rxxafxy 8
| | | |
Db 2 RQIAFYG 8

RESULT 2
ID 062721 PRELIMINARY: PRT: 8 AA.
AC 062721;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PROHIBITIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FISHER;
 RX MEDLINE=955331633; PubMed=7607556;
 RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
 RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
 RA McClung J.K.;
 RT "Regions of evolutionary conservation between the rat and human
 RT prohibitin-encoding genes.";
 RL Gene 158:291-294(1995).
 DR EMBL, 017178; AAA86692.1; -.
 FT NON_TER
 SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 45.7%; Score 16; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 11
 DB 2 WR 3

RESULT 3
 ID 095945 PRELIMINARY; PRT; 7 AA.
 AC 095945:
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INSIDE INTRON 5 (FRAGMENT).
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Mitochondrion.
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonlitz S.G., Coruzzi G., Thalerfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system. Structure and
 RT nucleotide sequence of the gene coding for subunit 1 of yeast
 RT cytochrome oxidase.";
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL, V00694; CAA24066.1; -.
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 37.1%; Score 13; DB 8; Length 7;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 1:
 DB 4 WK 5

RESULT 4
 ID P82929 PRELIMINARY; PRT; 8 AA.
 AC P82929:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LIVER;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremull L.L.;
 RT "Small subunit of the mammalian mitochondrial ribosome. Identification
 RT of the full complement ribosomal proteins present.";
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.
 CC -i- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 37.1%; Score 13; DB 6; Length 8;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 11
 DB 2 WGITLF 7

RESULT 5
 ID P70243 PRELIMINARY; PRT; 8 AA.
 AC P70243:
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE SKELETAL MUSCLE-SPECIFIC CALCIUM CHANNEL (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Ophoff R.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL, X98325; CAA66969.1; -.
 KW Calcium channel.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
 1:
 DB 7 WQ 8

RESULT 6
 ID Q9QVD3 PRELIMINARY; PRT; 8 AA.
 AC Q9QVD3:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
 OS Rattus sp.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCB TaxID=10118;
RN (1)
RX MEDLINE=92202192; PubMed=1313009;
RA Kanamatsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative Inositol 1,4,5-trisphosphate binding proteins in rat brain
cytosol."
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 8 AA; 1047 MW; D72415B806C37041 CRC64;

Query Match 34.3%; Score 12; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 2
DB 3 W 4

RESULT 7
P82096 PRELIMINARY; PRT: 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ELECTRIN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
OX NCB TaxID=104895;
RN (1)
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 5 W 5

RESULT 8
O49223 PRELIMINARY; PRT: 7 AA.
AC O49223;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
DE Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCB TaxID=3847;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN CV. ESSEX; TISSUE=ROOTS;
RX MEDLINE=91367679; PubMed=1891369;
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RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins."
RL Nucleic Acids Res. 19:4769-4769(1991).
RN (12)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOTS;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF047050; AAC03556.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 31.4%; Score 11; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 2 W 2

RESULT 9
P82065 PRELIMINARY; PRT: 7 AA.
AC P82065;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TRITOPHYLLIN 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyllidae;
OC Litoria.
OX NCB TaxID=104895;
RN (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: MAY ACT AS A NEUROMODULATOR OR NEUROTRANSMITTER.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KW Amphibian skin; Amidation; Neuropeptide.
FT MOD_RES 1
FT MOD_RES 1 PYROGLUTAMINE CARBOXYLIC ACID.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 31.4%; Score 11; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 4 W 4

RESULT 10
O85406 PRELIMINARY; PRT: 8 AA.
AC O85406;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
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OC Coxiella group; CoxIELla.
OX NCB1_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NINE MILE PHASE I;
RL Williams H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
   CoxIELla burnetii."
RT CoxIELla burnetii.
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF064963; AAD09947.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Query Match          31.4%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 4 w 4

RESULT 11
ID Q15888 PRELIMINARY; PRT; 8 AA.
AC Q15888;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
RL EMBL, L32069; AAA73878.1; -.
DR EMBL, L32069; AAA73878.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match          31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 6 w 6

RESULT 12
ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
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RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
RL EMBL, L32083; AAA73880.1; -.
DR EMBL, L32083; AAA73880.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 975 MW; 605EAC5BEA5A2D3 CRC64;

Query Match          31.4%; Score 11; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 w 1
DB 1 w 1

RESULT 13
ID Q9VRD2 PRELIMINARY; PRT; 8 AA.
AC Q9VRD2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE CG11666 PROTEIN.
GN CG11666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCB1_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Abpayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Split E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
DR EMBL: AB003569; AAF50870.1; -.
DR FlyBase: FBgn0040648; CG11666.
SQ SEQUENCE: 8 AA; 1062 MW; ED1B5B044004376 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 2 w 2

RESULT 14
P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
[1]
RN PERIPLANETA AMERICANA (American cockroach).
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA.
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RT Regul. Pept. 71:199-205(1997).
RL -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 32635B449D5A774 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 15
P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
[1]
RN PERIPLANETA AMERICANA (American cockroach).
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA.
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana."
RL Science 287:2185-2195(2000).
DR EMBL: AB003569; AAF50870.1; -.
DR FlyBase: FBgn0040648; CG11666.
SQ SEQUENCE: 8 AA; 1062 MW; ED1B5B044004376 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 16
P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
[1]
RN PERIPLANETA AMERICANA (American cockroach).
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA.
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";
RT Regul. Pept. 71:199-205(1997).
RL -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365A5B9D5BDDA CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 17
P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
NCBI_TaxID=6978;

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RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinsins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 18
P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE KININ-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinsins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.
CC KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 865 MW; C76365B449CDC775 CRC64;

Query Match 31.4%; Score 11; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 7 w 7

RESULT 19
O02831 PRELIMINARY; PRT; 8 AA.
AC O02831;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).

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```

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metarantha M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
FT SEQUENCE 1
FT SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 2 w 2

RESULT 20
O9TRV3 PRELIMINARY; PRT; 8 AA.
AC O9TRV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGF-B-6.
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
DE SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 31.4%; Score 11; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
Db 5 w 5

RESULT 21
O9TD02 PRELIMINARY; PRT; 8 AA.
AC O9TD02;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Terranatos dolichopterus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxID=61836;
RN [1]

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```
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RL (Alburninomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL: AF092421; AAF03041.1; -.
KW Mitochondrion.
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DD44056 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 8; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 22
O9T4Y2 PRELIMINARY; PRT; 8 AA.
ID O9T4Y2;
AC O9T4Y2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE COL GENE PRODUCT (FRAGMENT).
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:89354669; PubMed:2766382;
RA Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL Curr. Ganc. 15:193-206(1989).
DR EMBL: X16886; CAA34767.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1114 MW; F0C9D36415B736D6 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 8; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 6 w 6

RESULT 23
O35835 PRELIMINARY; PRT; 8 AA.
ID O35835;
AC O35835;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORF1 PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE:98008057; PubMed:9581555;
RA Hospital V., Prat A., Jonile C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
```

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RT NRD convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL: X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EALB1ADC5A5B6 CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 11; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 8 w 8

RESULT 24
P82598 PRELIMINARY; PRT; 8 AA.
ID P82598;
AC P82598;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE 3KRDA NON-ARGINASE GROWTH INHIBITORY FACTOR (NAGIF)(FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=20198203; PubMed=10731662;
RA Kim K.-Y., Choi I., Kim S.-S.;
RT "Purification and characterization of a novel inhibitor of the
RT proliferation of hepatic stellate cells.";
RL J. Biochem. 127:23-27(2000).
CC -1- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
CC ENDOMETRIAL CELLS AND 3T6 FIBROBLASTS.
CC -1- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
CC PROTEIN.
FT NON_TER 8
SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match
Best Local Similarity 31.4%; Score 11; DB 11; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 w 1
DB 7 w 7

RESULT 25
Q9ET18 PRELIMINARY; PRT; 8 AA.
ID Q9ET18;
AC Q9ET18;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEUROPEPTIDE Y (FRAGMENT).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Taylor B.A., Wnek C., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RT (New Zealand obese) and the SM (small) mouse strains.";
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF286200; AAG01474.1; -.
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FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1033 MW; 297685A76AAB1734 CRC64;

Query Match 31.48; Score 11; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 W 1
DB 8 W 8

Search completed: January 14, 2002, 07:53:46
Job time: 726 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:43:17 ; Search time 80.55 Seconds
(without alignments)
7.357 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 35
Sequence: 1 wrxxafxx 8

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 50 summaries

Database :
1: A_Geneseq.1101:*
2: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT:*
4: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT:*
5: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT:*
6: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT:*
7: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT:*
8: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT:*
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21: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT:*
22: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT:*
23: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	85.7	8	21	AAB06583	Claudin-3 cell adh
2	30	85.7	8	21	AAB06636	Claudin-3 cyclic c
3	30	85.7	8	21	AAB06645	Claudin-4 cell adh
4	30	85.7	8	21	AAB06658	Claudin-4 cyclic c
5	27	77.1	8	21	AAB06764	Claudin-6/9 cell a
6	27	77.1	8	21	AAB06814	Claudin-6/9 cyclic
7	27	77.1	8	21	AAB06916	Claudin cell adhes
8	25	71.4	6	21	AAB06581	Claudin-3 cell adh
9	25	71.4	6	21	AAB06634	Claudin-3 cyclic c
10	25	71.4	6	21	AAB06643	Claudin-4 cell adh
11	25	71.4	6	21	AAB06656	Claudin-4 cyclic c

12	25	71.4	7	21	AAB06582	Claudin-3 cell adh
13	25	71.4	7	21	AAB06635	Claudin-3 cyclic c
14	25	71.4	7	21	AAB06644	Claudin-4 cell adh
15	25	71.4	7	21	AAB06697	Claudin-4 cyclic c
16	25	71.4	8	21	AAB06521	Claudin-2 cell adh
17	25	71.4	8	21	AAB06574	Claudin-2 cyclic c
18	25	71.4	8	21	AAB06590	Claudin-3 cyclic c
19	25	71.4	8	21	AAB06599	Claudin-3 cyclic c
20	25	71.4	8	21	AAB06608	Claudin-3 cyclic c
21	25	71.4	8	21	AAB06617	Claudin-3 cyclic c
22	25	71.4	8	21	AAB06626	Claudin-3 cyclic c
23	25	71.4	8	21	AAB06652	Claudin-4 cyclic c
24	25	71.4	8	21	AAB06661	Claudin-4 cyclic c
25	25	71.4	8	21	AAB06670	Claudin-4 cyclic c
26	25	71.4	8	21	AAB06679	Claudin-4 cyclic c
27	25	71.4	8	21	AAB06688	Claudin-4 cyclic c
28	25	71.4	8	21	AAB06879	Claudin-8 cell adh
29	25	71.4	8	21	AAB06897	Claudin-8 cyclic c
30	25	71.4	8	21	AAB06918	Claudin-8 cell adh
31	24	68.6	8	21	AAB06426	Claudin-1 cell adh
32	24	68.6	8	21	AAB06512	Claudin-1 cyclic c
33	22	62.9	6	21	AAB06762	Claudin-6/9 cell a
34	22	62.9	6	21	AAB06812	Claudin-6/9 cyclic
35	22	62.9	7	21	AAB06763	Claudin-6/9 cell a
36	22	62.9	7	21	AAB06813	Claudin-6/9 cyclic
37	22	62.9	8	21	AAB06770	Claudin-6/9 cyclic
38	22	62.9	8	21	AAB06779	Claudin-6/9 cyclic
39	22	62.9	8	21	AAB06787	Claudin-6/9 cyclic
40	22	62.9	8	21	AAB06796	Claudin-6/9 cyclic
41	22	62.9	8	21	AAB06804	Claudin-6/9 cyclic
42	21	60.0	6	21	AAB06704	Claudin-5 cell adh
43	21	60.0	6	21	AAB06754	Claudin-5 cyclic c
44	21	60.0	7	21	AAB06705	Claudin-5 cell adh
45	21	60.0	7	21	AAB06755	Claudin-5 cyclic c
46	21	60.0	8	21	AAB06419	Claudin-1 cell adh
47	21	60.0	8	21	AAB06479	Claudin-1 cyclic c
48	21	60.0	8	21	AAB06706	Claudin-5 cell adh
49	21	60.0	8	21	AAB06712	Claudin-5 cyclic c
50	21	60.0	8	21	AAB06721	Claudin-5 cyclic c

ALIGNMENTS

RESULT 1
ID AAB06583 standard; peptide: 8 AA.
XX
AC AAB06583;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 58.
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW Car sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 52; Page 99; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 wrxxafxg 8
DB 1 wrvsafig 8

RESULT 2
AAB06636
ID AAB06636 standard; peptide; 8 AA.
XX
AC AAB06636;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 269.
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 wrxxafxg 8
DB 1 wrvsafig 8

RESULT 3
AAB06645
ID AAB06645 standard; peptide; 8 AA.
XX
AC AAB06645;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 50.
XX
XX Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 58; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 85.7%; Score 30; DB 21; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 wrxxafxg 8
DB 1 wrvtafig 8

xx	RESULT	4	!
xx	AAB0698	standard; peptide: 8 AA.	
xx	AAB0698		
xx	28-SEP-2000	(first entry)	
xx			
xx	Claudin-4	cyclic cell adhesion recognition sequence SEQ ID NO: 216.	
xx	Claudin-4	modulating agent; cell adhesion recognition sequence;	
xx	CAR sequence; autoimmune disease; inflammatory disease; cancer;		
xx	graft rejection; cyclic.		
xx	Mammalia.		
xx	MO200026360-A1.		
xx	11-MAY-2000.		
xx	03-NOV-1999;	99WO-CA01029.	
xx	03-NOV-1998;	98US-0185908.	
xx	30-MAR-1999;	99US-0282029.	
xx	(ADHE-) ADHEREX TECHNOLOGIES INC.		
xx	Bluschuck OW, Symonds JM, Gour BJ;		
xx	WPI: 2000-365610/31.		
xx	Antibody modulation of claudin-mediated cell adhesion for increasing		
xx	vasopermeability, for delivering drugs to tumors and the nervous system		
xx	and across the skin -		
xx	Claim 101; Page 101; 121pp; English.		
xx	The present invention relates to the use of peptides as claudin-mediated		
xx	cell adhesion modulators. The claudin-4 group of proteins are cadherins,		
xx	which are membrane glycoproteins involved in cell adhesion. In some		
xx	situations, cell adhesion occurs at abnormal levels, and these peptides		
xx	can be used to modulate these levels, and thus treat autoimmune diseases,		
xx	inflammatory diseases and cancer, and aid wound healing and implant		
xx	adhesion. In addition, they can also be used to facilitate drug delivery		
xx	to the desired target site. The present sequence has a cyclic		
xx	conformation.		
xx	Sequence	8 AA;	
xx			
xx	Query Match	85.7%;	Score 30; DB 21; Length 8;
xx	Best Local Similarity	62.5%;	Pred. No. 4.3e+05;
xx	Matches	5; Conservative	0; Mismatches 3; Indels 0; Gaps 0.
xx			
xx	QY	1 wrxaxfxg 8	
xx			
xx	Db	1 wrvtafig 8	
xx			
xx	RESULT	5	
xx	AAB06764		
xx	AAB06764	standard; peptide: 8 AA.	
xx	AAB06764;		
xx	28-SEP-2000	(first entry)	
xx			
xx	Claudin-6/9	cell adhesion recognition sequence SEQ ID NO: 335.	
xx	Claudin-6	modulating agent; claudin-9 modulating agent;	
xx	cell adhesion recognition sequence; CAR sequence; autoimmune disease;		
xx	inflammatory disease; cancer; graft rejection.		

OS	Mammalia.
XX	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaeschuck OW, Symonds JM, Gour BJ;
DR	WPI: 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
Pt	and across the skin -
XX	
PS	Claim 70; Page 103; 121pp; English.
XX	
CC	The present invention relates to the use of peptides as claudin-mediated
CC	cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC	are cadherins, which are membrane glycoproteins involved in cell
CC	adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC	and these peptides can be used to modulate these levels, and thus treat
CC	autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC	healing and implant adhesion. In addition, they can also be used to
CC	facilitate drug delivery to the desired target site.
XX	
SQ	Sequence 8 AA:
Query Match	77.18; Score 27; DB 21; Length 8;
Best Local Similarity	50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
OY	1 wrxxafxg 8 : DB 1 wkvtatfg 8
RESULT 6	
AAB06814	
ID AAB06814	standard; peptide: 8 AA.
XX	
AC AAB06814;	
XX	
DT 28-SEP-2000	(first entry)
XX	
Claudin-6/9	cyclic cell adhesion recognition sequence SEQ ID NO: 385.
XX	
KM	claudin-6 modulating agent; claudin-9 modulating agent;
KW	cell adhesion recognition sequence; CAR sequence; autoimmune disease;
KM	inflammatory disease; cancer; graft rejection; cyclic.
XX	
OS	Mammalia.
OS	
PN	WO200026360-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaeschuck OW, Symonds JM, Gour BJ;
XX	

DR WPI; 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 73; Page 104; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
CC are cadherins, which are membrane glycoproteins involved in cell
CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
CC and these peptides can be used to modulate these levels, and thus treat
CC autoimmune diseases, inflammatory diseases and cancer, and aid wound
CC healing and implant adhesion. In addition, they can also be used to
CC facilitate drug delivery to the desired target site. The present
CC sequence has a cyclic conformation.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxafxg 8
1: |||
Db 1 wkvtatfg 8

RESULT 7
AAB06916
ID AAB06916 standard; Protein; 8 AA.
XX
AC AAB06916;
XX
DT 05-OCT-2000 (first entry)
XX

DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 50.

KW Claudin modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Synthetic.

PH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 8
FT /note= "C-terminal amide"
XX

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 71; Page 103; 121pp; English.

CC The present sequence is a peptide which can be used in a claudin-mediated
CC cell adhesion modulator. The claudin group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and this peptide
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, it can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 27; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 wrxxafxg 8
1: |||
Db 1 wkvtatfg 8

RESULT 8
AAB06581
ID AAB06581 standard; peptide; 6 AA.
XX
AC AAB06581;
XX
DT 28-SEP-2000 (first entry)
XX

DE Claudin-3 cell adhesion recognition sequence SEQ ID NO: 56.

KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA01029.

XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX Claim 52; Page 99; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX

SQ Sequence 6 AA;

Query Match 71.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 || 11
Db 1 wrvsaf 6

RESULT 9
AAB06634
ID AAB06634 standard; peptide: 6 AA.
XX
AC AAB06634;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 267.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
XX OS
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 6 AA;

Query Match 71.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 || 11
Db 1 wrvsaf 6

RESULT 10
AAB06643
ID AAB06643 standard; peptide: 6 AA.
XX
AC AAB06643;
XX
DT 28-SEP-2000 (first entry)
XX

DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 48.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
XX OS
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 58; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
SQ Sequence 6 AA;

Query Match 71.4%; Score 25; DB 21; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 || 11
Db 1 wrvsaf 6

RESULT 11
AAB06696
ID AAB06696 standard; peptide: 6 AA.
XX
AC AAB06696;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 214.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
XX OS
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.

Query Match Similarity	71.48;	Score 25;	DB 21;	Length 6;
Best Local Similarity	66.78;	Pred. No.	4.3e+05;	
Matches	4;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;
OY	1 wrxxaf	6		
	1 wrvtaf	6		
	Db			

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
CC
CC Sequence 7 AA;
CC
CC

```

Query Match Similarity      71.4%; Score 25; DB 21; Length 7;
Best Local Similarity      66.7%; Pred. No. 4.3e+05;
Matches      4; Conservative      0; Mismatches      2; Indels      0; Gaps      0.

OY      1 wrxaf 6
        11 11
        12 12
        13 13
        14 14
        15 15
        16 16
        17 vsaf 6

Db

RESULT 13
AAB06635
ID AAB06635 standard; peptide: 7 AA.
XX
XX AAB06635;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 268.
XX
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
      graft rejection; cyclic.

```

Query Match	Best Local Similarity	71.4%; 66.7%;	Score 25; Pred No. 4.3e+05;	DB 21; Length 7;
Result 13				
AAB06635				
ID	AAB06635 standard; peptide; 7 AA.			
XX				
AC	AAB06635;			
XX				
DT	28-SEP-2000 (first entry)			
XX				
DE	Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 268.			
KW	Claudin-3 modulating agent; cell adhesion recognition sequence;			
KW	CAR sequence; autoimmune disease; inflammatory disease; cancer;			
KW	graft rejection; cyclic.			
XX				
OS	Mammalia.			
XX				
PN	WO200026360-A1.			
XX				
PD	11-MAY-2000.			
XX				
PF	03-NOV-1999; 99WO-CA01029.			
XX				
PR	03-NOV-1998; 98US-0185908.			
PR	30-MAR-1999; 99US-0282029.			
XX				
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.			
XX				
PI	Blaschuck OW, Symonds JM, Gour BJ;			
DR	WPI; 2000-365610/31.			
XX				
PT	Antibody modulation of claudin-mediated cell adhesion for increasing			
PT	vasopermeability, for delivering drugs to tumors and the nervous system			
PT	and across the skin -			
XX				
PS	Claim 55; Page 100; 121pp; English.			
XX				
CC	The present invention relates to the use of peptides as claudin-mediated			
CC	cell adhesion modulators. The claudin-3 group of proteins are cadherins,			
CC	which are membrane glycoproteins involved in cell adhesion. In some			
CC	situations, cell adhesion occurs at abnormal levels, and these peptides			
CC	can be used to modulate these levels, and thus treat autoimmune diseases			
CC	inflammatory diseases and cancer, and aid wound healing and implant			
CC	adhesion. In addition, they can also be used to facilitate drug delivery			
CC	to the desired target site. The present sequence has a cyclic			
CC	conformation.			
XX				
XX				
SO	Sequence 7 AA;			

Matches : 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
|| ||
Db 1 wrvsaf 6

RESULT 14
AAB06644
ID AAB06644 standard; peptide; 7 AA.
XX
AC AAB06644;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cell adhesion recognition sequence SEQ ID NO: 49.
XX

KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.

XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.

XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX
PS Claim 58; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.

XX
SQ Sequence 7 AA;

Query Match 71.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
|| ||
Db 1 wrvsaf 6

RESULT 15
AAB06697
ID AAB06697 standard; peptide; 7 AA.
XX
AC AAB06697;
XX
DT 28-SEP-2000 (first entry)
XX

DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 215.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

XX Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.

XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.

XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.

XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

XX
SQ Sequence 7 AA;
XX
Query Match 71.4%; Score 25; DB 21; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
|| ||
Db 1 wrvsaf 6

RESULT 16
AAB06521
ID AAB06521 standard; peptide; 8 AA.
XX
AC AAB06521;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cell adhesion recognition sequence SEQ ID NO: 42.

XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.

XX Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.

XX
PF 03-NOV-1999; 99WO-CA01029.
XX

PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 46; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;
XX
OY 1 wrxxafxg 8
| | : : |
Db 1 wrtssyvg 8
XX
RESULT 17
AAB06574
ID AAB06574 standard; peptide; 8 AA.
XX
AC AAB06574;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 163.
XX
KW Claudin-2 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 49; Page 98; 121pp; English.
XX

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-2 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;
XX

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 37.5%; Pred. No. 4.3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxafxg 8
| | : : |
Db 1 wrtssyvg 8

RESULT 18
AAB06590
ID AAB06590 standard; peptide; 8 AA.
XX
AC AAB06590;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 223.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 99; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;
XX

Query Match 71.4%; Score 25; DB 21; Length 8;

Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvsaf 7

RESULT 19
AAB06599
ID AAB06599 standard; peptide: 8 AA.

AC AAB06599;

DT 28-SEP-2000 (first entry)

DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 232.

KW Claudin-3 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 55; Page 99; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SQ Sequence 8 AA;

Query Match Best Local Similarity 71.4%; Score 25; DB 21; Length 8;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvsaf 7

RESULT 20

AAB06608
ID AAB06608 standard; peptide: 8 AA.

AC AAB06608;

XX

DT 28-SEP-2000 (first entry)

DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 241.

KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

PS Claim 55; Page 99; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SQ Sequence 8 AA;

Query Match Best Local Similarity 71.4%; Score 25; DB 21; Length 8;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvsaf 7

RESULT 21

AAB06617
ID AAB06617 standard; peptide: 8 AA.

AC AAB06617;

DT 28-SEP-2000 (first entry)

DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 250.

KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

XX

PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 55; Page 100; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 wrxxaf 6
|||
Db 2 wrvsaf 7

RESULT 22
AAB06626
ID AAB06626 standard; peptide; 8 AA.
XX
AC AAB06626;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 259.
XX
KW Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
XX WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -

XX
XX Claim 55; Page 100; 121pp; English.
PS
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 wrxxaf 6
|||
Db 2 wrvsaf 7

RESULT 23
AAB06652
ID AAB06652 standard; peptide; 8 AA.
XX
AC AAB06652;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 170.
XX
KW Claudin-4 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
XX WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 61; Page 101; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-4 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvraf 7

RESULT 24

AAB06661
ID AAB06661 standard; peptide; 8 AA.

XX AC AAB06661;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 179.

XX KW Claudin-4 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.

XX OS Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OM, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

XX PS Claim 61; Page 101; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-4 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site. The present sequence has a cyclic
conformation.

CC SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvraf 7

RESULT 25

AAB06670
ID AAB06670 standard; peptide; 8 AA.

XX AC AAB06670;

XX DT 28-SEP-2000 (first entry)

XX DE Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 188.

XX KW Claudin-4 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.

XX OS Mammalia.

XX PN WO200026360-A1.

XX PD 11-MAY-2000.

XX PF 03-NOV-1999; 99WO-CA01029.

XX PR 03-NOV-1998; 98US-0185908.

XX PR 30-MAR-1999; 99US-0282029.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OM, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

XX PS Claim 61; Page 101; 121pp; English.

CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-4 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site. The present sequence has a cyclic
conformation.

CC SQ Sequence 8 AA;

Query Match 71.4%; Score 25; DB 21; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxaf 6
11 11
Db 2 wrvraf 7

Search completed: January 14, 2002, 07:43:17
Job time: 428 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 14, 2002, 07:41:37 : Search time 39.77 Seconds
(without alignments)
4.527 Million cell updates/sec

Title: 09-185908-1h
Perfect score: 35
Sequence: 1 wrxxafxg 8

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/prodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.1	5	1	US-08-190-802A-263	Sequence 263, App
2	57.1	5	4	US-08-477-346-263	Sequence 263, App
3	54.3	6	1	US-08-089-994A-12	Sequence 12, Appl
4	54.3	6	5	PCT-US94-07605-12	Sequence 12, Appl
5	54.3	8	1	US-08-633-760-3	Sequence 3, Appl
6	51.4	5	4	US-09-020-880-44	Sequence 44, Appl
7	51.4	7	4	US-09-139-802-65	Sequence 65, Appl
8	48.6	6	4	US-09-189-0608-58	Sequence 58, Appl
9	48.6	8	3	US-08-335-733D-23	Sequence 23, Appl
10	48.6	8	3	US-08-335-733D-24	Sequence 24, Appl
11	48.6	8	3	US-08-335-733D-25	Sequence 25, Appl
12	45.7	3	1	US-08-165-545-8	Sequence 8, Appl
13	45.7	3	1	US-08-305-768-27	Sequence 27, Appl
14	45.7	3	1	US-08-256-771-17	Sequence 17, Appl
15	45.7	3	1	US-08-381-084-17	Sequence 17, Appl
16	45.7	3	2	US-08-871-163-27	Sequence 27, Appl
17	45.7	3	3	US-08-767-903-27	Sequence 27, Appl
18	45.7	3	5	PCT-US95-11724-27	Sequence 27, Appl
19	45.7	4	1	US-08-165-545-7	Sequence 7, Appl
20	45.7	4	1	US-08-190-802A-265	Sequence 265, App
21	45.7	4	1	US-08-215-137-11	Sequence 11, Appl
22	45.7	4	1	US-08-256-771-16	Sequence 16, Appl
23	45.7	4	1	US-08-222-851-22	Sequence 22, Appl
24	45.7	4	1	US-08-381-084-16	Sequence 16, Appl
25	45.7	4	2	US-08-592-646A-62	Sequence 62, Appl
26	45.7	4	2	US-08-637-759B-108	Sequence 108, App
27	45.7	4	3	US-08-871-355A-108	Sequence 108, App

28	16	45.7	4	3	US-08-981-122-24	Sequence 24, Appl
29	16	45.7	4	3	US-08-981-122-28	Sequence 28, Appl
30	16	45.7	4	4	US-09-329-350-3	Sequence 3, Appl
31	16	45.7	4	4	US-08-591-632-40	Sequence 40, Appl
32	16	45.7	4	4	US-08-591-632-42	Sequence 42, Appl
33	16	45.7	4	4	US-08-477-346-265	Sequence 265, App
34	16	45.7	4	4	US-08-682-767-25	Sequence 25, App
35	16	45.7	5	1	US-07-851-941-1	Sequence 1, Appl
36	16	45.7	5	1	US-07-851-941-2	Sequence 2, Appl
37	16	45.7	5	1	US-07-851-941-3	Sequence 3, Appl
38	16	45.7	5	1	US-08-190-802A-264	Sequence 264, App
39	16	45.7	5	3	US-08-907-403A-7	Sequence 7, Appl
40	16	45.7	5	3	US-08-894-172-34	Sequence 34, Appl
41	16	45.7	5	3	US-08-981-122-12	Sequence 12, Appl
42	16	45.7	5	3	US-08-981-122-16	Sequence 16, Appl
43	16	45.7	5	3	US-08-981-122-19	Sequence 19, Appl
44	16	45.7	5	3	US-08-981-122-20	Sequence 20, Appl
45	16	45.7	5	3	US-08-981-122-26	Sequence 26, Appl
46	16	45.7	5	3	US-08-981-122-33	Sequence 33, Appl
47	16	45.7	5	3	US-08-981-122-36	Sequence 36, Appl
48	16	45.7	5	3	US-08-981-122-89	Sequence 89, Appl
49	16	45.7	5	4	US-09-020-880-39	Sequence 39, Appl
50	16	45.7	5	4	US-08-672-850-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-190-802A-263
; Sequence 263, Application US/08190802A
; Patent No. 5319003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: Wd-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 86000-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTAA peptide
; US-08-190-802A-263

Query Match 57.1%; Score 20; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
1 1 1
Db 1 WRTAA 5

RESULT 2

US-08-477-346-263
; Sequence 263, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Theorof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTAA peptide
US-08-477-346-263

Query Match 57.1%; Score 20; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
1 1 1
Db 1 WRTAA 5

RESULT 3

US-08-089-994A-12
; Sequence 12, Application US/08089994A

; Patent No. 5380668
; GENERAL INFORMATION:
; APPLICANT: Hertron, James N.
; TITLE OF INVENTION: Compounds Having the Antigenicity of
; TITLE OF INVENTION: hCG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Utah Technology
; ADDRESS: Transfer Office
; STREET: 421 Wakara Way, Suite 170
; CITY: Salt Lake City
; STATE: UT
; COUNTRY: USA
; ZIP: 84108

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 144mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,994A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 2224
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PM04UT
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-089-994A-12

Query Match 54.3%; Score 19; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
1 1 1
Db 2 WREAA 6

RESULT 4

PCT-US94-07605-12
; Sequence 12, Application PC/TUS9407605
; GENERAL INFORMATION:
; APPLICANT: Hertron, James N.
; TITLE OF INVENTION: Compounds Having the Antigenicity of
; TITLE OF INVENTION: hCG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Utah Technology
; ADDRESS: Transfer Office
; STREET: 421 Wakara Way, Suite 170
; CITY: Salt Lake City
; STATE: UT
; COUNTRY: USA
; ZIP: 84108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:

APPLCATION NUMBER: PCT/US94/07605
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/089,994
FILING DATE: 6 Jul 1993
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33,041
REFERENCE/DOCKET NUMBER: 2224
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-07605-12

Query Match 54.3% Score 19; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
| | |
Db 2 WREAL 6

RESULT 5
US-08-633-760-3
; Sequence 3, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
; APPLICANT: NIMA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: FUJIMURA, TAKAO
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: NOGUCHI, YUJI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,760
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-760-3

Query Match 54.3% Score 19; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
| | |
Db 2 WREAL 6

RESULT 6
US-09-020-880-44
; Sequence 44, Application US/09020880A
; Patent No. 6136558
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Silkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 14918-720CON1
; CURRENT APPLICATION NUMBER: US/09/020,880A
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: US 60/037,581
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 5
; TYPE: PRT
; ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-44

Query Match 51.4% Score 18; DB 4; Length 5;
Best Local Similarity 60.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 wrxxa 5
| | |
Db 1 WRLVA 5

RESULT 7
US-09-139-802-65
; Sequence 65, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-139-802-65

Query Match          51.4%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 wrxxa 5
      |||
      1 wrvla 5

RESULT 8
US-09-189-060B-58
; Sequence 58, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method of providing No. 6270968el DNA sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Prokaryotic
; NAME/KEY: UNSURE
; LOCATION: (1)...(6)
; OTHER INFORMATION: Xaa = Phe or Tyr
US-09-189-060B-58

Query Match          48.6%; Score 17; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 wrxxaf 6
      |||
      1 WRXDMF 6

RESULT 9
US-08-335-733D-23
; Sequence 23, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-335-733D-23

Query Match          48.6%; Score 17; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 wrxxaf 6
      |||
      3 WRSELY 8

RESULT 10
US-08-335-733D-24
; Sequence 24, Application US/08335733D
; Patent No. 6042831
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,733D
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLeod, Janet M
; REGISTRATION NUMBER: 35,263
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2500
; TELEFAX: 212-765-2519
; TELEX:
```

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:
 US-08-335-733D-24

Query Match 48.6%; Score 17; DB 3; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.6e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 11 :
 Db 2 WRSELY 7

RESULT 11

US-08-335-733D-25
 ; Sequence 25, Application US/08335733D
 ; Patent No. 6042831
 ; GENERAL INFORMATION:
 ; APPLICANT: Beretta, Alberto
 ; TITLE OF INVENTION: HIV PROTEIN EPITOPES
 ; NUMBER OF SEQUENCES: 90
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Bolts, L.L.P.
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10112-0228
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/335,733D
 ; FILING DATE: 10-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MacLeod, Janet M
 ; REGISTRATION NUMBER: 35,263
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-408-2500
 ; TELEFAX: 212-765-2519
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: Internal
 ; ORIGINAL SOURCE:
 ; US-08-335-733D-25

Query Match 48.6%; Score 17; DB 3; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.6e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 wrxxaf 6
 11 :
 Db 1 WRSELY 6

RESULT 12

US-08-165-545-8
 ; Sequence 8, Application US/08165545
 ; Patent No. 5424396
 ; GENERAL INFORMATION:
 ; APPLICANT: Mamoru TOMITA et al.
 ; TITLE OF INVENTION: Antimicrobial Peptide and
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Displaywrite
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/165,545
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/871,981
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-8850
 ; TELEFAX:
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; HYPOTHETICAL:
 ; ANTI-SENSE:
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM:
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:
 ; TISSUE TYPE:
 ; CELL TYPE:
 ; CELL LINE:
 ; ORGANELLE:
 ; IMMEDIATE SOURCE:
 ; LIBRARY:
 ; CLONE:
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT:
 ; MAP POSITION:
 ; UNITS:
 ; FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-8

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 13
US-08-305-768-27
Sequence 27, Application US/08305768
Patent No. 5602097
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antifungal Peptides
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,768
FILING DATE: 12-SEPT-1994
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-305-768-27

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 1 wr 2

RESULT 14
US-08-256-771-17
Sequence 17, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-256-771-17

Query Match 45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 wr 2
11
Db 2 wr 3

RESULT 15
US-08-381-984-17
Sequence 17, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note="the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a fragment thereof
US-08-381-984-17
```

```
Query Match          45.7%; Score 16; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 wr 2
   11
DB 2 wr 3
```

```
RESULT 16
US-08-871-163-27
; Sequence 27, Application US/08871163
; Patent No. 5885782
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,163
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-871-163-27
```

```
Query Match          45.7%; Score 16; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 wr 2
   11
DB 1 wr 2
```

```
RESULT 17
US-08-767-903-27
; Sequence 27, Application US/08767903
; Patent No. 6020312
```

```

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 47
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,903
; FILING DATE:
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-767-903-27
```

```
Query Match          45.7%; Score 16; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 wr 2
   11
DB 1 wr 2
```

```
RESULT 18
PCT-US95-11724-27
; Sequence 27, Application PC/TUS9511724
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antifungal Peptides
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11724
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-11724-27
```

```
Query Match          45.7%; Score 16; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 wr 2
   11
DB 1 wr 2
```

```
RESULT 19
US-08-165-545-7
; Sequence 7, Application US/08165545
; Patent No. 5424396
; GENERAL INFORMATION:
```

APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptide and
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 KB
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,545
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,981
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:

PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-165-545-7
Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 wr 2
Db 3 wr 4
RESULT 20
US-08-190-802A-265
; Sequence 265, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fadian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: WRTA peptide
; US-08-190-802A-265
Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 wr 2
Db 1 wr 2
RESULT 21
US-08-215-137-11
; Sequence 11, Application US/08215137


```
; Patent No. 5614370
; GENERAL INFORMATION:
; APPLICANT: Konealis, Zenon
; APPLICANT: Siciliano, Salvatore J
; APPLICANT: Springer, Martin S
; TITLE OF INVENTION: ASSAY TO IDENTIFY HUMAN C5A ANTAGONISTS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Ave., P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,137
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: 19108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3901
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= TIC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /label= dCha
; OTHER INFORMATION: /note= "D-cyclohexylalanine"
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= dArg
; OTHER INFORMATION: /note= "D-arginine"
; US-08-215-137-11

Query Match      45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-256-771-16

Query Match      45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
US-08-222-851-22
; Sequence 22, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
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US-08-256-771-16
; Sequence 16, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,851
FILING DATE: 05-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28600-20200.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 494-0792
TELEX: 90-4030 MRSNFORSMW
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-851-22

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 WR 4

RESULT 24
US-08-381-984-16
Sequence 16, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note="the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment the
US-08-381-984-16

Query Match 45.7%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 WR 4

RESULT 25
US-08-592-646A-62
Sequence 62, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOHNER-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-62

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 wr 2
11
DB 3 WR 4

Search completed: January 14, 2002, 07:41:37
Job time: 458 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: January 14, 2002, 06:24:42 ; Search time 93.18 Seconds
(without alignments)
6.360 Million cell updates/sec

Title: US-09-185-908-34

Perfect score: 48

Sequence: 1 WKIYSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 50 summaries

Database : A_Geneseq_1101:*

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2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	8	21	AA806419	Claudin-1 cell adh
2	48	100.0	8	21	AA806479	Claudin-1 cyclc c
3	48	100.0	9	21	AA806420	Claudin-1 cell adh
4	48	100.0	10	21	AA806436	Claudin-1 cyclc c
5	48	100.0	10	21	AA806445	Claudin-1 cyclc c
6	48	100.0	10	21	AA806454	Claudin-1 cyclc c
7	48	100.0	10	21	AA806463	Claudin-1 cyclc c
8	48	100.0	10	21	AA806472	Claudin-1 cyclc c
9	48	100.0	10	21	AA806481	Claudin-1 cyclc c
10	48	100.0	21	21	AA806490	Murine clodin 1 pr
11	45	93.8	8	21	AA806426	Claudin-1 cell adh

12	45	93.8	8	21	AA806512	Claudin-1 cyclc c
13	45	93.8	10	21	AA806427	Claudin-1 cell adh
14	45	93.8	10	21	AA806485	Claudin-1 cyclc c
15	45	93.8	10	21	AA806491	Claudin-1 cyclc c
16	45	93.8	10	21	AA806497	Claudin-1 cyclc c
17	45	93.8	10	21	AA806503	Claudin-1 cyclc c
18	45	93.8	10	21	AA806509	Claudin-1 cyclc c
19	45	93.8	71	20	AA138421	Human secreted pro
20	45	93.8	211	20	AAV41726	Human PRO944 prote
21	45	93.8	211	20	AAV04143	Human Tango-73 pro
22	45	93.8	211	20	AA899653	Human senescence f
23	45	93.8	211	20	AA844282	Human PRO944 (UN04
24	45	93.8	211	20	AAV68679	A human molecule a
25	45	93.8	212	20	AAV38430	Human secreted pro
26	45	93.8	212	20	AAV76130	Human secreted pro
27	42	87.5	7	21	AA806418	Claudin-1 cell adh
28	42	87.5	7	21	AA806478	Claudin-1 cyclc c
29	42	87.5	9	21	AA806435	Claudin-1 cyclc c
30	42	87.5	9	21	AA806444	Claudin-1 cyclc c
31	42	87.5	9	21	AA806453	Claudin-1 cyclc c
32	42	87.5	9	21	AA806462	Claudin-1 cyclc c
33	42	87.5	9	21	AA806471	Claudin-1 cyclc c
34	39	81.2	7	21	AA806425	Claudin-1 cell adh
35	39	81.2	7	21	AA806511	Claudin-1 cyclc c
36	39	81.2	9	21	AA806484	Claudin-1 cyclc c
37	39	81.2	9	21	AA806490	Claudin-1 cyclc c
38	39	81.2	9	21	AA806496	Claudin-1 cyclc c
39	39	81.2	9	21	AA806502	Claudin-1 cyclc c
40	39	81.2	9	21	AA806508	Claudin-1 cyclc c
41	39	81.2	513	11	AA804585	Aquaticus Aquari
42	39	81.2	513	12	AA813181	Aquaticus Aquari
43	39	81.2	513	16	AA867653	Aquaticus Aquari
44	38	79.2	6	21	AA806417	Claudin-1 cell adh
45	38	79.2	6	21	AA806477	Claudin-1 cyclc c
46	38	79.2	8	21	AA806434	Claudin-1 cyclc c
47	38	79.2	8	21	AA806443	Claudin-1 cyclc c
48	38	79.2	8	21	AA806452	Claudin-1 cyclc c
49	38	79.2	8	21	AA806461	Claudin-1 cyclc c
50	38	79.2	8	21	AA806470	Claudin-1 cyclc c

ALIGNMENTS

RESULT 1
AA806419
ID AA806419 standard; peptide: 8 AA.
XX
AC AA806419;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW Cdk sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
PN WO200026330-A1.
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 48; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1 wkIysyag 8

RESULT 2
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
DR Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 48; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1 wkIysyag 8

RESULT 3
AAB06420
ID AAB06420 standard; peptide; 9 AA.
XX
AC AAB06420;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 476.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
DR Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1 wkIysyag 8

RESULT * 4
 AAB06436
 ID AAB06436 standard; peptide: 10 AA.
 XX
 AC AAB06436:
 XX
 DT 28-SEP-2000 (first entry)
 XX
 DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 67.
 XX
 KW Claudin-1 modulating agent; cell adhesion recognition sequence;
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
 KW graft rejection; cyclic.
 XX
 OS Mammalia.
 XX
 PN WO200026360-A1.
 PD 11-MAY-2000.
 XX
 PE 03-NOV-1999; 99WO-CA01029.
 XX
 PR 03-NOV-1998; 98US-0185908.
 PR 30-MAR-1999; 99US-0282029.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuck OW, Symonds JM, Gour BJ:
 DR WPI; 2000-369610/31.
 XX
 PT Antibody modulation of claudin-mediated cell adhesion for increasing
 PT vasopermeability, for delivering drugs to tumors and the nervous system
 PT and across the skin -
 XX
 XX Claim 43; Page 96; 121pp; English.
 XX
 XX The present invention relates to the use of peptides as claudin-mediated
 XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
 XX which are membrane glycoproteins involved in cell adhesion. In some
 XX situations, cell adhesion occurs at abnormal levels, and these peptides
 XX can be used to modulate these levels, and thus treat autoimmune diseases,
 XX inflammatory diseases and cancer, and aid wound healing and implant
 XX adhesion. In addition, they can also be used to facilitate drug delivery
 XX to the desired target site. The present sequence has a cyclic
 XX conformation.
 XX
 XX Sequence 10 AA:
 XX

Query Match	100.0%	Score 48;	DB 21;	Length 10;
Best Local Similarity	100.0%;	Pred. NO. 0.0054;		
Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.
QY	1 WKIYSYAG 8			
	2 WKIYSYAG 9			
Db				
RESULT 5				
AAB06445				
ID AAB06445	standard; peptide: 10 AA.			
XX				
AC AAB06445;				
XX				
DT 28-SEP-2000	(first entry)			
XX				
DE Claudin-1	cyclic cell adhesion recognition sequence SHQ ID NO: 76.			
XX				
KW Claudin-1	modulating agent; cell adhesion recognition sequence;			
KW CAR	sequence; autoimmune disease; inflammatory disease; cancer;			
KW graft	rejection; cyclic.			
XX				

XX	Mammalia
XX	
PN	WO200028660-A1.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-CA01029.
XX	
PR	03-NOV-1998; 98US-0185908.
XX	
PR	30-MAR-1999; 99US-0282029.
XX	
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.
XX	
PI	Blaschuck OW, Symonds JM, Gour BJ;
DR	WPI; 2000-365610/31.
XX	
PT	Antibody modulation of claudin-mediated cell adhesion for increasing
PT	vasopermeability, for delivering drugs to tumors and the nervous system
PT	and across the skin -
XX	
PS	Claim 43; Page 96; 121pp; English.
XX	

The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation.

XX	Sequence	10 AA;
XX		
XX		

Query Match	100.0%	Score 48;	DB 21;	Length 10;
Best Local Similarity	100.0%;	Pred. NO. 0.0054;		
Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 WKIYSYAG 8			
Db	2 wkIysyag 9			
RESULT 6				
AAB06454				
ID AAB06454	standard; peptide; 10 AA.			
XX				
AC AAB06454;				
XX				
DT 28-SEP-2000	(first entry)			
XX				
DE Claudin-1	cyclic cell adhesion recognition sequence SEQ ID NO: 85.			
XX				
KM Claudin-1	modulating agent; cell adhesion recognition sequence;			
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;				
KW graft rejection; cyclic.				
XX				
OS Mammalia.				
XX				
PN WC200028360-A1.				
XX				
XX 11-MAY-2000.				
XX				
PF 03-NOV-1999;	99WO-CA01029.			
XX				
PR 03-NOV-1998;	98US-0185908.			
PR 30-MAR-1999;	99US-0282029.			
XX				
PA (ADHE-) ADHEREX TECHNOLOGIES INC.				
XX				
PI Blaschuck OW, Symonds JM, Gour BJ;				

XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 96; 121pp; English.
PS
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 48; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 2 wkIysyag 9

RESULT 7
AAB06463
ID AAB06463 standard; peptide; 10 AA.
XX
XX AAB06463;
XX
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 94.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 10 AA;
SQ

CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 48; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 2 wkIysyag 9

RESULT 8
AAB06472
ID AAB06472 standard; peptide; 10 AA.
XX
XX AAB06472;
XX
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 103.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX 03-NOV-1999; 99WO-CA01029.
PF
XX 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 48; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
Db 2 wkIysyag 9

Db * 2 wklysyag 9

RESULT 9
AAB06911
ID AAB06911 standard; protein; 10 AA.
XX
AC AAB06911;
XX
DT 05-OCT-2000 (first entry)
XX
DE Claudin cell adhesion recognition modulating sequence SEQ ID NO: 475.
XX
KW Claudin modulating agent; cell adhesion recognition sequence;
KM CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="N-terminal acetyl or hydrogen"
FT Modified-site 10 /note="C-terminal amide"
FT
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI: 2000-365610/31.
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vascopermeability, for delivering drugs to tumors and the nervous system
XX and across the skin -
XX
XX Disclosure; Page 19; 121pp; English.
XX
XX PS The present sequence is a peptide which can be used in a claudin-mediated
XX cell adhesion modulator. The claudin group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and this peptide
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, it can also be used to facilitate drug delivery
XX to the desired target site.
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| | | | | | | |
DB 1 wklysyag 8

RESULT 10
AAV51675
ID AAV51675 standard; protein; 211 AA.
XX
XX AAV51675;
XX

DT 02-JUN-2000 (first entry)
XX
XX murine clodin 1 protein.
XX
XX Clodin 1; murine; tight junction-constituting membrane protein;
XX medicine.
XX
XX Mus sp.
XX
XX JP2000032484-A.
XX
XX 02-FEB-2000.
XX
XX 26-JUN-1998; 98JP-0179847.
XX
XX 15-MAY-1998; 98JP-0133215.
XX
XX (EISA) EISAI CO LTD.
XX
XX WPI: 2000-285512/25.
XX
XX N-PSDB: AA289136.
XX
XX Tight junction-constituting membrane protein clodin family - useful in
XX the medical field
XX
XX Claim 1; Page 10; 22pp; Japanese.
XX
XX This invention describes novel murine nucleic acid sequences encoding the
XX clodin family of tight junction (TJ)-constituting membrane protein. The
XX membrane protein can be used in medical field. This sequence represents
XX the clodin 1 protein described in the method of the invention.
XX
XX Sequence 211 AA;

Query Match 100.0%; Score 48; DB 21; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.13; Length 211;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYAG 8
| | | | | | | |
DB 30 wklysyag 37

RESULT 11
AAB06426
ID AAB06426 standard; peptide; 8 AA.
XX
XX AAB06426;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection.
XX
XX Mammalia.
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI; 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 93.8%; Score 45; DB 21; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
I:|||||
Db 1 wriysyag 8

RESULT 12
AAB06512
ID AAB06512 standard; peptide; 8 AA.
XX
AC AAB06512;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 93.8%; Score 45; DB 21; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
I:|||||
Db 1 wriysyag 8

RESULT 13
AAB06427
ID AAB06427 standard; peptide; 9 AA.
XX
AC AAB06427;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 486.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 9 AA;

Query Match 93.8%; Score 45; DB 21; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
I:|||||
Db 1 wriysyag 8

RESULT 14
AAB06485
ID AAB06485 standard; peptide; 10 AA.
XX
XX AAB06485;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 492.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 43; Page 96; 121pp; English.
PS
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
CC
XX
XX Sequence 10 AA;
SQ

Query Match 93.8%; Score 45; DB 21; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
1:|||||
Db 2 wrlsysag 9

RESULT 15
AAB06491
ID AAB06491 standard; peptide; 10 AA.
XX
XX AAB06491;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 498.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX

OS Mammalia.
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
XX Claim 43; Page 96; 121pp; English.
PS
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
CC
XX
XX Sequence 10 AA;
SQ

Query Match 93.8%; Score 45; DB 21; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
1:|||||
Db 2 wrlsysag 9

RESULT 16
AAB06497
ID AAB06497 standard; peptide; 10 AA.
XX
XX AAB06497;
AC
XX
XX 28-SEP-2000 (first entry)
DT
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 504.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuck OW, Symonds JM, Gour BJ;
PI

XX WPI: 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
CC
SQ Sequence 10 AA;
XX
XX
Query Match 93.8%; Score 45; DB 21; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1:|||||
2 wriysyag 9
XX
XX
RESULT 17
AAB06503
ID AAB06503 standard; peptide; 10 AA.
XX
AC AAB06503;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 510.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
XX
XX
Query Match 93.8%; Score 45; DB 21; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1:|||||
2 wriysyag 9
XX
XX
RESULT 18
AAB06509
ID AAB06509 standard; peptide; 10 AA.
XX
AC AAB06509;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 516.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 10 AA;
XX
XX
Query Match 93.8%; Score 45; DB 21; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
Db 1:|||||

Db *2 wrllyayag 9

RESULT 19
ID AAY38421
AC AAY38421
XX AAY38421: standard; Protein; 71 AA.

XX 30-SEP-1999 (first entry)

DE Human secreted protein encoded by gene No. 36.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX OS

PN W09935158-A1.

PD 15-JUL-1999.

XX 06-JAN-1999; 99WO-US00108.

XX 07-JAN-1998; 98US-0070704.

PR 07-JAN-1998; 98US-0070657.

PR 07-JAN-1998; 98US-0070658.

PR 07-JAN-1998; 98US-0070692.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Brewer LA, Duan RD, Edner R, Lafleur DW, Ni J;

PI Olsen HS, Rosen CA, Ruden SM, Soppet DR;

XX WPI: 1999-444190/37.

DR N-PSDB: AA206254.

XX New isolated human genes and the secreted polypeptides they encode

XX Clalm 11; Page 195; 227pp; English.

XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AA206210) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 36 novel genes and their fragments (nucleic
CC acid sequences: AA206219-206263; amino acid sequences AAY38386-Y38498)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 36
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AA206219 for described uses).

XX Sequence 71 AA:

Query Match 93.8%; Score 45; DB 20; Length 71;

Best Local Similarity 87.5%; Pred. No: 0.15; Mismatches 0; Gaps 0;

Matches 7; Conservative 1; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
I:|||||
Db 30 wrllyayag 37

RESULT 20

AAV41726
ID AAV41726 standard; Protein; 211 AA.

XX AAV41726;

AC AAV41726;

XX 07-DEC-1999 (first entry)

DE Human PRO944 protein sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.

XX Homo sapiens.

XX W09946281-A2.

PD 16-SEP-1999.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1998; 98US-0077450.

PR 11-MAR-1998; 98US-0077632.

PR 11-MAR-1998; 98US-0077641.

PR 11-MAR-1998; 98US-0077649.

PR 12-MAR-1998; 98US-0077791.

PR 13-MAR-1998; 98US-0078004.

PR 17-MAR-1998; 98US-0040220.

PR 20-MAR-1998; 98US-0078886.

PR 20-MAR-1998; 98US-0078910.

PR 20-MAR-1998; 98US-0078936.

PR 20-MAR-1998; 98US-0078939.

PR 25-MAR-1998; 98US-0079294.

PR 26-MAR-1998; 98US-0079655.

PR 27-MAR-1998; 98US-0079663.

PR 27-MAR-1998; 98US-0079664.

PR 27-MAR-1998; 98US-0079689.

PR 27-MAR-1998; 98US-0079728.

PR 27-MAR-1998; 98US-0079786.

PR 30-MAR-1998; 98US-0079920.

PR 30-MAR-1998; 98US-0079922.

PR 31-MAR-1998; 98US-0080105.

PR 31-MAR-1998; 98US-0080107.

PR 31-MAR-1998; 98US-0080165.

PR 31-MAR-1998; 98US-0080194.

PR 01-APR-1998; 98US-0080327.

PR 01-APR-1998; 98US-0080328.

PR 01-APR-1998; 98US-0080333.

PR 01-APR-1998; 98US-0080334.

PR 08-APR-1998; 98US-0081049.

PR 08-APR-1998; 98US-0081070.

PR 08-APR-1998; 98US-0081071.

PR 09-APR-1998; 98US-0081195.

PR 09-APR-1998; 98US-0081203.

PR 09-APR-1998; 98US-0081229.

PR 15-APR-1998; 98US-0081817.

PR 15-APR-1998; 98US-0081838.

PR 15-APR-1998; 98US-0081952.

PR 15-APR-1998; 98US-0081955.

PR 21-APR-1998; 98US-0082568.

PR 21-APR-1998; 98US-0082569.

PR 22-APR-1998; 98US-0082700.

PR 22-APR-1998; 98US-0082704.

PR 23-APR-1998; 98US-0082804.

PR 23-APR-1998; 98US-0082767.

PR 23-APR-1998; 98US-0082796.

PR 27-APR-1998; 98US-0083336.

PR 28-APR-1998; 98US-0083322.

PR 29-APR-1998; 98US-0083392.

PR 29-APR-1998; 98US-0083495.

PR 29-APR-1998; 98US-0083496.

PR	29-APR-1998;	98US-00834199.
PR	29-APR-1998;	98US-0083500.
PR	29-APR-1998;	98US-0083545.
PR	29-APR-1998;	98US-0083554.
PR	29-APR-1998;	98US-0083558.
PR	29-APR-1998;	98US-0083559.
PR	30-APR-1998;	98US-0083742.
PR	05-MAY-1998;	98US-0084366.
PR	06-MAY-1998;	98US-0084414.
PR	06-MAY-1998;	98US-0084441.
PR	07-MAY-1998;	98US-0084598.
PR	07-MAY-1998;	98US-0084600.
PR	07-MAY-1998;	98US-0084627.
PR	07-MAY-1998;	98US-0084637.
PR	07-MAY-1998;	98US-0084639.
PR	07-MAY-1998;	98US-0084640.
PR	07-MAY-1998;	98US-0084643.
PR	13-MAY-1998;	98US-0085323.
PR	13-MAY-1998;	98US-0085338.
PR	13-MAY-1998;	98US-0085339.
PR	15-MAY-1998;	98US-0085573.
PR	15-MAY-1998;	98US-0085579.
PR	15-MAY-1998;	98US-0085580.
PR	15-MAY-1998;	98US-0085582.
PR	15-MAY-1998;	98US-0085589.
PR	15-MAY-1998;	98US-0085697.
PR	15-MAY-1998;	98US-0085700.
PR	15-MAY-1998;	98US-0085704.
PR	18-MAY-1998;	98US-0086023.
PR	22-MAY-1998;	98US-0086392.
PR	22-MAY-1998;	98US-0086414.
PR	22-MAY-1998;	98US-0086430.
PR	22-MAY-1998;	98US-0086486.
PR	28-MAY-1998;	98US-0087098.
PR	28-MAY-1998;	98US-0087106.
PR	28-MAY-1998;	98US-0087208.
PR	30-JUL-1998;	98US-0094651.
PR	11-SEP-1998;	98US-0100038.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Wood Wt, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX		
DR	WPI: 1999-551358/46.	
XX		
DR	N-PSDB; AAZ34118.	
XX		
PT	New secreted and transmembrane polypeptides and their polynucleotides,	
PT	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders -	
XX		
PS	Claim 12; Fig 98; 530pp; English.	
XX		
CC	The present invention describes secreted and transmembrane polypeptides	
CC	and their polynucleotides. The nucleotide sequences are useful as	
CC	sources of probes, primers, for chromosome mapping, and for generation	
CC	of antisense sequences. They can also be used to create transgenic	
CC	animals. The proteins can be used to treat a variety of diseases and	
CC	disorders, depending on their function. Diseases that may be treated	
CC	include blood coagulation disorders, cancers and cellular adhesion	
CC	disorders. They may also be used to raise antibodies. AAZ3891 to	
CC	AAZ34338, and AAY1685 to AAY41774 represent polynucleotide and	
CC	polypeptide sequence given in the exemplification of the present	
CC	invention.	
XX		
SQ	Sequence 211 AA;	

Query Match	93.88;	Score 45;	DB 20;	Length 211;
Best Local Similarity	87.58;	Pred. No. 0.48;		
Matches 7; Conservative	1;	Mismatches	0;	Indels 0; Gaps 0;
QY	1 WKIYTAG 8			
	1:			

```

Db      30 wrtlysyag 37

RESULT  21
ID      AAY04143
        AAY04143 standard; Protein; 211 AA.
XX
AC      AAY04143;
XX
DT      15-JUN-1999 (first entry)
XX
DE      Human Tango-73 protein.
XX
KW      Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
        detection.
XX
RN      Homo sapiens.
XX
OS      Homo sapiens.
XX
PN      W09907850-A1.
XX
PD      18-FEB-1999.
XX
PF      06-AUG-1998; 98WO-US16502.
XX
PR      05-SEP-1997; 97US-0058108.
XX
PR      06-AUG-1997; 97US-0054966.
XX
PA      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI      Goodenarl ADJ, Holtzman DA;
XX
DR      WPI; 1999-167426/14.
XX
DR      N-PSDB; AAX19956.
XX
PT      New TANGO polypeptides and nucleic acids encoding them - useful as
        diagnostic agents and for treating disorders caused by aberrant
        expression of TANGO
XX
PS      Claim 8; Fig 2; 84pp; English.
XX
CC      The present sequence represents human Tango-73. Tango polypeptides are
        useful for identifying compounds which bind the polypeptide via direct
        binding, competition binding assays or Tango-71, -73, -74, 76 or -83-
        mediated signal transduction. Tango polypeptides are also useful for
        identifying modulating compounds by determining effect on Tango activity.
        CC      Tango polypeptides and nucleic acids are useful for diagnosing diseases
        CC      related to aberrant expression of Tango, and Tango polypeptides are
        CC      useful for raising antibodies which can be used in diagnostic assays for
        CC      detection of Tango, and also for generating anti-idiotypic antibodies for
        CC      prevention and protection.
XX
SQ      Sequence 211 AA;

Query Match 93.8%; Score 45; DB 20; Length 211;
Best Local Similarity 87.5%; Pred. No. 0.48;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0

OY      1 WKIYSYAG 8
        |:|||||
DB      30 wrtlysyag 37

RESULT  22
ID      AAW99653
        AAW99653 standard; Protein; 211 AA.
XX
AC      AAW99653;
XX
DT      21-MAY-1999 (first entry)
XX
DE      Human senescence factor p23 protein.
XX

```

KW	Human; senescence factor; p23; cancer; persistent inflammation;
KV	proliferative disorder; degenerative disorder.
XX	
OS	Homo sapiens.
XX	
PN	MO9907893-A1.
XX	
PD	18-FEB-1999.
XX	
PF	05-AUG-1998; 98WO-US16343.
XX	
PR	08-AUG-1997; 97US-0908873.
XX	
PA	(UNITW) UNIV WASHINGTON.
XX	
PI	Hostler S, Kubbles M, Swisshelm K;
XX	
OR	WPI; 1999-167454/14.
DR	N-PSDB; AAX19461.
XX	
PT	Newly isolated nucleic acid molecule (designated p23) encoding a p23
XX	polypeptide - useful for inducing a senescence phenotype in a cell
SS	Claim 3; Page 35; 44pp; English.

The present sequence is human senescence factor p23. An expression vector for p23 is useful for inducing a senescent phenotype in a cell (preferably eukaryotic). This may help in regulating diseases, including cancer, persistent inflammation, and various proliferative and degenerative disorders. These transgenic cells are useful in gene therapy for treating cancer, particularly where antisense oligonucleotides are useful for blocking normal or mutant p23 expression in cancer cells or other proliferating cells. Transgenic cells are also useful for producing the p23 polypeptide in large quantities. The antibodies are useful for raising antiserum against p23, and for identifying senescent cells in culture and tissue biopsies. The p23 polynucleotides are useful for modulating or altering p23 activity in a cell, and for identifying and isolating the whole gene encoding p23, and variants of p23. Assays based on p23 elements, which detect p23 levels and activity are useful as diagnostic markers for staging tumours determining prognosis, and/or predicting therapeutic success. These elements also provide an assay for detecting chromosomal rearrangements in chromosome 3 in a human cell. The isolation of the p23 polynucleotide permits the manipulation of malignant growth in cancer.

SQ **Sequence** **211** **AA;**

Query Match	93.8%	Score 45	DB 20	Length 211
Best Local Similarity	87.5%	Pred. No. 0.48		
Matches 7	Conservative	1	Mismatches	0
			Indels	0
			Gaps	0

```
QY      1 WKIYSYAG 8
Db      30 WrlYsyag 37
```

RESULT	23
AAB44282	
ID	AAB44282 standard; Protein; 211 AA

AC AAB44282;

DT 08-FEB-2001 (first entry)

Human PRO944 (UNQ481) protein sequence SEQ ID NO:270

Kw Human; secreted protein; transmembrane protein; PRO; EST; cytosolic
Kw expressed sequence tag; detection; cancer.

Homo sapiens.

PN WO2000053756-A2

XX	14-SEP-2000.
PD	
XX	
PF	18-FEB-2000; 2000WO-US04341

PR	12-MAR-1999;	9900-US050528
PR	12-MAR-1999;	9900-US123857
PR	29-MAR-1999;	9900-US126773
PR	21-APR-1999;	9900-US103432
PR	28-APR-1999;	9900-US131445
PR	14-MAY-1999;	9900-US134287
PR	23-JUN-1999;	9900-US141037
PR	25-JUL-1999;	9900-US145698
PR	29-OCT-1999;	9900-US162506
PR	30-NOV-1999;	9900-US283113
PR	02-DEC-1999;	9900-US285511
PR	12-DEC-1999;	9900-US285511
PR	16-DEC-1999;	9900-US285655
PR	30-DEC-1999;	9900-US300955
PR	30-DEC-1999;	9900-US312433
PR	05-JAN-2000;	2000OWO-US031274
PR	05-JAN-2000;	2000OWO-US002199
PR	06-JAN-2000;	2000OWO-US003776
PR	06-JAN-2000;	2000OWO-US003766

PA (GETH) GENENTECH INC.

PI Ashtkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Flyvbjerg E, Fong S, Gao W, Gerber H, Gertlissen ME;
PI Goddard A, Godowski PU, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DC, Stewart TA, Tunas D, Williams PM, Wood WJ;

DR WPI; 2000-611443/
DR N-PSDB; AAC78513.

PT Novel PRO polypeptides and polynucleotides used in detection methods
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 12; Fig 9B; 636pp; English.

Claim 12; Fig 98; 636pp; English.

CC AAC784850 to AAC78559, represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC7887 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.

Sequence 211 AA;

Query Match	93.8%	Score 45;	DB 21;	Length 211;
Best Local Similarity	87.5%	Pred. No. 0.48;		
Matches	7;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;

```
QY      1 WKIYSYAG 8
Db      30 wriysyag 37
```

RESULT 24

ID AAY68679 standard; Protein; 211 AA.

AC AAY68679;

DT 05-MAY-2000 (first entry)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 06:42:06 ; Search time 40.81 Seconds
(without alignments)
14.521 Million cell updates/sec

Title: US-09-185-908-34

Perfect score: 48
Sequence: 1 WKIYSYAG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT:*

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21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	48	100.0	8 21 AAB06419	Claudin-1 cell adh
2	48	100.0	8 21 AAB06479	Claudin-1 cyclc c
3	45	93.8	8 21 AAB06426	Claudin-1 cell adh
4	45	93.8	8 21 AAB06512	Claudin-1 cyclc c
5	42	87.5	7 21 AAB06418	Claudin-1 cell adh
6	42	87.5	7 21 AAB06478	Claudin-1 cyclc c
7	39	81.2	7 21 AAB06425	Claudin-1 cell adh
8	39	81.2	7 21 AAB06511	Claudin-1 cyclc c
9	38	79.2	6 21 AAB06417	Claudin-1 cell adh
10	38	79.2	6 21 AAB06477	Claudin-1 cyclc c
11	38	79.2	8 21 AAB06434	Claudin-1 cyclc c

12	38	79.2	8 21 AAB06443	Claudin-1 cyclc c
13	38	79.2	8 21 AAB06452	Claudin-1 cyclc c
14	38	79.2	8 21 AAB06461	Claudin-1 cyclc c
15	38	79.2	8 21 AAB06470	Claudin-1 cyclc c
16	37	77.1	7 21 AAB06416	Claudin-1 cell adh
17	37	77.1	7 21 AAB06476	Claudin-1 cyclc c
18	37	77.1	8 21 AAB06439	Claudin-1 cyclc c
19	37	77.1	8 21 AAB06448	Claudin-1 cyclc c
20	35	72.9	6 21 AAB06424	Claudin-1 cell adh
21	35	72.9	6 21 AAB06510	Claudin-1 cyclc c
22	35	72.9	8 21 AAB06483	Claudin-1 cyclc c
23	35	72.9	8 21 AAB06495	Claudin-1 cyclc c
24	35	72.9	8 21 AAB06495	Claudin-1 cyclc c
25	35	72.9	8 21 AAB06501	Claudin-1 cyclc c
26	35	72.9	8 21 AAB06507	Claudin-1 cyclc c
27	34	70.8	7 21 AAB06423	Claudin-1 cell adh
28	33	68.8	8 21 AAB06466	Claudin-1 cyclc c
29	32	66.7	6 21 AAB06413	Claudin-1 cell adh
30	32	66.7	6 21 AAB06474	Claudin-1 cyclc c
31	32	66.7	8 21 AAB06430	Claudin-1 cyclc c
32	32	66.7	8 21 AAB06457	Claudin-1 cyclc c
33	32	66.7	8 21 AAB06823	Claudin-7 cell adh
34	32	66.7	8 21 AAB06876	Claudin-7 cyclc c
35	32	66.7	8 21 AAB06917	Claudin-7 cell adh
36	31	64.6	6 21 AAB06415	Claudin-1 cell adh
37	31	64.6	7 21 AAB06438	Claudin-1 cyclc c
38	31	64.6	7 21 AAB06447	Claudin-1 cyclc c
39	31	64.6	8 21 AAB06432	Claudin-1 cyclc c
40	31	64.6	8 21 AAB06441	Claudin-1 cyclc c
41	31	64.6	8 21 AAB06450	Claudin-1 cyclc c
42	31	64.6	8 21 AAB06459	Claudin-1 cyclc c
43	31	64.6	8 21 AAB06468	Claudin-1 cyclc c
44	30	62.5	6 4 AAB61317	Sequence of a cycl
45	29	60.4	6 7 AAB61337	Sequence of a novel
46	28	58.3	6 21 AAB06422	Claudin-1 cell adh
47	28	58.3	8 21 AAB06481	Claudin-1 cyclc c
48	28	58.3	8 21 AAB06487	Claudin-1 cyclc c
49	28	58.3	8 21 AAB06493	Claudin-1 cyclc c
50	28	58.3	8 21 AAB06499	Claudin-1 cyclc c

ALIGNMENTS

RESULT 1

AA06419

ID AAB06419 standard; peptide: 8 AA.

XX

AC AAB06419;

XX

DT 28-SEP-2000 (first entry)

XX

DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 34.

XX

XX Claudin-1 modulating agent; cell adhesion recognition sequence;

KW Cdr sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection.

XX

XX

XX Mammalia.

OS

XX

XX W020002860-A1.

FN

XX

PD 11-MAY-2000.

XX

PD 03-NOV-1999; 99WO-CA01029.

XX

PF 03-NOV-1999; 98US-0185908.

XX

PR 30-MAR-1999; 99US-0282029.

XX

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

PA

XX Blaschuck OW, Symonds JM, Gour BJ;

PI

XX

DR WPI; 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX
PS Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 48; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
|:|||||
Db 1 wkIysyag 8

RESULT 2
AAB06479
ID AAB06479 standard; peptide; 8 AA.
XX
AC AAB06479;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 110.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 48; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
|:|||||
Db 1 wkIysyag 8

RESULT 3
AAB06426
ID AAB06426 standard; peptide; 8 AA.
XX
AC AAB06426;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 485.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
DR
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 8 AA;

Query Match 93.8%; Score 45; DB 21; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYAG 8
|:|||||
Db 1 wkIysyag 8

RESULT 4

AB06512 standard; peptide: 8 AA.
AC AAB06512;
DT 28-SEP-2000 (first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 519.
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection; cyclic.
OS Mammalia.
PN WO200026360-A1.
PD 11-MAY-2000.
PF 03-NOV-1999; 99WO-CA01029.
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX Claim 43; Page 97; 121pp; English.
PS The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX Sequence 8 AA;
SO

Query Match 93.8%; Score 45; DB 21; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSYAG 8
I:|||||
Db 1 wklysyag 8
XX
RESULT 5
AAB06418
ID AAB06418 standard; peptide: 7 AA.
XX
AC AAB06418;
XX
DT 28-SEP-2000 (first entry)
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 33.
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection.
XX

OS Mammalia.

PN WO200026360-A1.
PD 11-MAY-2000.
PF 03-NOV-1999; 99WO-CA01029.
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX Claim 39; Page 96; 121pp; English.
PS The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX Sequence 7 AA;
SQ

Query Match 87.5%; Score 42; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSYA 7
I:|||||
Db 1 wklysy 7

RESULT 6

AAB06478
ID AAB06478 standard; peptide: 7 AA.
XX
AC AAB06478;
XX
DT 28-SEP-2000 (first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 109.
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection; cyclic.
XX
OS Mammalia.
PN WO200026360-A1.
PD 11-MAY-2000.
PF 03-NOV-1999; 99WO-CA01029.
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuck OW, Symonds JM, Gour BJ;
XX

DR WPI: 2000-365610/31.
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 7 AA;

Query Match 87.5%; Score 42; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYA 7
Db 1 wkIysya 7

RESULT 7
AAB06425
ID AAB06425 standard; peptide; 7 AA.
AC AAB06425;
DT 28-SEP-2000 (first entry)
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 484.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
OS Mammalia.
PN WO200026360-A1.
PD 11-MAY-2000.
PF 03-NOV-1999; 99WO-CA01029.
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 39; Page 96; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 7 AA;

Query Match 81.2%; Score 39; DB 21; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.3e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYA 7
Db 1 wriysya 7

RESULT 8
AAB06511
ID AAB06511 standard; peptide; 7 AA.
AC AAB06511;
DT 28-SEP-2000 (first entry)
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 518.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
PN WO200026360-A1.
PD 11-MAY-2000.
PF 03-NOV-1999; 99WO-CA01029.
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
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PA (ADHE-) ADHEREX TECHNOLOGIES INC.
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PI Blaschuck OW, Symonds JM, Gour BJ;
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DR WPI: 2000-365610/31.
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PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
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PS Claim 43; Page 97; 121pp; English.
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 7 AA;

Query Match 81.2%; Score 39; DB 21; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.3e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WKIYSYA 7
Db 1 wriysya 7

RESULT 9
AAB06417 standard; peptide: 6 AA.
XX
XX AAB06417;
AC
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 32.
DE
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PY
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
CC and across the skin -
CC
XX
XX Claim 39; Page 95; 121pp; English.
PS
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
CC
XX
XX Sequence 6 AA;
SQ

Query Match 79.2%; Score 38; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. NO. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WKIYSY 6
DB 1 WKIYSY 6

RESULT 10
AAB06477 standard; peptide: 6 AA.
ID AAB06477
XX
XX AAB06477;
AC
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 108.
DE
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX

OS Mammalia.
XX
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PY
XX Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
CC and across the skin -
CC
XX
XX Claim 43; Page 97; 121pp; English.
PS
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XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
CC
XX
XX Sequence 6 AA;
SQ

Query Match 79.2%; Score 38; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. NO. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WKIYSY 6
DB 1 WKIYSY 6

RESULT 11
AAB06434 standard; peptide: 8 AA.
ID AAB06434
XX
XX AAB06434;
AC
XX 28-SEP-2000 (first entry)
DT
XX
XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 65.
DE
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX WO200026360-A1.
PN
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA01029.
PE
XX
XX 03-NOV-1998; 98US-0185908.
PR
XX 30-MAR-1999; 99US-0282029.
PX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PY
XX Blaschuck OW, Symonds JM, Gour BJ;
PI

XX WPI; 2000-365610/31.
DR
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 79.2%; Score 38; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSY 6
Db 2 wkIysy 7

RESULT 12
AAB06443
ID AAB06443 standard; peptide; 8 AA.
XX
AC AAB06443;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SFQ ID NO: 74.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 79.2%; Score 38; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSY 6
Db 2 wkIysy 7

RESULT 13
AAB06452
ID AAB06452 standard; peptide; 8 AA.
XX
AC AAB06452;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SFQ ID NO: 83.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PF 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 79.2%; Score 38; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WKIYSY 6
Db 2 wkIysy 7

DB 2 wklysy 7

RESULT 14
ID AAB06461 standard; peptide: 8 AA.
XX AAB06461;
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 92.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
XX WO200026360-A1.
XX PN 11-MAY-2000.
XX PD 03-NOV-1999; 99WO-CA01029.
XX PE 03-NOV-1998; 98US-0185908.
XX PR 30-MAR-1999; 99US-0282029.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuck OW, Symonds JM, Gour BJ;
XX DR WPI: 2000-365610/31.
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SO Sequence 8 AA;

Query Match 79.2%; Score 38; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
|||||
DB 2 wklysy 7

RESULT 15
ID AAB06470 standard; peptide: 8 AA.
XX AAB06470;
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 101.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX PF 03-NOV-1999; 99WO-CA01029.
XX PR 03-NOV-1998; 98US-0185908.
XX PR 30-MAR-1999; 99US-0282029.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuck OW, Symonds JM, Gour BJ;
XX DR WPI: 2000-365610/31.
XX PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
XX Claim 43; Page 97; 121pp; English.

PS The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.

SO Sequence 8 AA;

Query Match 79.2%; Score 38; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
|||||
DB 2 wklysy 7

RESULT 16
ID AAB06416 standard; peptide: 7 AA.
XX AAB06416;
XX 28-SEP-2000 (first entry)
XX
DE Claudin-1 cell adhesion recognition sequence SEQ ID NO: 31.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection.
XX
XX Mammalia.
XX PN WO200026360-A1.
XX PD 11-MAY-2000.
XX PF 03-NOV-1999; 99WO-CA01029.
XX PR 03-NOV-1998; 98US-0185908.
XX PR 30-MAR-1999; 99US-0282029.
XX

PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX Blaschuck OW, Symonds JM, Gour BJ;
XX WPI; 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
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CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
SQ Sequence 7 AA;

Query Match 77.1%; Score 37; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KIYSTAG 8
| | | | | | |
Db 1 klysyag 7

RESULT 17
AAB06476
ID AAB06476 standard; peptide; 7 AA.
XX
AC AAB06476;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 107.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
XX
XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
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XX WPI; 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX PT and across the skin -
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CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site.
XX
XX
SQ Sequence 7 AA;

CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 7 AA;

Query Match 77.1%; Score 37; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KIYSTAG 8
| | | | | | |
Db 1 klysyag 7

RESULT 18
AAB06439
ID AAB06439 standard; peptide; 8 AA.
XX
AC AAB06439;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 70.
XX
XX Claudin-1 modulating agent; cell adhesion recognition sequence;
XX CAR sequence; autoimmune disease; inflammatory disease; cancer;
XX graft rejection; cyclic.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-CA01029.
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XX 03-NOV-1998; 98US-0185908.
XX 30-MAR-1999; 99US-0282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
XX
XX WPI; 2000-365610/31.
XX
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
XX vasopermeability, for delivering drugs to tumors and the nervous system
XX PT and across the skin -
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XX Claim 43; Page 96; 121pp; English.
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XX The present invention relates to the use of peptides as claudin-mediated
XX cell adhesion modulators. The claudin-1 group of proteins are cadherins,
XX which are membrane glycoproteins involved in cell adhesion. In some
XX situations, cell adhesion occurs at abnormal levels, and these peptides
XX can be used to modulate these levels, and thus treat autoimmune diseases,
XX inflammatory diseases and cancer, and aid wound healing and implant
XX adhesion. In addition, they can also be used to facilitate drug delivery
XX to the desired target site. The present sequence has a cyclic
XX conformation.
XX
XX
SQ Sequence 8 AA;

Query Match 77.1%; Score 37; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KITYSAG 8
KM |||||||
KW 1 kitysag 7
DB

RESULT 19

ID AAB06448 standard; peptide; 8 AA.

AC AAB06448;

DT 28-SEP-2000 (first entry)

XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 79.

DE Claudin-1 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

XX graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing

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PT and across the skin -

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CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site. The present sequence has a cyclic

CC conformation.

XX Sequence 8 AA;

XX Query Match 77.1%; Score 37; DB 21; Length 8;

XX Best Local Similarity 100.0%; Pred. No. 4.3e+05;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KITYSAG 8
KM |||||||
KW 1 kitysag 7
DB

RESULT 20

ID AAB06424 standard; peptide; 6 AA.

AC AAB06424;

DT 28-SEP-2000 (first entry)

XX Claudin-1 cell adhesion recognition sequence SEQ ID NO: 483.

XX Claudin-1 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

XX graft rejection.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuck OW, Symonds JM, Gour BJ;

DR WPI: 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing

PT vasopermeability, for delivering drugs to tumors and the nervous system

PT and across the skin -

PS Claim 39; Page 96; 121pp; English.

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CC situations, cell adhesion occurs at abnormal levels, and these peptides

CC can be used to modulate these levels, and thus treat autoimmune diseases,

CC inflammatory diseases and cancer, and aid wound healing and implant

CC adhesion. In addition, they can also be used to facilitate drug delivery

CC to the desired target site.

XX Sequence 6 AA;

XX Query Match 72.9%; Score 35; DB 21; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 4.3e+05;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIRSY 6
KM |||||||
KW 1 wrksy 6
DB

RESULT 21

ID AAB06510 standard; peptide; 6 AA.

AC AAB06510;

DT 28-SEP-2000 (first entry)

XX Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 517.

DE Claudin-1 modulating agent; cell adhesion recognition sequence;

KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

XX graft rejection; cyclic.

OS Mammalia.

PN WO200026360-A1.

PD 11-MAY-2000.

PE 03-NOV-1999; 99WO-CA01029.

PR 03-NOV-1998; 98US-0185908.

PR 30-MAR-1999; 99US-0282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA Blaschuck OW, Symonds JM, Gour BJ;
PI WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 97; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 6 AA;

Query Match 72.9%; Score 35; DB 21; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
Db 1 wrlysy 6

RESULT 22
AAB06483
ID AAB06483 standard; peptide; 8 AA.
XX
AC AAB06483;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 490.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated

CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 72.9%; Score 35; DB 21; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
Db 2 wrlysy 7

RESULT 23
AAB06489
ID AAB06489 standard; peptide; 8 AA.
XX
AC AAB06489;
XX
DT 28-SEP-2000 (first entry)
XX
DE Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 496.
XX
KW Claudin-1 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
OS Mammalia.
XX
PN WO200026360-A1.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-CA01029.
XX
PR 03-NOV-1998; 98US-0185908.
PR 30-MAR-1999; 99US-0282029.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuck OW, Symonds JM, Gour BJ;
XX
DR WPI: 2000-365610/31.
XX
PT Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin -
XX
PS Claim 43; Page 96; 121pp; English.
XX
CC The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-1 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation.
XX
SQ Sequence 8 AA;

Query Match 72.9%; Score 35; DB 21; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.3e+05;

Matches 5: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
1:||||
Db 2 wriysy 7

RESULT 24

AAB06495 standard; peptide; 8 AA.

AAB06495;

28-SEP-2000 (first entry)

Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 502.

Claudin-1 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection; cyclic.

Mammalia.

WO200026360-A1.

11-MAY-2000.

03-NOV-1999; 99WO-CA01029.

03-NOV-1998; 98US-0185908.

30-MAR-1999; 99US-0282029.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Blaschuck OW, Symonds JM, Gour BJ;

WPI: 2000-365610/31.

Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

Claim 43; Page 97; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-1 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site. The present sequence has a cyclic
conformation.

Sequence 8 AA:

Query Match 72.9%; Score 35; DB 21; Length 8;
Best local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
1:||||
Db 2 wriysy 7

RESULT 25

AAB06501 standard; peptide; 8 AA.

AAB06501;

28-SEP-2000 (first entry)

Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 508.
Claudin-1 modulating agent; cell adhesion recognition sequence;
CAR sequence; autoimmune disease; inflammatory disease; cancer;
graft rejection; cyclic.

Mammalia.

WO200026360-A1.

11-MAY-2000.

03-NOV-1999; 99WO-CA01029.

03-NOV-1998; 98US-0185908.

30-MAR-1999; 99US-0282029.

(ADHE-) ADHEREX TECHNOLOGIES INC.

Blaschuck OW, Symonds JM, Gour BJ;

WPI: 2000-365610/31.

Antibody modulation of claudin-mediated cell adhesion for increasing
vasopermeability, for delivering drugs to tumors and the nervous system
and across the skin -

Claim 43; Page 97; 121pp; English.

The present invention relates to the use of peptides as claudin-mediated
cell adhesion modulators. The claudin-1 group of proteins are cadherins,
which are membrane glycoproteins involved in cell adhesion. In some
situations, cell adhesion occurs at abnormal levels, and these peptides
can be used to modulate these levels, and thus treat autoimmune diseases,
inflammatory diseases and cancer, and aid wound healing and implant
adhesion. In addition, they can also be used to facilitate drug delivery
to the desired target site. The present sequence has a cyclic
conformation.

Sequence 8 AA:

Query Match 72.9%; Score 35; DB 21; Length 8;
Best local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 WKIYSY 6
1:||||
Db 2 wriysy 7

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wxxxyxg1

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